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RESULT CARESULT CARES
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Best Local s
Matches 5
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Submitted (JUL-2000) to the EMBL
EMBL; AF257136; AAF91353.1; -
EMBL; AF139987; AAF75558.1; -
EMBL; AF1399664; AAF99331.1; -
MGD; MGI:1926679; Wbscr5.
MGD; MGI:1926679; Wbscr5.
SEQUENCE 203 AA; 22876 MW; 1
                                                                                                                                                                                                                                                                                                                                         Q20551 PRELIMINARY;
Q20551;
Q1-NOV-1996 (TIEMBLIEL 0
01-MAR-2002 (TIEMBLIEL 2)
01-JUN-2002 (TIEMBLIEL 2)
Hypothetical 23.0 kDa pro-
F48B9.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JHL0
Q9JHL0;
Q1-OCT-2000
Q1-OCT-2000
Q1-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6J;
SOURCE J.L., DeSilva U., Miller W., Green E.;
Doyle J.L., DeSilva U., Miller W., Green E.;
"Divergent Human and Mouse Orthologs of a Novel Gene
"Divergent Human and Mouse Orthologs of a Novel Gene
Reside within the Genomic Interval Commonly Deleted i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WBSCR15 protein (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ES-129/SVJI;
Martindale D.W., Wilson M.D.,
Duranio V., Koop B.F.;
                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Miller N.;
                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                               "Genome sequence of the nematode investigating biology. The C. ele Science 282:2012-2018(1998).
                                                                                                                                                               None;
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Comparative genomic sequence and (LIMK1-RFC2) of human chromosome Mamm. Genome 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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129/SV;
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Similarity 100.0%;
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0 (TrembLrel. 15,
1 (TrembLrel. 17,
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Rodentia;
  elegans
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Pred.
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elegans Sequenc
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    F48B9.";
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Sequencing Consort
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                                                                                                                                                                                                                                                                                                  Rhabditida;
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                                                                                                                      Consortium
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in Williams
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Murinae; Mus
                                                                                                                                                                                                                                                                                                    Rhabditoidea;
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RESULT 199
Q35872
ID Q35872
AC Q35872
DT 01-NOV
DT 01-NOV
DT 01-UT
DE ABC-ty
GN ORF206
OS Lycope
GO Mitoch
OC Eukary
OC Sperma
OC Asteri
OX NCBI.T
RN [1]
RP SEQUEN
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Q9N7Q9
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Matches
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01-OCT-2000 (TrEMBLrel. 15, Li
01-DEC-2001 (TrEMBLrel. 19, La
Possible hypothetical protein
LM28.132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Direct Submission.";
Submitted (JAN-2002) to the EMBL/(Submitted (JAN-2002);
EMBL; U40955; AAA81747.2; -.
HSSP; P26367; 6PAX.
InterPro; IPRO01523; Paired_box.
Pfam; PF00292; PAX; 1.
SMART; SM00351; PAX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9N7Q9
Q9N7Q9;
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                                                Lycopersicon esculentum (Tomato).
Mitochondrion.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                           Q35872;
Q35872;
Q1-NOV-1996 (TrEMBLrel. 01,
O1-NOV-1996 (TrEMBLrel. 01,
O1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
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Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murphy L., Quail M., Harris Submitted (JUL-2000) to the EMBL; AL390935; CAC00878.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-FRIEDLIN;
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SEQUENCE 204 AA; 22990 MW;
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    N.A.
                                                                                                                                                                            transporter
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to the
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Last annotation update)
in mj1404 (Fragment).
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Pred. No. 5.3
0; Mismatches
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58
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                                                                                                 Tracheophyta;
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                                                                                                                                                                                                                                                MEDLINE=21548291; PubMed=11689642;
Farina S.F., Gao G.P., Xiang Z.Q., Rux J.J., Burnett
Alvira M.R., Marsh J., Ertl H.C., Wilson J.M.;
"Replication-defective vector based on a chimpanzee
J., Virol. 75:11603-11613(2001).
                                                                                                                                                                                                                                                                                                                                                               PVII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 408:816-820(2000).

EMBL; AC068901; AAG50893.1; -.

Interpro; IPR004252; Transposase_24

Pfam; PF03004; Transposase_24; 1.
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RESULT 195
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DE Beta-9
OS Carica
OC Eukary
OC Sperma
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OC STRAUM
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SEQUENCE
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ EMBL; AF079874; AAC28739.1;
InterPro; IPR001944; GH.35.
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01-NOV-1998 (TrEMBLrel. 21, Las

01-JUN-2002 (TrEMBLrel. 21, Las

Beta-galactosidase (Fragment).
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D'Innocenzo M.,
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Eukaryota; Viridiplantae; Streptophyta;
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EMBL; AE009015; AAL41471.1; -
Hypothetical protein; Complete
SEQUENCE 201 AA; 21160 MW;
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MEDLINE=21608550; PubMed=11743193;
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Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
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STRAIN-KI;

MEDLINE-9931039; PubMed-10382966;

Kawarabbyasi Y., Hino Y., Horikawa H., Yamazaki S., Haiki
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A.
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota F
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Q9UJB9;
01-MAY-2000
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01-MAR-2002
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ862K6.11 (Continues in Em:AL031681 as dJ138B7.3)
DJ138B7.3.
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r fungi.";
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RP SEQUEN
RA SIZUK!
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                                              RESULT 192
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DT 01-JUN
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O9C7M6,
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r 01-JUN-2001 (TrEMBLrel. 17, Lr
r 01-JUN-2002 (TrEMBLrel. 21, Lr
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Matches 5
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Best Local S
Matches 5
SEQUENCE FROM N.A.

STRAIN-CY. COLUMBIA;

STRAIN-CY. COLUMBIA;

MEDLINE-21016719; Pubmed-11130712;

MEDLINE-21016719; Pubmed-11130712;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Chin C.W.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Buehler E., Chan A., Canway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

Gill J.E., Goldsmith A.D., Haass B., Hansen N.F., Hughes B., Huizar L.,

Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

"In Converse Converse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashi Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka Nakamura Y., Isogai T., Sugano S.; NuEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases EMBL; AK025804; BAB15240.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, CDNA: FLJ72151 fis, clone HHomo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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ilarity 100.0%;
Conservative
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Pred. No. 5.2
0; Mismatches
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RESULT 187
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A peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
A Quaggio R.B., Roberto P.G., Rodrigues V. de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva H.C., Silvestri M.L.Z., Siqueira W.J., de Souza A.P.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-
                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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Chloroplast.
Eukaryota; Viridiplantae; St
Lycopodiophyta; Lycopodiopsi
NCBI_TaxID=37429;
                           Q9LII3
Q9LII3;
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q95C95;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF313605; AAL26206.1;
InterPro; IPR001912; Riboson
InterPro; IPR002942; S4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relatives to seed plants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pryer K.M., Schneider Hunt J.S., Sipes S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q95C95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast; Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGRO1017; rpsD_bact; 1.
PROSITE; PS00632; RIBOSOMAL_S4; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Horsetails
                                                                                                                                                                                                                                                                      133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 ньсрн
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186
                                                                                                                                                                                                                                                                                                                             10 PESRA 14
                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                      PESRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00163; Ribosomal_S4; 1. PF01479; S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0:0-0(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 100 5; Conservative
                                                                                                                                                                                                                                                                      137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158
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                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation updat

omal protein 4 (Fragment).
                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schneider H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopodiopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22312 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribosomal_S4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                           15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptophyta; Embryophyta; Tracheophyta;
psida; Lycopodiales; Lycopodiaceae; Huper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith A.R., Cranfill R., Wolf P.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        club
                           Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                   Score 5; DB 8; Pred. No. 5e+
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      0
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Pred. No.
                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   683CFFE60130679E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     moss).
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                                                                                                                     195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192
                                                                                                                                                                                                                                                                                                                                                                                                           DB 8; 1
o. 5e+02;
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5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 192;
                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     closest living
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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                  RESULT 188
Q950R1
ID 0950R1
AC Q950R1
AC Q950R1
O1-DEC
DT 01-DEC
DT 01-DEC
DE 01196
GN 0RF196
GN Spizel
OG Mitch
OC Eukary
OC Spizel
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Best Local S
Matches 5
                                                                                                                                                                                                 Q950R1;
Q950R1;
01-DEC-2001
01-DEC-2001
01-DEC-2001
Splzetrom, Mitochondrion.

Eukaryota; Fungi; Chytridiomycota; Eukaryota; Fungi; Chytridiomyceta; Spizellomyces.
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TAC and B
                                                                                                               ORF196.
Spizellomyces
                                                                                                                                                                         Orf196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Arabidopsis cDNA clones.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001303; BAB02214.1; -.
EMBL; AY054138; AAL06799.1; -.
EMBL; AF380644; AAK55725.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Shinn P., Banh J., Bowser L., Carrinci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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6)[ARP43227.1 (AR3918560/K24M9_5).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR000923; BlueCu_1.
PROSITE; PS00196; COPPER_BLUE;
SEQUENCE 195 AA; 21876 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-COLUMBIA;
Kaneko T., Kato T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Arabidopsis ORF clones.";
Submitted (AUG-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structural analysis
Sequence features of
TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                    (TrEMBLrel. 19,
(TrEMBLrel. 19,
(TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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the regions of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Nakamura Y., Asamizu
EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 5; DB 10; I
Pred. No. 5.1e+02;
0; Mismatches 0;
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854707849DA9CAD1 CRC64;
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Matches 5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BALB/C;
STRAIN-BALB/C;
MEDLINE-20381309; PubMed-10922053;
Cinquanta M., Royescalli A.C., Kozak C.A., Nirenberg M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-MAR-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U. EMBL; U65068; AAC52829.2; HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97008065; PubMed-8855241;
Rovescalli A.C., Asoh S., Nirenberg M.;
"Cloning and characterization of four murine homeobox Proc. Natl. Acad. Sci. U.S.A. 93:10691-10696(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 189 AA;
                                                                                                                                                                               PROSITE; PS00027; HOMEOBOX_1;
PROSITE; PS50071; HOMEOBOX_2;
SEQUENCE 190 AA; 20391 MW;
                                                                                                                                                                                                                                                                                                                   TRANSFAC; T03309; -...
MGD; MGI:108012; Og9x.
InterPro; IPR001356; Homeobox.
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                                                                                                                                                                                                                                                     SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                        ProDom;
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MEDLINE=21156231; PubMed=11258796;
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                                                                                      Similarity
5; Conserv
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Similarity 100.0%;
5; Conservative
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Pred. No
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Pred. No.
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                                                                                                                                                                                                                             UNKNOWN_1.
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o. 4.9e+02;
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Tanaka M., Tobe T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes..
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Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M.,
Coutinho L.L., Cristofani M., Dias Neto E., Docena C., El Dorry H.,
Pacincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Fraga J.S., Franca S.C., Franco M.H.S., Gomes S.L., Gruber A.,
A Krieger J.E., Kutajima J.P.,
A Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
A Lemos E.G.M., Lemos M.Y.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
A Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
A Menck C.F.M., Majai M.A., Nascimento A.L.T.O., Netto L.E.S.,
A Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
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OJJJ29;

OJ-OCT-2000 (TrEMBLrel. 15, Created)

OL-OCT-2000 (TrEMBLrel. 15, Last sequence update)

OJ-JUN-2001 (TrEMBLrel. 17, Last annotation update)

Wbscr5 alternative spliced product (Williams-Beuren
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01-OCT-2000
01-MAR-2002
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Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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Martindale D.W., Wilson M.D.,
Duranio V., Koop B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20365717; PubMed=10910347;
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100.0%; Pr
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Sciurognathi; Muridae;
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01-MAR-2002

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RESULT 181
Q9ZUE1
ID Q9ZUE1
AC Q9ZUE1
AC Q9ZUE1
DT Q1-MAY
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RN [1]
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Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen, Howing B., Koo T., Lam B., Lee J Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
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STRAIN-SPRAGUE DAWLEY;
MEDLINE-20381309; PubMed-10922053;
MEDLINE-20381309; PubMed-10922053;
MEDLINE-2038130; PubMed-10922053;
MEDLINE-2038150; PubMed-109250;
MEDLINE-2038150; PubMed-109250;
MEDLINE-2038150; PubMed-109250; Pu
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01-MAY-1999 (TIEMBLIEL 10, Last sequence update)
01-OCT-2000 (TIEMBLIEL 15, Last annotation update)
Hypothetical 20.9 kDa protein F508.9 (F28c11.16).
F508.9.
                                                                                                                                                                                                                                         Theologis
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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VARIANT
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PROSITE; PS00027; HOMEOBOX_1;
PROSITE; PS50071; HOMEOBOX_2;
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Proc. Natl. Acad. Sci. U.S..
EMBL; AF284338; AAG14459.1;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                 Submitted (DEC-1998)
                                                                                                                                                                                                                                                                     STRAIN=CV. COLUMBIA;
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kin, brain,
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Best Local S
Matches 5
                                              STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpattick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

"Genome Sciences"
                                                                                                                                                                                                                                                            Q8XAL7
Q8XAL7;
Q1-MAR-2002
Q1-MAR-2002
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                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=0157:H7 / E
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EMBL, AC005990; AAC98090.1; -. EMBL/AC005905 AAF9589.1; -.
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 SEQUENCE FROM N.A.
               Nature 409:529-533(2001).
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                                                                                                                                                                                                                     Escherichia coli 0157:H7.
Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical SEQUENCE 18
                                          'Genome
                                                                                                                                                                                           NCBI_TaxID=83334;
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                                         Escherichia coli 0157:H7.";
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01-NOV-1998 (TrEMBLrel. (
01-NOV-1998 (TrEMBLrel. (
F8M12.19 protein.
                                                                       Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheol Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                              081624
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Submitted (MAR-2001)
EMBL; BC004262; AAHO
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SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
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InterPro; IPR000182; GCN5acetyltransf.
Pfam; PF00583; Acetyltransf; 1.
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                                                                                                                                                                                                                                               081624;
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TISSUE-UTERUS;
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                                                      NCBI_TaxID=3702;
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183 AA; 20939 MW; 02AD828D376F3397 CRC64;
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No. 4.8e+02;
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hima K., Kimura T
A., Muraki A.,
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Q9ERS8;
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STRAIN - AS (2) / M145;

BentLey S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
actinomycetales; Streptomycineae; Streptomyces.
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Madsen C., Graves T., Cotton M., Modde T.;
"The sequence of A. thaliana F8M12.";
submitted (SEP-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of coelicolor A3(2).";
Nature 417:141-147(2002).
Nature AL355753; CAB90893.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9KYZ4;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9KYZ4
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22148 MW;
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the EMBL/GenBank/DDBJ
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NO. 4.9e+02;
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o. 4.8e+02;
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Last sequence update)

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Q92LB0;
Q92LB0;
Q92LB0;
Q1-DEC-2001 (TrEMBLrel. 19, C
Q1-DEC-2001 (TrEMBLrel. 19, L
Q1-MAR-2002 (TrEMBLrel. 20, L
Hypothetical protein R03164.
R03164 QR SMC03781.
                                                                                                                                                                                                                                                                                                                                                Capela D., Barioy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J. Bolstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss B., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
     Q9L0E7
                                                                                                                                                                                                                                                                                                          Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591793; CAC47743.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000520; Exonuclease,
Pfam; PF00929; Exonuclease; 1.
SMART; SM00479; EXOIII; 1.
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EMBL; X89773; CAA61915.2;
EMBL; U88964; AAB53416.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of a new interferon-inductible PML nuclear bodies-associated protein.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Pentecost B.T.;
                                                                                                                                                                                                                                                                                             InterPro; IPR003742; DUF163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                              67
                                                                                                                                11 ESRAA 15
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                                                                                              ESRAA
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                                                                                                                                                                                                                                          PF02590; DUF163; 1.
hetical protein; Complete
NCE 181 AA; 19513 MW;
                                                                                                                                                                . Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
5; Conserv
                                                                                              71
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     PRELIMINARY;
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100.0%;
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0; Mismatches
                                                                                                                                                                  0;
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Last annotation updat
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Pred. No.
   PRT;
                                                                                                                                                                                                                                    proteome.
F45B6D0D60303B75 CRC64;
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   181
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b. 4.7e+02;
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.7e+02;
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RESULT
Q9BTA6
ID Q9BTA6
ID Q9
AC Q9
DT 01
DT 01
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DT 01
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the mccoelicolor A3(2).",
Nature 417:141-147(2002).
EMBL; AL161803; CAB82063.1;
INCOEPTO; IPRO01932; PP2C-1ike.
InterPro; IPR001230; Pranyl_site.
SMART; SM00331; PP2C_SIG: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM M.145;
STRAIN=83(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                   01-JUN-2001 (TrEMBLrel. 17, C. 01-JUN-2001 (TrEMBLrel. 17, L. 01-JUN-2001 (TrEMBLrel. 17, L. Similar to cactin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00294; PRI
Hypothetical protein.
SEQUENCE 181 AA; 1
                                                  Homo sapiens
                                                                                                                                               Q9BTA6;
                                                                                                                                                                  Q9BTA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9L0E7;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein SCO4695.
SCO4695 OR SCD31.20.
 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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Cerdeno A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                  PRELIMINARY;
                                                  (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomycineae; Streptomycetaceae; Streptomyces.
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                    Primates;
                                   Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                     18977 MW;
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                                                                                      Created)
Last sequence
Last annotation
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EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                               Score 5;
                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                     B915019A97814814 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN_1
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                                                                                        sequence update) annotation updat
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Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9VKY6 PRELIMINARY;
O9VKY6;
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
O1-JUN-2002 (TrEMBLrel. 2
CG13141 protein.
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STRAIN-ZOBELL ATCC
MEDLINE-97107629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (respiratory nitrite reductase) from Pseudomonas Eur. J. Blochem. 232:737-746(1995).
EMBL; Z73914; CAA98149.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ZOBELL ATCC 14405;
MEDLINE-96028114; PubMed-7588711;
MEDLINE-96028114; PubMed-7588711;
Palmedo G., Seither P., Koerner H., Matthews
Timkovich R., Zumft W.G.;
"Resolution of the nirD locus for heme dl syr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence and analysis of an internal 9.7-kb segment from denitrification gene cluster of Pseudomonas stutzeri."; Biochim. Biophys. Acta 1277:6-12(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muso:
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000382; CytC_oxdse_III; 1. PROSITE; PS50253; COX3; 1. SEQUENCE 175 AA; 19485 MW; 24E2E
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Pfam; PF00510; COX3; 1.
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Glockner A.B., Zumft W.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
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5; Conser
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ilarity 100.0%;
Conservative
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13,
21,
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NO. 4.6e+02;
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RESULT 172
Q802T0
ID Q002T0
AC Q802T0
O1-JUN
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DT Q1-JUN
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RP SEQUER
RC TISSUE
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RL Submitt
DR EMBL;
SQ SEQUER
RESULT 173
000441
ID 000441
AC 000441
DT 01-VUL
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DT 01-DEC
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A Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Wooddage T., Wolfey K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Wooddage T., Wolfey K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Wooddage T., Wolfey K.C., Wu D., Yang S., Yao Q.A.,
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Clabs R.A., Wyers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).

BUBL; AE003628; AAF52920.1;
Science S. FNDON032766. CG1314.1
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Best Local S
Matches 5
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OBOZTO;
O1-JUN-2002 (TrEMBLrel. 21, C:
O1-JUN-2002 (TrEMBLrel. 21, L:
O1-JUN-2002 (TrEMBLrel. 21, L:
Similar to unknown (Protein for Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NOBI_TaxID-10090;
                                                                                              000441
000441; 000586;
01-JUL-1997 (TIEMBLEEL 04, C)
01-MAY-2000 (TIEMBLEEL 13, Le
01-DEC-2001 (TIEMBLEEL 19, Le
ISG20 protein (Interferon stil
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Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC024802; AAH24802.1;
SEQUENCE 176 AA; 19102 MW; 9B309EAE9E585AC6 CRC64;
                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003628; AAF52920.1; -. F1yBase; FB9n0032226; CG13141. InterPro; IPR003654; Homeo_OAR. SEQUENCE 176 AA; 17810 MW;
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                                NCBI_TaxID=9606;
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                                                Chordata;
Primates;
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Rodentia;
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stimulated gene) (20KD).
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for IMAGE: 3908182).
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                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM

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NESULT 167
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AC OS2386
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OT 01-UN
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OS Lactob
OC Bacter
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01-MAY-2000
01-MAR-2002
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Strausberg R
Submitted (SI
                            MEDLINE=20036896; PubMed=10567266; White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Woffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                 Q9RRQ6;
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Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases EMBL; AF037091; AAB91419.1;
SEQUENCE 172 AA; 19966 MW; F8B392A3FB9E2FF4 CRC64;
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EMBL; BC014429; AAH14429.1; -
InterPro; IPR000369; ISK_Channel.
Pfam; PF02060; ISK_Channel; 1.
SEQUENCE 170 AA; 18439 MW; 4F
  "Genome sequence radiodurans R1.";
                     Fraser C
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                           Deinococcaceae;
NCBI_TaxID=1299;
                                                                                                                                               Bacteria; Thermus/Deinococcus
                                                                                                                                                         Deinococcus radiodurans
                                                                                                                                                                          Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-ATCC7469;
                                                                                                                                                                                                                                                                                                                                                                                                                              Lactobacillus rhamnosus.
Bacteria; Firmicutes; Ba
Lactobacillaceae; Lactob
MCBI_TaxID=47715;
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01-JUN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Lactobacillus.
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18439 MW; 4F6C94F87BF71B52 CRC64;
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Best Local :
Pseudomonas.
NCBI_TaxID=316;
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P95548;
01-MAY-1997
01-MAY-1997
01-MAR-2002
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Q9W6F2;
Q1-NOV-1999
01-NOV-1999
01-JUN-2002
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Sofer L., Burnside J.;
Submitted (JAN-1999) to the EMBL/Ge
EMBL; AF120211; AA031645.1; -
InterPro; IPR000712; Bc12_BH.
InterPro; IPR0002475; Bc12_family.
Pfam; PF00452; Bc1-2; 1.
SMART; SM00337; BCL; 1.
Pseudomonas stutzeri (Pseudomonas perfectomarina)
Bacteria; Proteobacteria; gamma subdivision; Pseu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein Al.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 286:1571-1577(1999).
EMBL; AE002073; AAF11973.1; -.
TIGR; DR4432; -.
InterPro; IPR000182; GCN5acetyltransf.
Pfam; PF00583; Acetyltransf; 1.
Hypothetical protein; Complete proteome.
BYDOTHETICAL PROTEIN; CAMPILET PROTEOME.
173 AA; 18755 MW; 42FEA6DFA4E4A77D CRC64;
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MEDLINE=99190706; PubMed=10090728;
Lee R.M., Gillet G., Burnside J.,
                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50062; BCL2_FAMILY; PROSITE; PS01258; BH2; 1.
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leognathae; Galliformes; Phasianidae; Phasiani
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death in t
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RESULT 163
Q06234
AC Q06238
AC Q06238
AC Q06238
DT 01-NO)
DT 01-NO
RESULT
097194
ID 097
AC 097
DT 01
DT 01
DT 01
DT 01
DT 01
CON 12
CON 12
CON 12
CON 14
CON 16

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Best Local
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                                                                                       O97194
PKELLINI.
O97194;
O97194;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
"""nothetical 19.1 kDa protein.
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Q06236;
Q1-NOV-1996
Leishmania major.
Eukaryota; Euglenc
NCBI_TaxID=5664;
(1)
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Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
Louis E.J., Messenguy F., Mewes H.W., Miosga T., Mostl D.,
Muller Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
Vlerendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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YLR164W OR L9632.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cherry J.M.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ
EMBL; U51921; AAB67488.1; -.
SGD; S0004154; YLR164W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston
Submitted
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5; Conserv
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                                                                        Euglenozoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                        Kinetoplastida;
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Last sequence update)
Last annotation update)
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Pred. No
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o. 4.5e+02;
                                                                        Trypanosomatidae;
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                                                                            Leishmania.
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RESULT 166
Q96CC4
ID Q96CC4
AC Q96CC4
DT 01-DEC
DT 01-DEC
DT 01-UN
DE Simila
DE gene 4
OS Homo s
OC Eukary
OC Mammal
OX NCBI_T
RN [1]
RP SEQUEN
                                                                                                                                                                                                                                                                                                      RESULT 165
Q8WWG9
ID Q8WWG9
AC Q8WWG9
DT 01-MAR
DT 01-MAR
DT 01-JUN
DE POLASS
GN KCNEA.
OS HOMO S
OC EUKARY
OC MAMMAI
OX NCBLT
RN [1]
RP SEQUEN
RC TISSUE
RA HUI K.
RL SUBMI K.
RL SUBMI K.
RL SUBMI K.
RF PRINTS
DR PRINTS
SQ SEQUEN
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Matches 5
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Best Local S
Matches 5
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TISSUE-KIDNEY, AND HEART;
TISSUE-KIDNEY, AND HEART;
Hui R., Teng S., Lin C., Ma L., Zhen
Submitted (DEC-2001) to the EMBL/Gen
LEMBL, AV065987; AAL49979.1; -..
R Interpro; IPR000369; ISK_Channel.
R PRINTS; PR00168; KCNECHANNEL.
R PRINTS; PR00168; KCNECHANNEL.
                                                 Q96CC4 PKELLING
Q96CC4;
Q96CC4;
Q96CC4;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to potassium voltage-gated channel, IsK-r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A physical map of the Leishmania Genome Res. 8:135-145(1998).
EMBL; AL139794; CAC22659.1; -.
Hypothetical protein.
SEQUENCE 168 AA; 19126 MW; 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ivens A.C., Lewis Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ivens A.C., Murphy L., Quail M.,
Rajandream M.A., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8WWG9;
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                                    Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potassium voltage-gated
                         NCBI_TaxID=9606;
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5; Conservative
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5; Conser
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   N.A
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S.M., Bagherzadeh
                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Primates;
                                       Primates;
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20, Last sequence update)
21, Last annotation updat
channel-like protein.
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Pred. No. 4.5
0; Mismatches
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                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; V. Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             950E3FAE9715EA98
                                                                                                                                                                                                                                                                                                         1C6FBCF87298F6C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   Zhen
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No.
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                                                                                                                                                                                                                                                                  DB 4; Le
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                                                                                                                                                                                                                                                                                                                                                                                                                             Vertebrata;
i; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Friedlin
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IsK-related
                                                                                                                                                                                                                                                         0
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                                                                                    subfamily,
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RESULT 160
024121
ID 024121
AC 024121
DT 01-JAN
DT 01-DEC
DE Transc
OS Nicoti
OC Sperm
OC Sperm
OC ASter
OX NCBL/
RN [1]
RP SEQUE
RA BOTIS
BRI Submi
DR Inter
DR Ffam;
SQ SEQUE
RESULT
Q9CCZO
ID Q9
AC Q9
DT 01
DT 01
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DT 01
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Matches 5
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Best Local
O9CCZO;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Conserved hypotehical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=20504483; PubMed=11016950;

Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Ballga N.S., Thorsson V., Sbrogna J.,

Shukla H.D., Lasky S.R., Ballga N.S., Thorsson V., Sbrogna J.,

Shukla H.D., Lasky S.R., Ballga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Isenbarger T.A., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Ebhardt H., Lowe T.M., Liang P., Klay M., Hood L., DasSarma S.;

"Genome sequence of Halobacterium species NRC-1.",

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                     Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
Ricotiana plumbaginifolia (Leadwort-leaved tobacco).
Rukaryota; Viriddiplantae; Streptophyta; Embryophyta; espermatophyta; Magnoliophyta; eudicotyledons; core asteridae; euasterids I; Solanales; Solanaceae; Nico
                                                                                                                                                                                                                                                                                                                                                                                                                                             O24121;
O1-JAN-1998 (TrEMBLrel. 05,
O1-JAN-1998 (TrEMBLrel. 05,
O1-DEC-2001 (TrEMBLrel. 19,
Transcription factor
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Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                        Q9CCZ0
                                                                                                                                                                                                                                                                                    Submitted (OCT-1996) to the EMBL; Y09106; CAA70323.1; InterPro; IPR002715; NAC.
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NCBI_TaxID=64091;
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01-MAR-2001
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Borisjuk N.V.;
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ilarity 100.0%;
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17859 MW;
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Pred. No. 4.4
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Pred. No.
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edons; core eudicots;
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Q9LH78;
Q1-H78;
Q1-CT-2000 (TrEMBLrel. 15,
Q1-CT-2000 (TrEMBLrel. 15,
Q1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                    Similarity to transposon protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II, Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                   "Structural analysis
Sequence features of
TAC and BAC clones.";
                                                                                                                                                                                  Submitted
                                                                                                                                                                                            Kaneko
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Massive gene decay in the leprosy Nature 409:1007-1011(2001).
EMBL; AL583926; CAC32186.1; -.
Leproma; ML2654; -.
                                                                        DNA
                                                                                                                       Nakamura Y.;
                                                                                                                                               STRAIN-COLUMBIA;
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                       STRAIN-COLUMBIA;
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Pfam; PF00149; Metallophos;
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Barrell B.G.;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                          and BAC clones.";
Res. 7:217-221(2000).
                                                AP002061; BAB02643
ICE 167 AA; 1971
Similarity
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O58905;
01-AUG-1998 (TrEMBLrel. 0
01-AUG-1998 (TrEMBLrel. 0
01-MAR-2002 (TrEMBLrel. 2
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eulemur fulvus (brown lemur).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Eulemur.
NCBI_TaxID=13515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
                                                                                                                                                    PROSITE; | Receptor.
                                                                                                                                                                                                                                                   "The olfactory receptor gene repertoire in primates and Evidence for reduction of the functional fraction in pri Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000). EMBL; AF179771; AAF40354.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
01-dectory receptor (Fragment).
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thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
EMBL; AP000005; BAA30291.1; -.
                                                                                                                                                                                                          Pfam; PF00001
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-20183981; PubMed-10706615;
Rouquier S., Blancher A., Giorgi D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 1
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0001; 7tm_1; 1.
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161 AA;
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ilarity 100.0%;
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17687 MW;
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A217DD7F21CD0E95
                                                                              3A67FBF76F3BB069 CRC64;
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RESULT 158
Q96129
ID Q96129
AC Q96129
DT 01-DEC
DT 01-DEC
DT 01-MAR
DE Unknow
OS HOMO S
OC EUKALTY
OC MAMMMAI
OX NCBL_T
RN [1]
RN [1]
RP SEQUEN
RC TISSUE
RA Straus
RL Submit
DR Interf
FT NON_TEL
SQ SEQUEN
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053000
                                                          RESULT 159
Q9HSQ8
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Best Local S
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Best Local S
Matches 5
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01-JUN-1998 (
01-JUN-1998 (
01-AUG-1998 (
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Q96129;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (Protein for IMAGE:4301250) (Fragment)
Homo sapiens (Human)
Q9HSQ8;
01-MAR-2001
                                     905н60
                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2001) to the EMBL/GenBank/DDBJ EMBL; BC007864; AAH07864.1; -. InterPro; IPR004822; Histone_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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Escherichia
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TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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GTrEMBLrel.
GTrEMBLrel.
                                                                                                                                                                                                                                                                                                  163 AA;
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ilarity 100.0%;
Conservative
(TrEMBLrel.
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                                         PRELIMINARY;
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100.0%; Pr
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07,
  16,
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0; Mismatches
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0; Mismatches
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                  70AD52C6D9575A47 CRC64;
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b. 4.4e+02;
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.4e+02;
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Rosidae;

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RESULT 153
1004218
ID 004218
AC 004218
DT 01-JUL
DT 01-JUL
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OR VSV5
ID VSV5
ID VSV5
ID VSV5
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 004218;
004218;
01-JUL-1997
01-JUL-1997
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01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                               InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004359; HIS_KIN_sig.
Pfam; PF02518; HATPase_c; 1.
PROSITE; P850109; HIS_KIN; 1.
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21562662; PubMed=11705980;
Kies S., Otto M., Vuong C., Gotz F.;
"Identification of the sigB Operon in S
Construction and Characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8VSV5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR004359; HIS_KIN_sig.
Pfam; PF02518; HATPase_c; 1.
SMART; SM00387; HATPase_c; 1.
SEQUENCE 159 AA; 17922 MW; EA
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                              Infect.
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nes 5; Conserv
                                                                                                                                                                                                  Local Similarity
les 5; Conserv
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                                                                                                                                                                  1 SHLGP
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2 (TrEMBLrel.
2 (TrEMBLrel.
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 (TrEMBLrel.
                                                    PRELIMINARY;
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183:2624-2633(2001).
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Bartscht K., Sab
                                                                                                                                                                                                                                                                   17924 MW;
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20,
21,
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annotation
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                                                    159
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o. 4.3e+02;
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a sigB Deletion
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b. 4.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                               epidermidis:
Mutant.";
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Q9F484
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Best Local S
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Best Local
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Q9F484;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                               EMBL; AI
HSSP; P(
NON_TER
                                                                                                                                                                              "Cloning and sequence of an alkaline from the marine bacterium Alteromonas Gene 136:247-251(1993).
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NON_TER
NON_TER
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Curr. Biol. 8:315-324(1998).
EMBL; U95144; AAG49963.1; -
InterPro; IPR000832; GPCR_sec
                                                                                                                                                                                                                             Tsujibo H., Miyamoto K., Okami Y., Inamori Y.;
                                                                                                                                                                                                                                                                                                                              rsujibo H., Miyamoto K., Okamoto T., Orikoshi H., Inamori Y.;
"A Serine Protease-Encoding Gene (april) of Alteromonas sp. S
Is Regulated by the Iron Uptake Regulator (Fur) Protein.";
Appl. Environ. Microbiol. 66:3778-3783(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alteromonas sp. (strain 0-7).
Bacteria; Proteobacteria; gam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=98189351; PubMed=9512416;
Plakidou-Dymock S., Dymock D., Hooley R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica napus (Rape).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                  STRAIN-0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FhuA (Fragment).
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                                                                                                                                                                                                                                                               MEDLINE=94124007; PubMed=8294010;
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20422186; PubMed=10966390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=29458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alteromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50261; G_PROTEIN_RECEP_F2_4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *A higher plant seven-transmembrane receptor that influences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative G-protein-coupled receptor (Fragment).
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                                                                                                                                                                  AB040412;
                                                 : Similarity
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                                                                                                                 160 AA;
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                                                                                                                   MW;
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                                                                  DB 2; Lei
o. 4.3e+02;
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D. 4.3e+02;
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                                                                               Length 160;
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Strain 0-7

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RESULT 149

Q9M9A2

ID 9Q9M9A2

AC Q9M9A2

AC Q9M9A2

DT 01-CCT

DT 01-DCC

DE F27J115

OS Arabid

OC Eukary

OC Eukary

OC Sperma

OC SPERMA

OC NCBL-T

RN [1]

RN [1]

RN [1]

RN [1]

RN Shinn

RA Shinn

RA Shinn

RA Conway

RA Lenz C

RA Palm C

RA FOrlum

RA Ecker

RT "Genome

RT I.";

RT SUBBL;

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Best Local
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9M9A2;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q48591 PRELIMINARY; PRT; 15
Q48591;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequer
Q1-NOV-1998 (TrEMBLrel. 08, Last annotation of 16S rRNA gene (5'end) (Fragment).
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SEQUENCE
                                                                                                                            Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khai Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen, Howing B., Koo T., Lam B., Leu Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri Joriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
  SEQUENCE 156 /
                                               Submitted
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9M9A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Gen. Microbiol. 139:200
EMBL; x65713; CAA46629.1;
NON_TER 1 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-NCDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus.";
                                                                                           Genomic sequence for Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Physiological and
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Similarity 100.0%;
5; Conservative
                                             (OCT-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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    AAF69704.1;
AA; 17611 M
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Pred. No
8192BEB1D5D7829E CRC64;
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No. 4.2e+02;
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                                                                                           BAC
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DT 01-MAR
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Q9F7V2;
01-MAR-2001
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MEDLINE-21608550; PubMed-11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr.,

Chen Y., Setubal J.C., Chen L., Wood G.E., Almeida N.F. Jr.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., W. Z., Romero P.,

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W.,

Cochumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.
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01-JUN-2002 (TrEMBLrel. 21, Las
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01-JUN-2002 (TrEMBLrel. 21, Las
Nitrogen regulatory protein PI
GLNB OR ATU1769 OR AGR_C_3252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cielo C., Slater S.;
"Genome sequence of the plant pathogen
Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
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NCBI_TaxID=176299;
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RESULT 145
Q9REL1
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Q1-MAY-2000 (TrEMBLrel. 13
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01-JUN-2002 (TrEMBLrel. 2
2-C-methyl-D-erythritol 2,
4.6.1.12).
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01-JUN-2002
01-JUN-2002
01-JUN-2002
 SEQUENCE FROM N.A. STRAIN-ATCC 27566; MEDLINE-20378653;
                                                                                                                                                                                                                                                                                   Lyase.
SEQUENCE
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                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Micrococcaceae; Micrococcus MCBI_TaxID-1273;
                                                                                                                                                                                                                                                                                                                                                                                                         Thermus thermophilus.
Bacteria; Thermus/Deinococcus
Thermaceae; Thermus.
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EMBL; AE010765; AAM04426.1; -.
                                                                                                                                                                                                                                                                                                                       Kishida H., Wada T., Unzai S., Kuzuyama T., Te
Yokoyama S., Tame J.R., Park S.;
"2-C-methyl-D-erythritol 2,4-cyclodiphosphate
thermophilus HBB.";
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                                                                         Micrococcus
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RESULT 147
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MEDLINE-96109443; PubMed-8619599;

MEDLINE-96109443; PubMed-8619599;

Noguchi N., Emura A., Matsuyama H., Ohara K., Sasatsu M.,

"Nucleotide sequence and characterization of erythromycin

determinant that encodes macrolide 2'-phosphotransferase I

escherichia colirase."

Antimicrob. Agents Chemother. 39:2359-2363(1995).

EMBL; D16251; BAA03774.2; -
"Nucleotide sequence of 2B g serotype Asia-1."; Submitted (NOV-1999) to the EMBL; AF207524; AAG35703.1;
                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ASIA1/IND 63/72;
Manju G., Venkataramanan
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                                                                                                                      Sanyal A.
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ler R.V.;
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Q9Y413;
Q9Y413;
Q1-NOV-1999 (TEMBLrel. 12, C
Q1-NOV-1999 (TEMBLrel. 12, L
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Hypothetical 18.0 kDa protein
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Hypothetical
SEQUENCE 14
Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. EMBL; #L050075; CAB43258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stanley E., Walsh L., Fitzge Submitted (APR-1999) to the EMBL; AF145034; AAF26608.1; HSSP; P02339; 1EYG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stanley E., Walsh L.,
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                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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"Identification of four loci isolated
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Pfam; PF00436; SSB; 1.
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                                                        FISSUE-KIDNEY;
                                                                          SEQUENCE FROM N.A.
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100.0%; Pr/
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Primates;
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15732 MW;
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D16371D9C4EBA237 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ODD3D7C394A53FF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148
                                                                                                                                                                                                                                                                                                              150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Lo
DB 16; Lo
DB 16; Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fitzgerald
                                                                                                                                                     Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                              Š
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                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Siphoviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacterlophage
                                      Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 143
Q8TS13
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Q923U3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local S
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-C2A / ATCC 35395 / DSM 2834;

MEDLINE-21929760; PubMed-11932238;

Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

Zimmer A., Barber R.D., Cann I., Graham D.E., Krzycki J.A.,
                                                                                                                                                                                                                                                                                                                                                                                      OBTS13 PRELIMINARY;
OBTS13;
O1-JUN-2002 (TIEMBLIEL. 2
O1-JUN-2002 (TIEMBLIEL. 2
O1-JUN-2002 (TIEMBLIEL. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRP5 (Fragment).
Cavia porcellus (Guinea pig).
Cavia Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q923U3
Q923U3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Expression of mRNA encoding Trp cation channe smooth muscle cells."; smooth muscle cells."; submitted (JUN-2001) to the EMBL/GenBank/DDBJ EMBL; AF395787; AAK84034.1; InterPro; IPR0002111; Cat_channel_TrpL. InterPro; IPR000365; M-thannel_nlg. InterPro; IPR001865; Ribosomal_S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Ong H.L., Brereton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                       Methanosarcinaceae;
NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                  Predicted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00520; ion_trans; 1.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ong H.L., Brereton H.M., "Expression of mRNA enco
                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                       Methanosarcina acetivorans
                                                                                                                                                                                                                                                                                                                                                MA0994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 LGPHR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LGPHR 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
150 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
17068 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18001 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rodentia;
                                                                                                                                                                                                                                                                              Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.3%;
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19,
20,
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ding Trp cation
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 5; DB 11;
Pred. No. 4.1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata;
Hystricognathi; Cavii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5F4E4DE03153CA65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B719BE32C5804913 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                    Methanosarcinales;
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on channels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         guinea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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RESULT 136
Q9NM50
ID Q9NM50
AC Q9NM50
DT 01-OCT
DT 01-OC
   AC OCCUPANT 
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Q942D1
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Best Local S
Matches 5
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Best Local
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                                                                                                                                                                                           STRAIN=CV.
Sasaki T.,
                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice), and Oryza sativa (Rice), and Dryza sativa (Japonica cultivar-group). Bukaryota, Viridiplantae; Streptophyta; En Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzea; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q942D1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
B1060H01.8 protein (OSJNBb0036G09.14 protein).
B1060H01.8 OR OSJNBB0036G09.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9NM50;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Possible hypothetical 63.6 kDa protein in aqpz-cspd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
SEQUENCE FROM N. STRAIN-CV. NIPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murphy L., Quail M., Harris Submitted (JUL-2000) to the EMBL; AL160493; CAB97860.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00710; NATPEPTIDES.
SMART; SM00183; NAT_PEP; 1.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
SEQUENCE 139 AA; 14881 MW; 4262B7771870E1FB CRC64;
                                                                                                 Submitted
                                                                                                                                  clone:B1060H01
                                                                                                                                                   Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4530,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q942D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leishmania major.
Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment).
LM26.242.
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Pfam; PF00212; ANP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U77596; AAC60341.1; -.
InterPro; IPR000663; Natr_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                             the EMBL/GenBank/DDBJ databases
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.8e+02;
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RESULT 138
Q9Z3G2
ID Q9Z3G2
AC Q9Z3G2
DT 01-MAX
DT 01-JUN
DE CYTM.
GN CYTM.
GN CYTM.
OS Synech
OC Bacter
OX NCBL_T
RN [1]
RP SEQUEN
RC STRAIN
RA Malakh
RL SUBmit
DR Intere
DR Intere
DR PROSIT
SQ SEQUEN
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Q8YP84
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Matches 5
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Malakhov M.P., Murata N.;
Sembli G., Malakhov M. 
                                                                                                                                                                                                                                                                                                                                                           Q8YP84;
01-MAR-2002
01-MAR-2002
01-MAR-2002
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Q9Z3G2;
Q1-MAY-1999
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21595285; PubMed=11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA,
clone:OSJNBb003669.";
Submitted (FEB-2001) to the EMBL/GenBank/DI
EMBL; AP003560; BAB68075.1;
EMBL; AP003369; BAB68075.1;
EMBL; AP003309; BAB89381.;
SEQUENCE 143 AA; 15266 MW; F25DC4382B14
                                                                                                                                                                                                                                                                   Anabaena sp. (strain PCC Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                      Hypothetical protein ALL4315.
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Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                 NCBI_TaxID=103690;
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01-JUN-2002
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(TrEMBLrel: 10,
(TrEMBLrel: 21,
                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last seq
(TrEMBLrel. 20, Last ann
l protein All4315.
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100.0%; F
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Nostocales;
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schrimi L.M., Staubli F., Suzuki R., Tomita M., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Hofmann M., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fijita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Hypothetical 15.7 kDa pro
                                             Znou X.M., Zhang P.P., J. Wan D.F., Gu J.R.;
"Novel human cDNA clones growth.";
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                          PP9943.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Eukaryota; Futheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J; TISSUE-EMBRYONIC MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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               Submitted (NOY-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF318380; AAL55887.1; -.
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                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                   NCBI_TaxID-9606;
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llarity 100.0%;
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                                                                                                H.Q.,
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Pred. No.
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Catarrhini;
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                                                                  function
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RESULT 135
P79799
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Q85071: 01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
P0678F11. 7 protein.
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"Cloning of an unusua...........;
coral snake Micrurus corallinus.";
niochem. 250:144-149(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Micrurus corallinus (Brazilian coral snake).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Lepidosauria; Squamata; Scleroglossa; Serpentes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group). Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsida Ehrhartoideae; Oryzeae; Oryza. NCBI_TaxID=39947;
                                                                                                                                           TISSUE-VENOM GLAND;
MEDLINE-98092299; P
HO P.L., Soares M.B
                                                                                                                                                                                                                                                                                                                                          coral
                                                                                                                                                                                                                                                                                                                                                    "Reverse biology applied to Micro
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Elapidae; Elapinae;
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Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                     9; PubMed=9432002;
M.B., Maack T., Gimenez
                                                                                                                                                                                                                                                                                                             Rev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Micrurus
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21,
21,
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Last annotation updat
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Pred. No.
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0. 3.8e+02;
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3.8e+(
                                                                                                                                                     Ι.,
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erpentes; Colubroidea;
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a; Poales; Poaceae;
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                                                                                                                                                     Puorto G.,
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                                                                                                                                                        Furtado M.F.,
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RESULT 130
052214
ID 052214
AC 052214
AC 052214
AC 052214
DT 01-JUN
DT 01-DEC
DE Hydrox
GN HABA.
OS Pseudo
OC Pseudo
OC Pseudo
OC Pseudo
OC STRAIN
RN [1]
RP SEQUEN
RCBLT
RN [1]
RP SEQUEN
RC STRAIN
RX MEDLIN
RX MEDLIN
RA Spain
RT "Seque
RT Hydrox
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Q8XIO4
ID Q8XIO4
AC C10Str
OC C10St
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Best Loc
Matches
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Best Local S
Matches 5
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Q8XI04;
Q8XI04;
Q8XI04;
Q1-MAR-2002 (TrEMBLrel. 20, Crest
Q1-MAR-2002 (TrEMBLrel. 20, Last
Q1-MAR-2002 (TrEMBLrel. 20, Last
Q1-MAR-2002 (TrEMBLrel. 20, Last
                                                                                                                                                                                                                                                                                                                                                                     052214;
052214;
01-JUN-1998
01-JUN-1998
01-DEC-2001
                                                                      MEDLINE=20336447; PubMed=10877793; Davis J.K., Paoli G.C., He Z., Nad Spain J.C.;
                                                                                                                                               STRAIN-JS45
                                                                                                                                                                                                                                                                        Pseudomonas pseudoalcaligenes
Bacteria; Proteobacteria; gamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimizu
Shiba T.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
Clostridiaceae; Clostridium.
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Pfam; PF00539; Tat; 1.

Activator; Nuclear protein; RNA-binding; Transcription regulation segulation 131 AA; 14742 MW; F931D793B0CF1D8B CRC64;
  *Sequence Analysis and Initial Characterization of Two Isozymes of Hydroxylaminobenzene Mutase from Pseudomonas pseudoalcaligenes JS4 Appl. Environ. Microbiol. 66:2965-2971(2000).
                           Hydroxylaminobenzene
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 Hydroxylaminobenzene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   flesh-eater.";
Proc. Natl. Acad. Sci. U.S.,
EMBL; AP003193; BAB82026.1;
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                                                                                                                                                                                                                           NCBI_TaxID=330;
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SEQUENCE 134 AA; 1
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Similarity 100.0%;
5; Conservative (
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., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
te genome sequence of Clostridium perfringens, an a
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                                                                                                                                                                                                                                                                                                                                                                   (TremBLrel. 06, Created)
(TremBLrel. 06, Last sequence update)
(TremBLrel. 19, Last annotation update)
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15780 MW; 13450C3B61886CF4 CRC64;
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                                                                                                                                                                                                                                                                        gamma subdivision; Pseudomonadaceae;
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0; Mismatches
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Pred. No. 3.7
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Last annotation update)
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                                                                                               Nadeau L.J.,
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NO. 3.6e+02;
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Best I
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Q9PGJ5;
01-OCT-2000
                                                                                                                                                                                                                        Complete
SEQUENCE
                                                                                                                                                                                                                                                                                               Pfam; PF00507;
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RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., RA Golauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M., RA RA Colauto N.B., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Ra Facincani A.P., Ferreira M.J.S., Forbme M., Furlan L.R., RA Fraya J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., RA Fraya J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., RA Garnier M., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Manchado M.A., Nascimento A.L.T.O., Netto L.E.S., RA Monck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Machado J.A., Nascimento A.L.T.O., Netto L.E.S., RA Mond A. Jr., de Oliveira R.A., Nascimento A.L.T.O., Netto L.E.S., RA Mond A.Y., Jeretra G.A.G., Pereira H.A. Jr., Pesquero J.B., RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., Pereira H.A. Jr., Pesquero J.B., RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.; RT Thereor. TpBO00400.) .
                                                                                                                                                                  PROSITE; PS00904; PPTA; UNKNOWN_1.
                                                                                                                                                                                                                      InterPro; IPR000440; Oxidored_q4.
InterPro; IPR002088; PPTA.
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                              DB 16; L<sub>1</sub>
), 3.7e+02;
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"The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
Proc. Natl. Acad. Sci. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-16M / ATCC 23456 / BIOTYPE
MEDLINE-20020109, PubMed-11756688;
DelVecchio V.G., Kapatral V., Redk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kestler H., Kodama
Lackner A., Regier
Submitted (JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimpanzee immuno
Viruses; Retroid
NCBI_TaxID=11723;
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01-DEC-2001
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                                                                                                                                                 Activator;
SEQUENCE
                                                                                                                                                                                                                                                          PROMOTER (BY SIMILARITY). EMBL; M33262; AAA47630.1; -.
                                                                                                                                                                                                                                                                                                                                                                   immunodeficiency virus.";
Science 248:1109-1112(1990)
                                                                                                                                                                                                                                                                                                                                                                                                        Kestler H., Kodama T., Ringler D., Marthas M., Pedersen N.C.,
Lackner A., Regier D., Sehgal P., Daniel M., King N., Desrosiers
"Induction of AIDS in Rhesus monkeys by molecularly cloned simiar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-239
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Bacteria; Proteobacteria;
Brucellaceae; Brucella.
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STPES
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5; Conserv
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130 AA;
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etroid viruses; Retroviridae; Lent
                                                           33.3%; Silarity 100.0%; Conservative 0;
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(TrEMBLrel. 19, Last annotation update)
(Transactivating regulatory protein).
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ilarity 100.0%;
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14599 MW;
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Pred. No. 3.5
0; Mismatches
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Pred. No.
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6196DF62F9F467E8
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No. 3.6e+02;
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Lentivirus.
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R) RNA ELEMENT AND
R ELONGATION FROM
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ing N., Desrosiers
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RESULT 128
Q90EX2
ID O90EX2
AC Q90EX2
AC Q90EX2
DT 01-DEC
DT 01-DEC
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DE TAT pr
GN TAT;
OS Simian
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Q90EX7;
Q1-DEC-2001
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01-DEC-2001
01-MAR-2002
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Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
-:- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINI
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMEN
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION
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Flaherty M.T., Hauer D.A., Mankowski J.L.,
"Molecular and biological characterization
molecular clone of simian immunodeficiency
J. Virol. 71:5790-5798(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simian immunodeficiency virus 17E-Fr. Viruses; Retroid viruses; Retroviridae; NCBI_TaxID-160753;
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Anderson M.G., Hauer D.A., Sharma D.P., Joag S.V., Narayan O. Zink M.C., Clements J.E.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AN ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM ACTIVATES TRANSCRIPTION INITIATION AND/OR
                                                                                                                         Anderson M.G., Hauer D., Sharma D.P., Jaink M.C., Clements J.E.; Zink M.C., of envelope changes acquired neuroadaption in rhesus macaques."; Virology 195:616-626(1993).
                                                                                                                                                                                                                                                                  Simian immunodeficiency virus 17E-Cl
Viruses; Retroid viruses; Retrovirid
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Pfam; PF00539; Tat; 1.
Activator; Nuclear protein; R
SEQUENCE 131 AA; 14800 MW;
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MEDLINE=93331720; Pubmed=8337835;
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100.0%; Pr
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of a neurovirulent
virus.";
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AC 011311
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H2-14.2 protein (
SEQUENCE FROM N.A.
STRAIN-C2A / ATCC 35395 / DSM 2834;
MEDLINE-21929760; PubMed-11932238;
Galagan J.E., Nusbaum C., Roy A., E
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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SEQUENCE
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Lopez-Estebaranz J.L., Esteban M., Martin Gallardo A.;
"A Random DNA Sequencing, Computer-Based Approach for the Gene
of a Gene Map of Molluscum Contagiosum Virus.";
Virus Genes 0:0-0(1997).
EMBL; U86896; AAB7941.1; -.

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NCBI_TaxID=10280;
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EMBL; AD000983; BAB65612.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 118 AA; 12734 MW; 5C91BACBE0104B42 CRC64;
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Q92RT8;
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          Hypothetical BMEI1918.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical SEQUENCE 1:
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Rhizobiaceae; Sinorhizobium.
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D3696FF6B96975FA CRC64;
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Q8XV40;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable periplasmic divalent cation tolerance protein
CUTA OR RSC2991 OR RSQ1125.
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21681879; PubMed-11823852; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Artiguenave F., Billault A., Brottier P., Camus J.C., Cattolico L., Arlat M., Billault A., Brottier P., Camus J.C., Cunnac S., Demange N. Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Molsan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; "Asture 415:497-502(2002).

EMBL: AL646073; Capl6700.1; -.

EMBL: AL646073; Capl6700.1; -.

EMBL: AL646073; CatAl; 1.
Rawlings N.D.;
Unpublished observations (JAN-1998).
-1- CATALYTIC ACTIVITY: HIPPURATE +
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Trifolium repens (Creeping white clover).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid:
eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae; Trifoli
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01-JUN-1998 (TremBLrel. 06, Last sequence update)
01-JUN-2002 (TremBLrel. 21, Last annotation update)
Putative HIPPURATE hydrolase (EC 3.5.1.32) (BENZOYLGLYCINE
                                                                             SEQUENCE FROM N.A. Koberstaedt A., Lenz Submitted (NOV-1992)
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                                  IDENTIFICATION, AND CONCEPTUAL TRANSLATION Rewlings N.D.;
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Pred. No. 3.2
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Pred. No.
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AC Q923U6
DT 01-DEC
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CAVIA
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OC MARMMAI
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RN [1]
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Q974P5;
Q1-DEC-2001
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Q923U4;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN_2002 (TrEMBLrel. 21,
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"Expression of mRNA encoding Trp cation channels in gui
smooth muscle cells.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF395786; AAK84033.1;
InterPro; IPR0002111; Cat_channel_TrpL.
InterPro; IPR000856; M+Channel_nlg.
InterPro; IPR001865; Ribosomal_S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMA/HIPO/HYUC FAMILY OF HYDROLASES.
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION EMBL; X68950; -; NOT_ANNOTATED_CDS.
Hypothetical protein; Hydrolase; Zinc.
63 ZINC (POTENTIAL)
  STRAIN=JCM 10545
PubMed=11572479;
                                                                                                                                               Sulfolobus tokodaii.
                                                                                                                                                                     Hypothetical ST0614.
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il protein ST0614.
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62; RIBOSOMAL_S2_1;
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ZINC (POTENTIAL).
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5. 3.3e+0
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RESULT 115
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Antimicrob. Agents Chemother. 45:2991-3000(2001).
EMBL; AY034138; AAK64885.1; -...
                                                                                                SEQUENCE
                                                                                                                                                         nucleus in flowering plants.";
Nature 408:354-357(2000).
EMBL; AF302137; AAG37233.1; -
                                                                                                                                                                                          MEDLINE-20548717; PubMed-11099041;
MEDLINE-20548717; PubMed-11099041;
Adams K.L., Daley D.O., Qiu Y.L., Whelan J., Palmer J.D.;
"Repeated, recent and diverse transfers of a mitochondrial gene
                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl Panicoideae; Andropogoneae; Zea.
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01-JUN-2002 (TrEMBLrel.
Ribosomal protein S10.
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01-MAR-2001
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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NCBI_TaxID=4577;
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Ribosomal_S10; 1.
- 17936 MW; F75BFFDBA6DCFA51 CRC64;
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Al Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Al Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Al Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ak Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ak Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ak Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ak Kuehl R., Catubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Ak Schriml L., M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Ak Schriml L., M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Ak Sakai K., Okido T., Frurno M., Aono H., Baldarelli R., Barsh G.,
Ak Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ak Blake J., Boffelli D., Bojunga N., Carninoi P., de Bonaldo M.F.,
Ak Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Ak Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Ak Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Ak Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Ak Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Ak Hayashizaki Y., Schida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local
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Q9D503;
Q1-JUN-2001
Q1-JUN-2001
Q1-JUN-2001
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                                                                                                                      EMBL;
                                                                                                                                                          Olofsson A., Mittelholzer C., Treiberg Berndt Mejerland T., Belak S.; Wejerland T., Belak S.; "Unusual, high genetic diversity of Aleutian J. Clin. Microbiol. 39:4145-4149(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NS1.
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Mus musculus (Mouse).
"harvota; Metazoa; Chordata;
"harvota; Rodentia;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Viruses; ssDNA viruses; Parv
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MGD; MGI:1922418; 4930533B18rik.
SEQUENCE 112 AA; 12360 MW; D31828B0D55BEC61
           SEQUENCE
                                                                                                                                                                                                                                                                                                                        STRAIN=A2;
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=28314;
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki
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       112 AA;
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           MW;
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Sciurognathi; Muridae;
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           A6950872B9ED1790 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; L
b. 3.2e+02;
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P SQUIENCE FROM N.A.

C STRAIN-CO-92 / BIOVAR ORIENTALIS;

(X MEDLINE-21470413; PubMed-11586360;

RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

RA Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

RA Feltwell T., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

RA Leather S., Moule S., Oyston P.C.F., Whitehead S., Barrell B.G.;

"""""" Stevens K., Whitehead S., Barrell B.G.;
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Best Local S
Matches 5
                                                                                 "Genome sequence of Yersinia pestis, t)
Nature 413:523-527(2001).
EMBL; AJ414153; CAC92849.1; -.
InterPro; IPR003456; DUF143.
InterPro; IPR004394; Iojap.
Pfam; PF02410; DUF143; 1.
TIGRFAMS; TIGR00090; Iojap; 1.
Hypothetical protein; Complete proteome
SEQUENCE 105 AA; 11605 MW; A8A87A37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8ZDG2;

O1-MAR-2002 (TrEMBLrel. 20, C.

O1-MAR-2002 (TrEMBLrel. 21, L.

O1-JUN-2002 (TrEMBLrel. 21, L.

O1-JUN-2002 (TrEMBLrel. 21, L.
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01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paralichthys olivaceus (Flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Reukaryota; Metazoa; Chordata; Craniata; Pareleostei; Neoteleostei;
Acathopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
NCBI_TaxID-8255;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein YPO2606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     olivaceus.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AB055213; BAB62411.1; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kurokawa T., Suzuki T.;
"Development of neuropeptide Y related peptides in the digestive organs during the larval stage of Japanese flounder, Paralichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8ZDG2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yersinia pestis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
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;; PS00265; PANCREATIC_HORMONE_1;
;; PS50276; PANCREATIC_HORMONE_2;
E 97 AA; 10929 MW; 8703D0D393
  h 33.3%;
Similarity 100.0%;
'5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteobacteria;
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Score 5; DB 10; Pred. No. 3e+10; Mismatches
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01-MAR-2001 (TrEMBLrel. 10
01-MAR-2001 (TrEMBLrel. 10
01-JUN-2002 (TrEMBLrel. 20
01-JUN-2002 (TrEMBLrel. 20
                                                                                                                       nucleus in flowering plants.";
Nature 408:354-357(2000).
EMBL; AF287341; AAG23319.1; -.
InterPro; IPR001848; Ribosomal_S10
Pfam; PF00338; Ribosomal_S10; 1.
PRINTS; PR00971; RIBOSOMALS10;
PrODom; PD001972; RIBOSOMALS10; 1
PEQUENCE 109 AA; 12684 MW; 7EB
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Q99494;
01-MAY-1997
01-MAY-1997
01-DEC-2001
                                                                                                                                                                                                                                                                                                   Adams K.L., Daley D.O., Qiu Y.L., Whelan "Repeated, recent and diverse transfers
                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays (Maize).
Eukaryota; Viridiplantae; Strept
Spermatophyta; Magnoliophyta; Li
Spermatophyta; Magnoliophyta; Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9FUT8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lockshin B., Boyd N.R., Shie massociation of dopamine train with smoking.",
Am. J. Hum. Genet. 0:0-0(0).
EMBL, Y10141; CAA71229.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                      MEDLINE=20548717; PubMed=11099041;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Lerman C., Ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
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                                              Conservative
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N.R., Shields
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Primates;
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/ta; Liliopsida;
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0; Mismatches
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5. 3e+02;
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a; Poales; Poaceae;
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mitochondrial
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RESULT 107
Q50101
ID Q50101
AC Q50101
DT 01-NOV
DT 01-FEE
DE HYPOTH
GN U650J.
OS Mycoba
OC Actinc
OX NCBI_1
RN [1]
RP SEQUEN
RA SMITH
DR SUBDIT
DR SEQUEN
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Q9N001
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DT 01-OC
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Best Local
                                                                                                        Smith D.R., Robison K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
EMBL; U15184; AAA63068.1; -.
Hypothetical protein.
SEQUENCE 95 AA; 10229 MW; 1037F851EFA214C2 CRC64;
                                                                                                                                                                                                                                                              Mycobacterium leprae.
Mycobacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                    Q50101 PRELIMINARY; PRT; 95 AA. Q50101; O1-NOV-1996 (TrEMBLrel. 01, Created) O1-NOV-1996 (TrEMBLrel. 01, Last sequence update) O1-FEB-1997 (TrEMBLrel. 02, Last annotation updat Hypothetical 10.2 kDa protein U650J. U650J.
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TISSUB-CEREBELLUM CORTEX;
OSAGA N., HJAB M., KUSUGA J., Tanuma R.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical 9.6 kDa protein.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monk Macara fascicularis (Crab eating macaque) (Cynomolgus monk Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalla; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ EMBL; AB046646; BAB03564.1; -.
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01-OCT-2000
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01-OCT-2000
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                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                      Local Similarity 100 tes 5; Conservative
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87 AA; 9072 MW; 4I
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5. 2.6e+02;
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Q90WF2
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Best Local
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Q8SC82;
01-JUN-2002
01-JUN-2002
Q90WF2;
                                                                                                                                                                                                                                                                                                         "Genomic sequence of Shiga toxin 2-converting Escherichia coli (0157:H7 Okayama strain and co Shiga toxin 2-converting phages."; submitted (DEC-2001) to the EMBL/GenBank/DDBJ EMBL; AP004402; BAB87902.1; -. Hypothetical protein. SEQUENCE 96 AA; 10747 MW; 567C7F96EA9A70F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9N8N8;
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01-JUN-2002 (TrEMBLrel. 21, La
01-JUN-2002 (TrEMBLrel. 21, La
Hypothetical 10.7 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sato T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=STX2 PHAGE-I;
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Yamasaki S., Takeda Y.;
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                      PRT;
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Q1-DEC-2001 (TrEMBLrel. 2
Q1-JUN-2002 (TrEMBLrel. 2
Glucokinase (Fragment).
Equus caballus (Horse).
Equus caballus (Horse).
Eukaryota; Wetazoa; Chord
Mammalia; Eutheria; Peris
NCBI_TaxID-9796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mikko S., Roed K., Schmutz S., Andersson L.;
"Genetic diversity at major histocompatibility complex DRB some domesticated and wild ruminant species.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF012723; AAB66616.1; -.
HSSP; P13758; 1DLH.
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NCBI_TaxID-9870;
                                                          SEQUENCE FROM N.A.
MEDLINE=21314992; PubMed=11421942;
Shubitowski D.M., Venta P.J., Doug
"Polymorphism identification withi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00969; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
Glycoprotein; MHC II; Transmembrane
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                                                          C.L., Z
equine
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                                                 zhou R.-X., Ewart S. gene-specific seque
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Best Local
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Q8YFP6;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
MAR-2002 (TrEMBLREL 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pı
NCBI_TaxID=9606;
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Kinase.
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01-DEC-2001 (TremBLrel. 19, Last
01-JUN-2002 (TremBLrel. 21, Last
Similar to interferon stimulated
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                                    SEQUENCE FROM N.A.
STRAIN-16M / ATCC 23456 / BIOTYPE 1;
STRAIN-16M / ATCC 23456 / BIOTYPE 1;
MEDLINE-20020109; PubMed-11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Rez Ivanova N., Anderson I., Bhattacharyya A., Bernal A., Mazur M., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson Selkov E., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY008787, AAG43039.1; -. InterPro; IPRO01312; Hexokinase. Pfam; PF00349; hexokinase; 1. ProDom; PD001109; Hexokinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-2001) to the EMBL/
EMBL; BC016341; AAH16341.1; .
InterPro; IPR000520; Exonuclease.
Pfam; PF00929; Exonuclease; 1.
                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                            Brucella melitensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Last annotation updat
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Catarrhini; Hominidae
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                                                                  Letesson
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Reznik G
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Best Local
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01-MAR-2002 (TrEMBLrel. 2

01-MAR-2002 (TrEMBLrel. 2

01-JUN-2002 (TrEMBLrel. 2

MHC class II DR alpha 1 d
     SEQUENCE FROM N.A. Schmutz S., Andersson L.;
Mikko S., Roed K., Schmutz S., Andersson L.;
Mikko S., Roed K., Schmutz S., Andersson L.;
"Genetic diversity at major histocompatibility complex DRB
some domesticated and wild ruminant species.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF012716; AAB66609.1;
EMBL; AF012716; AAB66609.1;
InterPro; IPR000353; MHC_II_beta.
Pfam; PF00969; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
Glycoprotein; MHC II; Transmembrane.
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01-JAN-1998
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wei Z., Happ G.;
"MHC variation in reindeer and caribou.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ
EMBL; AF458948; AAL67477.1;
Interpro; IPR000353; MHC_II_beta.
Pfam; PF00999; MHC_II_beta; 1.
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NCBI_TaxID=9870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rangifer tarandus (Reindeer) (Caribou).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; (Cetartiodactyla; Ruminantia; Pecora; Cervoide
Cervidae; Odocolleinae; Rangifer.
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                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9870;
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nilarity 100.0%;
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20, Last sequence update)
21, Last annotation update)
domain (Fragment).
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Pred. No. 2.4
0; Mismatches
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Pred. No.
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"Genetic diversity at major histocompartist; complex DRB loc
some domesticated and wild ruminant species.";

L Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF012717; AAB66610.1; -
R InterPro; IPR000353; MHC_II_beta.

R Pfam; pF00969; MHC_II_beta; 1.

R ProDom; PD000328; MHC_II_beta; 1.

Glycoprotein; MHC II; Transmembrane.

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SEQUENCE 83 AA; 9815 MW; 57BF9EEAD167E840 CRC64;
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Best Local :
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Best Local :
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O19222;
O1-JAN-1998 (TrEMBLrel. 05, C:
O1-JAN-1998 (TrEMBLrel. 05, L:
O1-DEC-2001 (TrEMBLrel. 19, L:
MHC II DR-beta 1 chain (Fragmu
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019221;
01-JAN-1998
          Mikko S., Roed K., Schmutz S., Andersson L.;
"Genetic diversity at major histocompatibility complex
some domesticated and wild ruminant species.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF012718; AAB66611.1;
InterPro; IPR000353; MHC_II_beta.
                                                                                                                                          Rangifer tarandus (Reindeer) (Caribou).
Eukaryota; Metazoa; Chordata; Cranitata;
Mammalia; Eutheria; Cetartiodactyla; Run
Cervidae; Odocoileinae; Rangifer.
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoide
Cervidae; Odocoileinae; Rangifer.
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01-DEC-2001
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-JAN-1998 (TrEMBLrel. 0
-DEC-2001 (TrEMBLrel. 1
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100.0%; Pr
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19,
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Last sequence update)
Last annotation update)
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Pred. No.
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Pred. No. 2.5
0; Mismatches
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                                                                                                                                                          Pecora; Cervoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9E796; PRELIMINARY;
Q9E796;
Q1-MAR-2001 (TrEMBLrel. 16, C
Q1-MAR-2001 (TrEMBLrel. 16, L
Q1-MAR-2001 (TrEMBLrel. 16, L
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O8XVKO:
01-MAR-2002 (TIEMBLIE). 2
01-MAR-2002 (TIEMBLIE). 2
01-MAR-2002 (TIEMBLIE). 2
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";
"Acture 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL646072; CAD16537.1; --
Hypothetical protein; Complete
SEQUENCE 71 AA; 7726 MW; BE
                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                         Core protein (Fragment).
Hepatitis C virus.
                               Roggendorf M.;
"Genotyping of hepatitis C virus isolates
J. Clin. Microbiol. 38:3581-3584(2000).
EMBL; AF233719; AAG24348.1; -.
NON TER
                                                                                                                                                           Ross R.S., Vi
Roggendorf M.
                                                                                                                                                                                                                    MEDLINE-20472685;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA positive-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21681879;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein RSc2830. RSC2830 OR RSO0275.
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                                                                                                                                                                                  172685; PubMed=11015367;
Viazov S.O., Holtzer C.
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     AA;
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ia; beta subdivision; Ralstonia
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Pred. No. 2.2
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BB8116A6554BB043 CRC64;
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5. 2.1e+02;
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b. 2.2e+02;
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Best Local :
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             Wei z., Happ G.;
"MHC variation in reindeer and caribou.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ-
EMBL; AF458945; AAL67474.1; -
Interpro; IPR000353; MHC_II_beta.
Pfam; PF000595; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
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01-NOV-1999
01-MAR-2002
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Fi Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Complete proteome. SEQUENCE 76 AA; 8245 MW; 9CBC49D7D4E8F559
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NCBI_TaxID=56636;
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ilarity 100.0%;
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domain (Fragment).
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MEDLINE=93250401; PubMed=8492091;

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Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai Indentification of the gene encoding the major capsid proinsect iridescent virus type 6 by polymerase chain react?

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DNA sequences of the genome
Virus Genes 6:19-32(1992).
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EMBL; AE005242; AAG54971.1; -.
EMBL; AP002552; BAB34098.1; -.
InterPro; IPR003456; DUF143.
InterPro; IPR004394; Iojap.
Pfam; PF02410; DUF143; I.
TIGRFAMS; TIGR00090; Iojap; 1.
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STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

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Grotbeck E.J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
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MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoy;

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe '

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DNA Dec 8.11-27/2011
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Jakob N.J., Mueller K., Bah
Submitted (SEP-2000) to the
EMBL; AF303741; AAK82141.1;
SEQUENCE 62 AA; 6641 MW;
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MEDLINE=21342599; PubMed=11448171;
Makob N.J., Muller K., Bahr U., Darai G.;
"Analysis of the First Complete DNA Sequence
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virus Genes 18:243-264(1999).
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409:529-533(2001).
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Iridescent Virus.";
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                                                                                                                                                                                                                                                                                                                                                            Yokoyama K.,
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Best Local S
Matches 5
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X MEDLINE-9928/316; PubMed-10360571;

X MEDLINE-9928/316; PubMed-10360571;

XA Haft D. H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.

XA Haft D. H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.

XA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.

X Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson

XA Heidelberg J. Sutton G.G., Fielschmann R.D., Eisen J.A., White

XA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteri

"Tevidence for lateral gene transfer between Archaea and Bacteri

"Tevidence of Thermotoga maritima.";

XL Nature 399:323-329(1999).

R EMBL; AE001735; AAD35696:1; -.

R TIGR; TM0611; -.

XO SEQUENCE 56 AA; 6468 MW; 346F85EB61A078A0 CRC64;
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09W280;
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01-WOV-1999 (TrEMBLrel. 22, La
01-MAR-2002 (TrEMBLrel. 20, La
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"A novel tetracycline resistance determinant, transferable R-plasmid from the fish pathogen submitted (OCT-1999) to the EMBL/GenBank/DDBJ EMBL; AJ250203; CAC80725.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
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Q14274;
Q1-NOV-1996
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O1-DEC-2001
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Q91FP4;
Q1-DEC-2001
01-DEC-2001
01-DEC-2001
SEQUENCE FROM N.A.
MEDILINE-89073752; PubMed-3201750;
MEDICINE-89073752; PubMed-3201750;
MIDICINE-89073752; PubMed-3201750;
MIDICINE-89073752; PubMed-3201750;
MIDICINE-3750;
MIDICINE-375
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                                                                                                                                                                                                                                                                        Delius H., Darai G.;

Molecular cloning and
iridescent virus type

the viral genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Med.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-87321126; PubMed-2820141;
Schnitzler P., Soltau J.B., Fischer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Insect iridescent virus type 6 induced toxic deg in mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Delius H., Darai G., Fluegel R.M.;

"DNA analysis of insect iridescent virus

permutation and terminal redundancy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chilo iridescent virus (CIV) (Insect iridescent virus type 6). Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
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Mammalia; Eutheria;
                                                                                                                                                                                                                              the viral genome.";
Virology 160:66-74(1987).
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MEDLINE-86174607; Pub
Lorbacher de Ruiz H.,
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H., Gelderblom H.,
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f: further evidence for c
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5. 1.9e+02;
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Franchini G., Gajdusek D.C.;
"Molecular phylogeny and dissemination of
virus type I viewed within the context of
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Human T-cell leukemia virus type II (HTLV-II).
Viruses; Retroid viruses; Retroviridae; Deltar
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Viruses; Retroid viruses; Retroviridae; Deltar
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"Endemic infection with human T-cell leukemia/lymphoma
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Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumo from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
EMBL; AE001585; AAD181644.1; -.
EMBL; AP002545; BAA98216-1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 51 AA; 5804 MW; 8229BE6536FCF0AE CRC64;
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"Partial nucleotide sequence analysis of the
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MEDLINE=96078239; PubMed=7576938;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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HPX-2.
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Submitted (MAY-1997) to the EMBL/GenBank/DDBJ data
EMBL; AF005396; AAB87754.1; -.
NON_TER 1
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EMBL: X74861; CAA52854.1; -.
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MEDLINE-94314219; F
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Endemic infection with human T-cell leukemia/lymphoma
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Love J., Poiesz B.;
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InterPro; IPRO00313; PWWP_domain.
InterPro; IPR001214; SET.
InterPro; IPR001265; Znf_PHD.
Pfam; PF00628; PHD; 3.
Pfam; PF00855; PWWP; 2.
Pfam; PF00855; PWWP; 2.
Pfam; PF00855; PWWP; 2.
Pfam; PF00855; PWWP; 1.
PROSITE; PS00190; CYTCCHROME_C; UNKNOW PROSITE; PS00190; SET; 1.
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01-JAN-1998 (TrEMBLrel. 05, 0
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01-JUN-2002 (TrEMBLrel. 21,
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InterPro; IPR001227; A
InterPro; IPR002198; A
InterPro; IPR004410; F
InterPro; IPR000794; K
InterPro; IPR003880; P
                                                                                           Pfam; PF02801; ketoacyl-synt_C; 3.
Pfam; PF02801; ketoacyl-synt_C; 3.
Pfam; PF00850; pp-binding; 3.
TIGRFAMs; TIGRF00128; fabD; 3.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
PROSITE; PS00075; ACP_DOMAIN; 3.
PROSITE; PS000606; B_KETOACYL_SYNTHASE; 2.
PROSITE; PS000012; PHOSPHOPANTETHEINE; UNKNOWN_1.
Oxidoreductase; Phosphopantetheine; Transferase.
SEQUENCE 4340 AA; 457589 MW; D59A734CB5FB795D CRC64;
3813 PESRAA 3818
                                                                                                                                                                                                                                   Pfam;
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J. Bacteriol. 179:7515-7522(1997).
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-NRRL-2821;
MEDLINE-98053867; PubMed-9393718;
Kakavas S.J., Katz L., Stassi D.;
                                                                                                                                                                                                                                                                                                                        (SDR) FAMILY.
EMBL; AF016585; #
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Bacteria; Firmicutes; A
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                                                                                                                                                                                                         PF00698; Acyl_transf; 3.
PF00106; adh_short; 2.
PF00109; ketoacyl-synt; 3.
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Similarity 100.0%;
6; Conservative
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                        15
                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomycineae;
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transf; 3.
                                                                                                                                                                                                                                                                                   Ac_transferase.
ADH_short.
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                                                                                                                                                                                                                                                                                                                                               THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                               Score 6; DB 2; Pred. No. 5.5
0; Mismatches
                                                0;
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Last annotation updat
1 and 2.
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                                                            DB 2; Le
o. 5.5e+02;
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3.7e+02;
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RESULT 022463
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P70635
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01-JAN-1998 (
01-JAN-1998 (
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                                                                                                                                                            EMBL; AFO
NON_TER
SEQUENCE
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MEDLINE=96305362; PubMed=8706714;

Dirks R.P.H., Kraft H.J., Van Genesen S.T., Klok E.J., Pfundt Schoenmakers J.G.G., Lubsen N.H.;

"The cooperation between two silencers creates an enhancer ele that controls both the lens-preferred and the differentiation specific expression of the rat betaB2-crystallin gene.";

Eur. J. Biochem. 239:23-32(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
NON_TER
SEQUENCE
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01-FEB-1997
01-DEC-2001
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                                                                                                                                                                                          Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF016328; AAB71681.1; -
NON TER 1 1 1
                                                                                                                                                                                                                                          "Barperm2.";
                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                         STRAIN-CV.
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Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barperm2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4513;
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(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                Conservative
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100.0%; Pr
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Pred. No
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R InterPro; IPRO00719; Euk_pkinase.
R InterPro; IPRO00478; ppz.
R InterPro; IPRO00967; pkinase_C.
R InterPro; IPRO00969; pkinase; l.
R Pfam; pF000595; ppz; l.
R Pfam; pF000699; pkinase; l.
R Pfam; pF000601; Euk_pkinase; l.
R SWART; SM002209; S_TKC; l.
R SWART; SM00220; S_TKC; l.
R SWART; SM00230; S_TK_X; l.
DR PROSITE; pS50106; pDZ; l.
DR PROSITE; PS50116; PROTEIN_KINASE_DOM; l.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; l.
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Best Local S
Matches 6
Query Match
Best Local Similarity
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01-DEC-2001
01-DEC-2001
01-JUN-2002
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                                                                                                                                                                                                                                 "A novel gene, NSD1, is fused to NUP98 in the t(5;11)(q35;p15.5) novo childhood acute myeLoid leukemia.";
Blood 98:1264-1267(2001)
EMBL; AF322907; AAK92049.1; -
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR000313; PWMP_domain.
InterPro; IPR001214; SET.
InterPro; IPR001214; SET.
InterPro; IPR001955; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=21384794; PubMed=11493482;

Jaju R.J., Fidler C., Haas O.A., Strickson A.J.,

Cross N.C., Cheng J.F., Aplan P.D., Kearney L., 1
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                                                                              PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1
PROSITE; PS50280; SET; 1.
SEQUENCE 2596 AA; 285024 MW; 1C412D841
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Eukaryota; Metazoa; (
Mammalia; Eutheria; E
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PF00856; SET; 1.
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Pred. No.
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Smith H.O.,
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Q26033;
01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96L73; PRELIMINARY;
Q96L73;
Q1-DEC-2001 (TIEMBLTel. 19,
Q1-DEC-2001 (TIEMBLTel. 19,
Q1-JUN-2002 (TIEMBLTel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1335 RSTPES 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95330813; PubMed=7606788; Su X.Z., Heatwole V.M., Werthelmer S.P., Guinet F., Peterson D.S., Ravetch J.A., Wellems T.E.; "The large diverse gene family var encodes proteins cytoadherence and antigenic variation of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa;
NCBI_TaxID=5833;
                     Nsd1
                                                                                                                                           "Identification and Characterization of a Novel Androgen Receptor Coregulator ARA267-alpha in Prostate Cancer Cells.";
J. Biol. Chem. 276:40417-40423(2001).
                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-21538797; Wang X., Yeh S., W
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                    protein NSD1).
ARA267B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Androgen receptor associated coregulator 267-b (Putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infected erythrocytes.";
Cell 82:89-100(1995).
                                                                                                  SEQUENCE FROM N.A. MEDLINE-21590373; PubMed-11733144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004258; | Pfam; PF03011; PFEMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                         "Molecular characterization
                                                             Matsumoto N.;
                                                                                   Kurotaki N.,
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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gene.";
279:197-204(2001)
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(TrEMBLrel. 01,
(TrEMBLrel. 19,
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                                                                                   Harada
                                                                                                                                                                                                                                                    Wu
                                                                                                                                                                                                                                                PubMed=11509567;
Wu G., Hsu C.-L.,
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100.0%;
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                                                                                   Yoshiura
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0; Mismatches
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                                           NSD1,
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                                           a human
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                                                                              s:
                                                                                                                                                                                                                                                Chang T.,
                                           homologue of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>.</u>.
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                                                                                                                                                                                                                                                    Yang Y.,
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SEQUENCE FKUT ALL STRAIN-CV. COLUMBIA; STRAIN-CV. COLUMBIA; STRAIN-CV. COLUMBIA; STRAIN-CV. COLUMBIA; PubMed=10617197; MEDLINE=20083487; PubMed=5.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; Salzberg S.L., Fraser C.M., Venter J.C.;
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064588;

01-AUG-1998 (TrEMBLrel. 07,

01-AUG-1998 (TrEMBLrel. 07,

01-MAR-2002 (TrEMBLrel. 20,
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InterPro; IPR004040; STY_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PP00069; pkinase; 1.
PRINTS; PR00100.
                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AT2G34680.
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Prodom; PD000001; Euk_pkinase; 1.

SMART; SM00221; STYKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
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Sato S., Nakamura
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Espermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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DDBJ databases
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RESULT
Q9VUQ9
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktargulu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktargulu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liux X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Pattman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
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Pterygota;
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01-MAR-2002
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01-MAY-2000
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PROSITE; PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN_1.

SEQUENCE 1680 AA; 183873 MW; E7296D84CA6B53E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COLUMBIA;
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0; Mismatches
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.5e+02;
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DNA Res. 7:331-338(2000).
EMBL; AP003006; BAB51853.1; -.
InterPro; IPR001450; 4Fe45_ferredoxin.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR001047; Prok_Mboxred.
Pfam; PF00111; fer2; 1.
Pfam; PF00384; molydop_binding; 1.
Pfam; PF01586; Molydop_binding; 1.
PROSITE; PS00198; 4FE45_FERREDOXIN; 2.
                                                                                                                               P79749 PRELIMINARY;
P79749;
01-MAY-1997 (TrEMBLrel. 03
01-MAY-1997 (TrEMBLrel. 03
01-JUN-2002 (TrEMBLrel. 21
Platelet-derived growth fi
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PDGFRBETA.

Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygil; Neopterygil; Teleostel; Euteleostel; Neoteleostel;

Acanthomorpha; Acanthopterygil; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00384; molybdopterin; 1.
Pfam; PF01568; Molydop_binding; 1.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; UNKNOWN_1.
Complete proteome.
SEQUENCE 970 AA; 106642 MW; 1E7CAF8FBBAC4E68 C:
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"Complete genome structure of the nitrogen-fixing symbiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
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Hypothetical protein.
SEQUENCE 938 AA; 106849
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Phyllobacteriaceae; Mesorhizobium.
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01-JUN-2002 (TrEMBLrel. 21
01-JUN-2002 (TrEMBLrel. 21
01-JUN-2002 (TrEMBLrel. 21
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Pfam; PF00047; dg; 3.

Pfam; PF0000001; Euk_pkinase; 2.

ProDom; PD000001; Euk_pkinase; 2.

SMART; SM00409; IG; 3.

SMART; SM00409; IG; 3.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00110; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00110; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

ATP-binding; Receptor; Transferase; Tyrosine-protein kinase.

ATP-binding; Receptor; Transferase; Tyrosine-protein kinase.
Q9LRY7
Q9LRY7;
01-OCT-2000
01-OCT-2000
                                                                                                                                                                     Receptor.
SEQUENCE
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"Conserved linkage between the puffer fish (Fugu r genes for platelet-derived growth factor receptor colony-stimulating factor receptor.";

Genome Res. 6:1185-1191(1996).
                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
Wang Y., Culty M.;
Submitted (MAR-2002) to
                                                                                                                                                                                                                                                      Eukaryota; Métazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
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EMBL; U63926; AAC60062.1;
HSSP; P11362; 1FGK.
InterPro; IPR000719; Euk_
                                                                                                                                                                                       Submitted (MAR-2002) to the EMBL; AY090783; AAM09098.1;
                                                                                                                                                                                                                                                                                         Rattus norvegicus
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InterPro; IPR003006;
InterPro; IPR001245;
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NCBI_TaxID=31033;
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Sciurognathi; Muridae;
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01-JUN-2000 (TYEMBLrel. 13, Last sequence update)
01-JUN-2002 (TYEMBLrel. 21, Last annotation update)
Putative transcriptional regulatory protein.
SCO0877 OR SCM1.10.
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Q9RD32;
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Signal.
SIGNAL
PRINTS; PRO0038; HTHLUXR.

PRODOM; PD000307; HTH_LUXR; 1.

SMART; SM00421; HTH_LUXR; 1.

DNA-binding; Transcription regulation
SEQUENCE 888 AA; 91963 MW; 7071FF
                                                                                                                                                              coelicolor A3(2).";
Nature 417:141-147(2002).
-1- SIMILARITY: BELONGS TO '
REGULATORS.
EMBL; AL133422; CAB62668.1;
                                                                                                                                                                                                                                                                                                                        Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M. Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S. Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K. Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A set of ordered cosmids and a detailed genetic the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97000351; PubMed-8843436; Redenbach M., Kieser H.M., Denapaite Kinashi H., Hopwood D.A.;
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Saunders D.C.
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Pfam; PF00196; GerE;
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m; PD000693; Glycoprot_B;
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Q8S5P5;
Q8S5P5;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
--harical 106.8 kDa protein.
STRAIN-CV. NIPPONBARE;

MCCombie W.R., de la Bastide M., Spiegel L., Preston R.

Kuit K., Nascimento L., Zutavern T., Balija V., Bell M.

Santos L., Miller B., Katzenberger F., Muller S., King

O'Shaughnessy A., Palmer L., Dedhia N.;

"Genomic sequence for Oryza sativa, Nipponbare strain,

OSJNBb0058B20, from chromosme 10, complete sequence.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
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01-FEB-1997
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzaa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-1996) to the EMBL; U60315; AAC55241.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-96325459; PubMe Senkevich T.G., Bugert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q98280
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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ugert J.J., Sisler J.R.,
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RNA stage; Poxviridae; Chordopoxvirinae;
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No. 1.5e+02;
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a; Poales; Poaceae;
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01-NOV-1996
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Cymbidium ringspot virus.
Viruses; ssRNA positive-strand viruses,
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SEQUENCE FROM N.A.
MEDLINE-96105357; PubMed-7503699;
Rubino L., Burgyan J., Russo M.;
"Molecular cloning and complete nucleotide sequence of carnatic "talian ringspot tombusvirus genomic and defective interfering
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                                                                                                                                    NCBI_TaxID=39443;
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Tombusvirus
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positive-strand viruses,
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sequence of Cymbidium :
es. 17:6383-6383(1989).
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                                                                                                                                                                                                                                                                                                                                        01-NOV-1996
01-NOV-1996
01-MAR-2002
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Q83291;
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01-OCT-2000
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                                                                                                                                    STRAIN-JM;
                                                                                                                                                           SEQUENCE
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"Isolation and characterization o Biochem. J. 357.617-623(2001).
EMBL; AJ293573; CAB97494.1; -
InterPro; IPR003323; OTU.
InterPro; IPR002533; Znf_A20.
SMART; SM00259; Znf_A20; 1.
PROSITE; PS50802; OTU; 1.
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01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
21nc finger protein Cezanne
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EMBL; X85215; CAAS9478.1; -.
InterPro; IPR002564; PV_RdRp.
Pfam; PF01615; PV_RdRp; 1.
SEQUENCE 851 AA; 95389 MW; OA
           "PCR-mediated cloning and sequencing of gene ecomplex gp100,gp60,gp48 (b-antigen).";
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ EMBL; x91985; CAA63039.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                            Viruses; dsDNA viruses,
Alphaherpesvirinae; Mar
 )85; CAA63039.1;
IPR000234; Glyco
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MBLrel. 01,
MBLrel. 20,
precursor.
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r E.R., Coadwell
                                                       Bakhtina M.M.,
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uses, no F
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94401
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Catarrhini; Hominidae
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Submitted (AUG-2001) to the EMBL/GenBar EMBL; AC087723; AAK95676.1;
InterPro; IPR004242; Transposase_21.
Pfam; PF02992; Transposase_21; 1.
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Q88485;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                                                                 MEDLINE=90281577; PubMed=2353450;
Hearne P.Q., Knorr D.A., Hillman B.I.,
"The complete genome structure and synt
clones of tomato bushy stunt virus.";
Virology 177:141-151(1990).
EMBL; M21958; AAB02535.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89163266; PubMed-2922927;
Hillman B.I., Hearne P., Rochon D., Morris T.J.;
"Organization of tomato bushy stunt virus genome:
the coat protein gene and the 3' terminus.";
Virology 169:42-50(1989).
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SEQUENCE FROM N.A.
Wing R.A., Yu Y., Soderlund C., Chen wing R.A., Yu Y., Oates R., Simmons
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Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative retrotransposable elements TNP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomato bushy stunt virus (strain Cherry) (TBSV).
Viruses; ssRNA positive-strand viruses, no DNA stage;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                         Pro; IPR002564; PV_RdRp.
PF01615; PV_RdRp: 1
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                                                        PV_RdRp; 1.
AA; 92251 MW;
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AA; 93019 P
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   40.0%;
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   Score
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                                                              D61AD04D5F94BC42 CRC64;
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of infectious
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Length 818;
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Best Local Similarity
Matches 6; Conserv
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Q96606;
Q1-FEB-1997
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Q1-FEB-2001
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Submitted (DEC-1996) to the E
EMBL; U80935; AAC32730.1; -.
Interpro; IPR002564; PV_RdRp.
Pfam; PF01615; PV_RdRp; 1.
             SEQUENCE FROM N.A.
STRALN-AMCV-BARI DR.GALLITELLI ISOLATE;
MEDLINE-94292901; PubMed-8021582;
Tavazza M., Lucioli A., Calogero A., Pa
                                                                                                         Artichoke mottled crinkle virus (AMCV). Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Szittya G., Salamon P., Burgyan J. "The complete nucleotide sequence genomic and defective interfering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20473138; PubMed=11018282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Havelda Z., Szittya G., Burgyan J., "Characterization of the molecular m "Characterization for the molecular in RNA-mediated symptom attenuation in J. Virol. 72:6251-6256(1998).
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01-MAY-1997
                                                                                 NCBI_TaxID=12142;
                                                                                                                                          Protein of 92 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-PEPPER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-PEPPER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98285798; PubMed=9621100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=12145;
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                             PV_RdRp; 1.
AA; 92566 MW;
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100.0%; Pr
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 genomic organization
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Last sequence update)
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                53C96D569E927CBB CRC64;
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and synthesis
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Best Local S
Matches 6
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Best Local S
Matches 6
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Submitted (JAN-2002) to the EMEMBL; AK074045; BAB84871.1; -
NON_TER 1
NON_TER 170813 MW
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O9E352:

O1-MAR-2001 (TrEMBLrel. 1

O1-MAR-2001 (TrEMBLrel. 1

O1-JUN-2001 (TrEMBLrel. 1

P92 protein.
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SEQUENCE FROM N.A.
LOUIE R., RedInbaugh M.G., Gordon D.T., Abt J.J., Ander:
"Maize Necrotic Streak Virus, a New Maize Virus with Si
Species of the Family Tombusviridae.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF266518; AAG21222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dev. Genes Evol. 0:0-0(2002).
EMBL; AB048247; BAB87180.1; -.
SEQUENCE 735 AA; 84337 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002
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                                                                                                                                                                                                  Viruses; ssRNA positive-strand NCBI_TaxID=137556;
                                                                                                                                                                                                                                                             Maize necrotic streak virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XEXT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The nucleotide sequence of
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CDNA cloning and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6;
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S., Shima N. distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
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16,
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, Last sequence up
, Last annotation
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Last annotation update)
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a long cDNA
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Pred. No
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Pred. No.
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                                                                                                                                                                                                                               viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4847E47E56F5D696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                             T., Abt J.J., Anderson R.J.; Maize Virus with Similarity
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O
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5. 1.2e+02;
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0. 1.3e+02;
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la; Pipoidea; Pipidae;
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RESULT 57
109874
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AC 09887
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DT 01-DE
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DT 01-DE
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OC Virus
OC NCBL
RN SEQUE
RA DAVId
RT "Mare
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RT TMATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q98Y44 PRELIMINARY;
Q98Y44;
01-JUN-2001 (TrEMBLrel. 17, 0
01-DEC-2001 (TrEMBLrel. 19, 1
01-MAR-2002 (TrEMBLrel. 20, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (OCT-2001) to the EMBL/Ge
EMBL; AR350325; AAR37556.2; -.
InterPro; IPR000324; Glycoprot_B.
Pfam; PF00606; Glycoprotein_B; 1.
ProDom; PD000693; Glycoprot_B; 1.
NON_TER 805
SEQUENCE 805 AA; 91111 MW; F88B
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                                                                                                                                                            "Marek's disease virus - turkey isolate, gB.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ
EMBL; AF350326; AAK37557.2; -
InterPro; IPR000234; Glycoprot_B.
Pfam; PF00606; Glycoprotein_B; 1.
ProDom; PD000693; Glycoprot_B; 1.
NON_TER 805 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses,
Alphaherpesvirinae; Mare
NCBI_TaxID=10390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein B (Fragment).
Turkey herpesvirus.
Viruses; dsDNA viruses, no F
Alphaherpesvirinae; Marek's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein B (Fragment). Turkey herpesvirus.
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01-DEC-2001 (TREMBLIGE: 19,
01-MAR-2002 (TREMBLIGE: 20,
                                                                                                                                                                                                                                                                                                                                                                                                Davidson I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alphaherpesvirinae;
NCBI_TaxID=10390;
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                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marek's disease virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          736 TPESRA 741
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 TPESRA 14
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   Similarity 6; Conser
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40.0%; Solution 100.0%; Solution 100.0%;
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                                                                                                                                 91115 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is - chicken isolate, gB gene.";
to the EMBL/GenBank/DDBJ databa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA stage; Herpesviridae; s disease-like viruses.
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0; Mismatches
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DR SMART; SM00220; S_TKC; 1.

DR SMART; SM002219; TyrKC; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

KW ATP-binding; Kinase; Transferase.

KW ATP-binding; Kinase; Transferase.

SPOURICE 614 AA; 67963 MW; C61DAD9A8B3A6B74 CRC64;

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SEQUENCE FROM N.A.
STRAIN-C2A / ATCC 35395 / DSM 2834;
MEDLINE-21929760; PubMed=11932238;
MEDLINE-21929760; PubMed=11932238;
Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Br Allen N., Naylor J., Stange-Thomann N., DeArellano K., John
                                                                                                                                                                                                                                                                                                                                                                                       Q8TJB4
Q8TJB4;
                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cleavage and polyadenylation specificity factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capsulatus SB1003.";
Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
EMBL; AF010496; AAC16163.1; -.
InterPro; IPR01440; TPR.
Pfam; PF00515; TPR; 2.
                                                                                                                                                                                          MA3874.
Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococo
Methanosarcinaceae; Methanosarcina
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 66.1 kDa protein.
Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter
                                                                                                                                                                    NCBI_TaxID=2214;
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Vlcek C., Paces V., Maltsev N., Paces J., Hasell
"Sequence of a 189 kb segment of the chromosome
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SEQUENCE FROM N.A.
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasu...
Nakamura Y., Wolk C.P., Kuritz T., Sasu...
Nakamura Y., Wolk C.P., Kuritz T., Sasu...
Natsunoto M., Kawashima K., Jiriguchi M., Ishikawa A., Kawashima K., Jiriguchi M., Matsunoto M., Watsuno A., Mura
Natsunoto M., Takazawa M., Yar
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                   Q8TES7 PRELIMINARY;
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Q1-JUN-2002 (TrEMBLrel. 21, C:
Q1-JUN-2002 (TrEMBLrel. 21, L:
Q1-JUN-2002 (TrEMBLrel. 21, L:
FLJ00103 protein (Fragment).
                                                                                                                                                                                                                                                                                                              Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Makazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AP003583; BAB72668.1;
InterPro; IPR001023; Hsp70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B.; "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity."; Genome Res. 12:532-542(2002).
                                                                                                                                                                                                                                                               PRODOM; PD000089; HSP70; 1.

PROSITE; PS00329; HSP70_2; UNKNOWN_1.

Hypothetical protein; Complete Proteome.

SEQUENCE 640 AA; 72075 MW; FF5D1160A2E98232 CRC64;
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01-MAR-2002
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FLJ00103

Homo sapiens (Human)

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RESULT ID 2211 OF STATE OF STA
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Best Local S
Matches 6
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Q9D2Z1;
Q9D2Z1;
O1-JUN-2001 (TrEMBLrel. 1
O1-JUN-2001 (TrEMBLrel. 1
O1-DEC-2001 (TrEMBLrel. 1
9130012009Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the model coelicolor A3(2).";
Nature 417:141-147(2002).
BMBL; AL132991; CAB61282.1;
InterPro; IPR000194; ATPase_a/bcentre.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004359; HIS_KIN_sig.
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
SEQUENCE FROM N.A.
STRAIN-C578L/6J; TISSUE-CECUM;
STRAIN-C51085660; PubMed-11217851;
MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K.
Arakawa'T., Hara A., Fukunishi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02518; HATPase_c; SMART; SM00387; HATPase_c; PROSITE; PS00152; ATPASE_A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redenbach M., Kieser H.M., Denapaite D., Eichner & Kinashl H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic athe 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
Cerdeno A.M., Parkhill
Submitted (NOV-1999) to
                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97000351; PubMed=8843436;
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Submitted (NOV-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A3(2);
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                                                                                                                                                                                                    Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conserv
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                                                                                                                                                           Chordata;
Rodentia;
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Shibata K.,
kunishi Y., F
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17,
19,
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the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                          Last sequence update)
                                                                                                                                                                                                                                                                                                                       Created)
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Pred. No.
                                                                                                                                                         Craniata; Ver
Sciurognathi;
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  Konno
Yoshino M., Itoh
Konno H., Adachi :
                                                                                                                                                                                                                                                                                                                                                                    577
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o. le+02;
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                                                                                                                                                       Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                    ĀΑ
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                                                                                                                                                                                                                                                                          update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 575;
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    , Ishii
Fukuda
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  s :
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RESULT 49
Q9FL63
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             DAGE OF THE PROPERTY OF THE PR
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RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Klehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Riug B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Riug B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Riug B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Riug B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Riug B., Ringwald M., Rodriguez I., Sakamoto N.,
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RA Nordone P., Riug B., Ringwald M., Rodriguez I., Sakamoto N.,
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Best Local
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InterPro; IPR003600; Ig_like.
InterPro; IPR003600; Ig_MHC.
Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 4.
SMART; SM00400; IG; 4.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
EMBL; AB010696; BAB11570.1; -.
EMBL; AB0106965 BAB11570.1; JOINED.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00560; LRR; 5.
Pfam; PF00069; pkinase; 1.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 11, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor-like protein kinase.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
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                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana features of the regions of 1,381,565 bp cover physically assigned Pl and TAC clones.";
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
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EMBL; AK018613; BAB31307.1;
                                                                                                                                                                                                                                                                                                                                                                                                       physically assigned P1 and DNA Res. 5:131-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaneko T., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98344145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pubmed=9679202;
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edons; core e
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01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 7
765D12A.4 protein.
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EMBL; AC011437; AAF04897.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome III BAC F7018 geno submitted (JAN-2001) to the EMBL/GenBank/DDBJ datab
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 13, Last sequence update)
0
                                                                 Submitted
                                                                                                                                                                                           Rhabditidae; Pel
NCBI_TaxID=6239;
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Rhabditidae; Peloderinae;
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01-MAY-2000
   SEQUENCE FROM N.A.
                                                                                                  Sulston
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
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databases.
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Best Local Similarity
Matches 6; Conser
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Best Local :
                                                                                                     O9RJQ2 PRELIMINARY;
O9RJQ2;
O1-MAY-2000 (TrEMBLrel. 13, C
O1-MAY-2000 (TrEMBLrel. 13, I
O1-JUN-2002 (TrEMBLrel. 21, I
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PROSITE;
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Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacterida
Actinomycetales; Streptomycineae; Streptomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okuyama H., Shimahara Y., Kawada N., Yamaoka Y.;
"Regulation of cell growth by redox-mediated extracellular
of platelet-derived growth factor receptor beta.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF359356; AAK43716.1;
                                                                     Putative sensor kinase. SC00588 OR SCF55.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
PROSITE; PS00240; RECEPTOR_TYR_KIN_III; UNKNOWN_1
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation update)
Platelet-derived growth factor receptor beta (Fragment).
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01-DEC-2001
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6; Conserv
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IPR001824; RTKinaseIII.
IPR001245; Tyr_pkinase.
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62986 MW;
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InterPro; IPR003135; ATP-grasp.
Pfam; PF02222; ATP-grasp; 1.
TIGRFAMS; TIGR01161; purK; 1.
Lyase; Complete proteome.
SEQUENCE 413 AA; 44581 MW; F2
                                                                               O99XK9 PRELIMINARY:
O99XK9
O1-JUN-2001 (TrEMBLrel. 1
O1-JUN-2001 (TrEMBLrel. 1
O1-JUN-2002 (TrEMBLrel. 2
PUTATIVE histidine-trna
HISS OR SPY2157.
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EMBL;
TIGR;
  Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Streptococaceae; Streptococcus.
NCBI_TaxID-1314;
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01-MAR 2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable phosphoribosylaminoimidazole carboxylase Af
protein (EC 4.1.1.21)
PURK OR RSC0576 OR RSC04889.
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Bacteria; Proteobacteria; beta subdivision; Ralstonia
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Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
AE005712; AAK22376.1; -.
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SEQUENCE FROM N.A.
STRAIN=SF370 / ATCC
STRAIN=21192684;
Q97NC9 PRELIMINARY;
Q97NC9;
Q1-OCT-2001 (TIEMBLTel. 18,
Q1-OCT-2001 (TIEMBLTel. 21,
Q1-JUN-2002 (TIEMBLTEL. 21,
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InterPro;
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InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004516; Hiss.
InterPro; IPR004516; Hiss.
InterPro; IPR002314; tRNA-synt_2b.
Pfam; PF03129; HGTP_anticodon; 1.
Pfam; PF00587; tRNA-synt_2b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Peldblyum T.V., Angiuoli S., Dickinson T., Hickey I Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";
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MEDLING-21192684; PUNMed-11296296;

Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,

Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,

Yuan X., Clifton S.W., Roe B.A., McLaughin R.;

"Complete genome sequence of an M1 strainin of Streptococcus pyogenes.";

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

ESEMBL, AE006634; AAK34794.1; -.
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EMBL; AE007501; AAK76180.1;
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MEDLINE=21357209; PubMed=11463916;
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Ligase; Complete proteome.
SEQUENCE 426 AA; 48200 MW; 3E0E3B3FFA9E948B C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                RA Azovedo V. Bertero M.G., Bessieres P., Bolotin A., M., Alioni G.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C. V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S. K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S. K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S. K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S. K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Choi S. K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Choi S. K., Codani J.J., Galleron N.,
RA Chim S.Y., Galser P., Goffeau A., Gollghtly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic C.,
RA Medina N., Mellado R.P., Mazuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moest D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle B., Rapoport G., Rey M., Reynolds S.,
RA Rabert M., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi A., Taconi E., Takagi T., Takahashi H., Takemaru K.,
RA Sato T., Scanlan E., Takagi T., Takahashi H., Takemaru K.,
RA Viari A., Wamanoto H., Vannier F., Vassarotti A.,
RA Viari A., Wandenboh M., Vannier F., Vassarotti A.,
RA Winters P., Wipat A., Vamanoto H., Vannier F., Vassarotti A.,
RA Winter S., Willey M., Vannier E., Wedler H., Weitzeneger T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
Kunst F., Ógasawara N., Yoshikawa H., Danchin A.; submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. EMBL; Y14081; CAA74477.1; -.
EMBL; Z99109; CAB12898.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           007569
007569;
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Bacteria; Firmicutes;
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                                                                                                                         STRAIN=168;
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Submitted (JUN-1997)
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                                                                                                                                             SEQUENCE
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                                                                                                                                                                               390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                    genome sequence of
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100.0%; Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus/Clostridium group; Bacillales;
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Last annotation update)
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Pred. No
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                                                                                                                                                                                                                    gram-positive bacterium
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databases
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ID Q9
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9AB45;
01-JUN-2001
01-JUN-2001
01-MAR-2002
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Q9UFF4;
01-MAY-2000
01-MAY-2000
01-DEC-2001
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.F. Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Ber Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698: PubMed-11259647;
Nierman W.C., Feldblyum T.V., Laub
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical CC0389.
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DKFZP434H071/,

Homo sapiens (Human).

Homo sapiens (Human).

Horia; Metazoa; Chordata;

Horia; Primates;
                                                                                                                                                                                                                                                                                                                                                     Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                        Caulobacter crescentus
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InterPro; IPR002653; Znf_A20;
SMART; SM00259; ZnF_A20; 1.
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Submitted (OCT-1999)
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                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=155892;
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TISSUE=TESTIS;
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6; Conserv
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l (TrEMBLrel. 17, 1
2 (TrEMBLrel. 20, 1
al protein CC0389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                             alpha subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment)
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Mismatches
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No.
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                                                                                                                                                                                                                                                                                                                                                                          Caulobacter group;
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                                                                                                                                                                         Nelson K.E.,
                                                                                                           k J.R.,
N.D., Ely B.,
                                                           Berry K.,
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                                                                                               "Retrotransposable elements o submitted (DEC-1998) to the EIEMBL; AF114171; AAD27563.1; -Hypothetical protein.
SEQUENCE 343 AA; 38484 MW;
                                                                                                                                                                                                                                                                                                                                   Q9XEP5
Q9XEP5
Q9XEP5;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-NOV-1999 (TrEMBLrel. 13, Last annotation update)
Q1-NOV-1999 (TrEMBLrel. 13, Last annotation update)
Hypothetical 38.5 kDa protein.
Sorghum bicolor (Sorghum) (Sorghum vulgare).
Sorghum bicolor (Sorghum) (Sorghum vulgare).
Sorghum bicolor (Sorghum) (Sorghum vulgare).
Spermatophyta; Magnollophyta; Lillopsida; Poales; Proceedings (Poales)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q856J9;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence u
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                                                                                                                                                                                                                         SEQUENCE FROM N.A. Llaca V., Lou A.,
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                                                                                                                                                                                                                                                                                               Panicoideae; Andropogoneae;
NCBI_TaxID=4558;
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315 AA; 36447 MW;
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  40.0%; S llarity 100.0%; Conservative 0;
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                                                                                                  38484 MW;
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                                                                                                                                                  , Messing J.;
s of Sorghum bicolor.
e EMBL/GenBank/DDBJ c
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; Poales; Poaceae;
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01-DEC-2001
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                                                                                                                                                                                                                                             Bindslev L.;
Thesis (2001), Department of Molecular University of Copenhagen, Copenhagen, D EMBL; AJ304829; CAC19660.1; -.
HSSP; P00515; 2APK.
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01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Bahr U., Darai G.;
"Analysis and Characterization of
Shrew) Herpesvirus.";
J. Virol. 75:4854-4870(2001).
PRINTS; PRO0103; CAMPKINASE.

SMART; SM00100; CNNP; 2.

PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; PROSITE; PS00888; CNMP_BINDING_1; 1.

PROSITE; PS00889; CNMP_BINDING_2; 2.

PROSITE; PS50042; CNMP_BINDING_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                    Blumeria graminis.
Eukaryota; Fungi; Ascomycoi
Erysiphales; Erysiphaceae;
NCBI_TaxID=34373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9HEP7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9HEP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Betaherpesvirinae.
NCBI_TaxID=10397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91TQ6
                                                                                                                                               InterPro; IPR000515; BPD_transp.
InterPro; IPR002373; CAMP_kin.
InterPro; IPR000295; CNMP_binding
Pfam; PF00027; CNMP_binding; 2.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKA regulatory subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tupaia herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ascomycota; Pezizciphaceae; Blumeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.0%;
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Last sequence up
Last annotation
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Last sequence uplast annotation
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pezizomycotina;
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RESULT
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Best Local
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Remillard P.E., Lacroix D.A.

Remillard (FEB-2001) to the

Submitted (FEB-2001) to the

-!- SUBCELLULAR LOCATION: TO

-!- SIMILARITY: BELONGS TO
            STRAIN-ATCC 1908) / CB15;

MEDLING-21173698; pubMed-11259647;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vanathevan J., Ermolaeva M., White (
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21, Exodeoxyribonuclease III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
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HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000001; Euk_pkinase;
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Platelet-derived growth
                                                                                                                                                                                                                                                                                                                                                                              Caulobacter crescentus
Bacteria; Proteobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9A6S2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9823; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9A6S2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BDK8;
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    AE005874; AAK23986.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF347051; AAK31152.1; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                       Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000719; Euk_pkinase.
IPR001824; RTKinaseIII.
IPR002290; Ser_thr_pkin
IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259
259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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2001) to the EMBL/GenBank/DDBJ databases.
LOCATION: TYPE I MEMBHANE PROTEIN (BY SIMILARITY).
BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259
28776
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17, Last sequence update)
21, Last annotation update)
factor receptor beta (Fragm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 52 
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                            subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
52;
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                                                                                                                                                                                                                                                                                                                                                                            Caulobacter group;
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RESULT 33
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Best Local :
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Q9R146;
01-MAY-2000 (TIEMBLIFEL 13, C
01-MAY-2000 (TIEMBLIFEL 13, L
01-JUN-2002 (TIEMBLIFEL 21, L
Hypothetical protein SCO0200.
SCO0200 OR SCJ12.12C.
                                                                                     STRAIN-A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins I
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor
warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.
       EMBL; AL109989; CAB53424.1; InterPro; IPR000041; Usp. Pfam; PF00582; Usp; 2.
                                           "Complete genome sequence coelicolor A3(2).";
Nature 417:141-147(2002).
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InterPro; IPR004042; ExoDNase_III.
InterPro; IPR004088; ExoIII_xth.
InterPro; IPR005135; Exo_endo_phos.
Pfam; PF03372; Exo_endo_phos; 1.
TIGRFAMs; TIGR00195; exoDNase_III; 1.
TIGRFAMs; TIGR00533; xth; 1.
PROSTTE; PS00728; AP_NUCLEASE_F1_3; UNKNOWN_1.
                                                                                                                                                                                                                                                                  Redenbach M., Kieser H.M.
Kinashi H., Hopwood D.A.;
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Actinomycetales; Streptomycineae;
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A Salanoubat M., Genin S., Arriguenave F., Camus J.C., Cattolico L.,
A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
A Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
RY "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RI Nature 415:497-502(2002).
DR RABL; AL646062; CAD14780.1; -.
DR InterPro; IPR000524; HTH_GntR.
DR PRINTS; PR00035; HTHGNTR.
DR PRINTS; PR000345; HTH_GNTR.; 1.
DR PROSITE: PS000443; HTH_GNTR.FAMILY; 1.
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O1-OCT-2001 (TremBLrel. 1
O1-OCT-2001 (TremBLrel. 1
O1-JUN-2002 (TremBLrel. 2
          ŚEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
MEDLINE-21082930; PubMed-11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kat
Kaneko T., Nakamura Y., Ishikawa A., Kawashima
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable transcriptional regulatory DNA-binding transcription
regulator protein
RSC1078 OR RSO4109.
                                                                                                                                                                                                                                                               Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision;
Phyllobacteriaceae; Mesorhizobium.
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Bacteria: Proteobacteria; beta subdivision; Ralstonia
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AC 092TU9;
AC 092TU9;
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable exodeoxyribonuclease III protein (EC 3.1.11.2).
DE Probable exodeoxyribonuclease III protein (EC 3.1.11.2).
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymB (megaplasmid 2).
OG Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OG Bacteria; Sinorhizobium.
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Interpro; IPR000097; APendonclsel.
Interpro; IPR004442; EXDDNsse_III.
Interpro; IPR0044489; EXOIII.xth.
Interpro; IPR005135; EXO_endo_phos.
Interpro; IPR005135; EXO_endo_phos.
Pfam; PF03372; EXO_endo_phos; 1.
TIGRFAMS; TIGR00195; exoDNsse_III; 1.
TIGRFAMS; TIGR00633; xth; 1.
PROSITE; PS00726; AP_NUCLEASE_F1_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                              PROSITE; PS00726; AP NUCLEASE F1_1; UNKNOWN_1.
Hydrolase; Plasmid; Complete proteome.
SEQUENCE 257 AA; 28866 MW; 162ABFBF88DC033
                                                                                                                                                                                                                                                                       Pfam; PF03372; Exo_endo_phos; 1. TIGRFAMS; TIGR00195; exoDNase_III; 1. TIGRFAMS; TIGR00633; xth; 1.
                                                                                                                                                                                                                                                                                                                                             fixing endosymbiont Sinorhizobium meliloti.";
proc. Natl. Acad. Sci. U.S.A. 98:9899-9894(2001).
EMBL; AL603646; CAC49796.1;
InterPro; IPR000097; APendoncisel.
InterPro; IPR0040442; EXODNASe_III.
InterPro; IPR0040818; EXOII_Xth.
InterPro; IPR005135; EXO_endo_phos.
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MEDLINE-93124536; PubMed-8419636;

Gessain A., Boeri E., Yanagihara R., Galio R.C., Franchini v.,

"Complete nucleotide sequence of a highly divergent human T-cell
leukemia (lymphotropic) virus type I (HTLV-I) variant from melanesia:
genetic and phylogenetic relationship to HTLV-I strains from other
geographical regions.";
J. Virol. 67:1015-1023(1993).

J. Virol. 67:1015-1023(1993).

NR 15: Length 240;
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Q1-DEC-2001 (TrEMBLrel. 19,
Q1-DEC-2001 (TrEMBLrel. 19,
Q1-DEC-2001 (TrEMBLrel. 19,
Similar to NGFI-A binding p
                                                                                                                                Eukaryota; Metazo
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NCBI_TaxID=9606;
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Human T-lymphotropic virus
Viruses; Retroid viruses; F
NCBI_TaxID=11908;
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EMBL; L41677; AAA98640.1; -
SEQUENCE 216 AA; 23977 M
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MEDILINE-95297146; PubMed=7539968;
Ciminale V., D'Agostino D.M., Zotti L., Franchini G., Felber B.K.,
Chieco-Bianchi L.;
"Expression and characterization of proteins produced by mRNAs splinto the X region of the human T-cell leukemia/lymphotropic virus
                                   TISSUE-MUSCLE;
                                                                       SEQUENCE FROM N.A.
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Best Local :
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                                                                                                                                                                                                                                                                              01-NOV-1996
01-NOV-1996
01-DEC-2001
                                 genome of LIL20/1)."
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                                           SEQUENCE FROM N.A.
STRAIN-MALAWI LIL20 /1;
DIXON L.K., Twigg S.R.F., Baylis S.A., V
Hammond J.M., Smith G.L.;
"Nucleotide sequence of a 55 kbp region
genome of a pathogenic African swine fev
                                                                                                                      "Duplicated genes within the variable right end of pathogenic isolate of African swine fever virus."; J. Gen. Virol. 74:2125-2130(1993).
                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-MALAWI LIL20 /1;
MEDLINE-94014996; PubMed-8409937;
                                                                                                                                                                                                                                                                                                                  Q65226;
Q65226;
          J. Gen. Virol. 7:1655-1684(1994).
EMBL; X71982; CAA50817.1; -
                                                                                                                                                                                                                                           African swine fever virus (
Viruses; dsDNA viruses, no
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
PX-TAX-ORF II fusion protein.
Human T-lymphotropic virus 1.
Viruses; Retroid viruses; Retroviridae; Deltaretr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC007756; AAH07756.1; -. SEQUENCE 241 AA; 25927 MW; DEF799BD103ED93C CRC64;
SEQUENCE
                                                                                                                                                                                                                                                                    ORF 14L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Protein isoforms encoded by the px region of human T-cell leukemia/lymphotropic virus type I.";
Proc. Natl. Acad. Sci. U.S. A. 89:8813-8817(1992).
SEQUENCE 241 AA; 26791 MW; 7607F1F66C55CF5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=92409607; PubMed=1528897;
                                                                                                                                                                                                                              NCBI_TaxID=10497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Franchini G.;
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 RSTPES
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6; Conservative
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DEF79E4705EE9FE1 CRC64;
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                                                                                                                                                         Dixon L.K.;
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                                                                                 Bristow
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REGULATORS.
EMBL; AF315580; AAK28495.1;
InterPro; IPR000485; ASNC_trans_reg.
Pfam; PF01037; ASNC_trans_reg; 1.
PRINTS; PR00033; HTHASNC; 1.
PRINTS; SM00344; HTH_ASNC; 1.
SMART; SM00344; HTH_ASNC; 1.
DNA-binding; Transcription regulation.
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Q9AHF1;
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9RRC1 PRELIMINARY; PRT; 168 AA.

O9RRC1;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MOLYDdenum cofactor biosynthesis protein C.
                                   STRAIN-R1;
STRAIN-R1;
MEDLINE-20036896; PubMed=10567266;
MEDLINE-20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Atavind L., Daly M.J., Minton K.W., Fleischmann R.E.
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Fraser C.M.;
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microbiology 147:1815-1824(2001).
-!- SIMILARITY: BELONGS TO THE ASNC FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae Rhizobiaceae; Rhizobium.
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Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Thermus/Deinococcus Deinococcaceae; Deinococcus.
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       "Genome sequence of
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                                                                                                                                                                                                                                                             J.D.,
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TIGR; DR2571; -.
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Pfam; PF01967; Moac; 1.
TIGRFAMs; TIGR00581; moac; 1.
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InterPro; IPR000345; CytC_heme_bind.
Pfam; PF01037; ASNC_trans_reg; 1.
PRINTS; PR00033; HTHASNC.
SMART; SM00344; HTH_ASNC; 1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
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EMBL; AL646080; CAD17796.1; -.
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01-MAR-2002 (TIEMBLIEL 20, Last sequence
01-JUN-2002 (TIEMBLIEL 21, Last annotati
Probable transcription regulator protein.
RSP0645 OR RS05577.
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Q9PXY6
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                  SEQUENCE
                                                                                                                                               Hypothetical protein CHAIN 5 1:
                                                                                                                                                                                                                                                           Desmyter J., Vandamme A.M.;
"The simian T-lymphotropic virus STLV-Pp1664 from Pan paniscus distinctly related to HTLV-2 but differs in genomic organization."
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J. Virol. 67:1015-1023(1993).
SEQUENCE 87 AA; 9988 MW; 34A239AC7EE7D9CD CRC64;
                                                                                                                                                                                                Virology 243:366-379(1998).
EMBL; Y14570; CAA74907.1;
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98229455; PubMed=9568035;
Van Brussel M., Salemi M., Liu H.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Protein isoforms encoded by the pX region of human leukemia/lymphotropic virus type 1."; Proc. Natl. Acad. Sci. U.S.A. 89:8813-8817(1992). SEQUENCE 87 AA; 10080 MW; 12DDEDBD6838B277 CRC64
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Human T-lymphotropic virus 1.
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus
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                                                                                                     POTENTIAL.; 23EC3D95B410CBAE CRC64;
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01-MAR-2002 (TremBirel 20, La
Hypothetical protein RA0220.
RA0220 OR SMA0412.
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Q9XX29;
01-NOV-1999 (TrEMBLrel. 12, C.
01-NOV-1999 (TrEMBLrel. 12, L.
01-DEC-2001 (TrEMBLrel. 19, L.
Y39ALA.18 protein.
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Q1-DEC-2001
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                                   "Genome seque...;
investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL031633; CAA21011.1;
EMBL; AL031633; CAA21011.1;
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MEDLINE-2136509; PubMed-11481432;
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells I
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBL; AE007215; AAK64878.1;
EMBL; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=99069613;
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Chennan M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Waynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYONIC I
MEDLINE-21085660; PubMed-11217851;
MEDLINE-21085660; PubMed-11217851;
MEDLINE-21085660; PubMed-11217811;
MEDLINE-21085660; PubMed-11217811;
MEDLINE-21085660; PubMed-1121781;
MEDLINE-21085660; PubMed-11217
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Mus musculus (Mouse).

Mus musculus (Mouse).

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O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
16 days embryo lung cDNA, RIKEN full-length enriched clone:8430430D21, full insert sequence (Fragment).
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Hypothetical protein
SEQUENCE 959 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a fu
Nature 409:685-690(2001).
EMBL; AKO18451; BAB31219.1; -.
MGD; MGI:88393; Chd1
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                              (TremBLrel. 04, Created)
(TremBLrel. 04, Last sequence update)
(TremBLrel. 21, Last annotation update)
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13;
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Q80794;
Q1-NOV-1996
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Q9PXZ8;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                        P13 II protein.
Human T-lymphotropic viru:
Viruses; Retroid viruses;
NCBI_TaxID=11908;
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Simian T-lymphotropic virus 1.
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus NCBI_TaxID=33747;
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      SEQUENCE FROM N.A. MEDLINE-93124536; Gessain A., Boeri
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Verschoor E.J., Warren K., Niphuis H.,
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                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
   PubMed=8419636;
E., Yanagihara
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Best Local S
Matches 7
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Best Local
                                          01-JUN-2002
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                                                                                                                       Q8S6U7
Q8S6U7;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative transcriptional regulator, LacI family pro
RB0557 OR SMB20817.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Plasmid pSymB (megaplasmid 2).
Bacteria: Proteobacteria; alpha subdivision; Rhizob
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SMART; SM00354; HTH_LACI; 1.

PROSITE; PS00356; HTH_LACI_FAMILY; UNKNOWN_1.

Hypothetical protein; Complete proteome.

SEQUENCE 343 AA; 37647 MW; CF301E166D2252
                           Putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000843; HTH_LacI.

Pfam; PF00356; lacI; 1.

PROSITE; PS00356; HTH_LACI_FAMILY; UNKNOWN_1.

Plasmid; Hypothetical protein; Complete proteome.

SEQUENCE 343 AA; 37381 MW; 714FF82A41E4522D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fixing endosymbiont Sinorhizobium meliloti."; Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001) EMBL; AL603644; CAC48957.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Golding B., Puehler A., Golding B., Puehler A., "The complete sequence of the 1,683-kb pSymB megaplasmid fixing endosymbiont Sinorhizobium meliloti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=1021;
MEDLINE=21396508; PubMed=11481431;
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DNA Res 7:331-338(2000).
EMBL; AP003007; BAB52218.1; -.
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Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot
Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Similarity 100.0%
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llarity 100.0%;
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CF301E166D225298
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Best Local
                                                                 SEQUENCE FROM 1445;
STRAIN-A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9RL12;
"Complete genome sequence of the coelicolor A3(2).";
Coelicolor A1(2).";
Nature 417:141-147(2002).
EMBL; AL117385; CAB55662.1; -.
InterPro; IPR000157; TIR_domain.
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01-MAY-2000 (TrEMBLrel. 21, L
01-JUN-2002 (TrEMBLrel. 21, L
Hypothetical protein SC00305.
SC00305 OR SC5G9.14.
                                                                                                                                                                                                                                                                             MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite D.,
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-A3(2);
Seeger K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2002) to the EMBL/GenBank/DDBJ EMBL; AC092172; AAM18162.1; -. SEQUENCE 738 AA; 83826 MW; 0626A5AC35C424
                                                                                                                                                                                                                                                                                                             STRAIN-A3(2)
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NCBI_TaxID=1902;
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"Rice Genomic Sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               James K.D.
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(SEP-1999) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomycineae;
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100.0%;
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                                                      Streptomyces
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                                                                                           Taylor K.,
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Best Local S
Matches 7
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Bentley S.D.,
Thomson N.R.,
                                                                                                                                                                                                             VIREB.
Wis musculus (Mouse).
Mus musculus (Mouse).
--harvota; Metazoa; Chordata;
--haria; Rodentia;
                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TREMBLIEL 21, 01-JUN-2002 (TREMBLIEL 21, 01-JUN-2002 (TREMBLIEL 21, Vomeronasal receptor VIRE8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the model coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL: AL590464; CAC36757.1; ...
InterPro; IPR001031; Thioesterase.
Pfam; PF00975; Thioesterase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REDLINE-98241550; PubMed-9573173;
Redenbach M., Ikeda K., Yamasaki M.,
"Cloning and physical mapping of the
linear plasmid SCP1.";
                       Vlr vomeronasal receptors.";
Nat. Neurosci. 5:134-140(2002).
EMBL; AY065508; AAL47913.1; -.
                                                                                  STRAIN=129X1/SVJ;

MEDLINE=21676859; PubMed-11802169;

Rodriguez I. Del Punta K., Rothman

"Multiple new and isolated families
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Tayl
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-A3(2);
Bentley S.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales;
NCBI_TaxID=1902;
    Receptor.
                                                                                                                                                                                                                                                                                                                                                                                               Q8R2A2;
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                                                                                                                                                                     SEQUENCE FROM N.A.
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Pred. No.
                                                                                                                                                                                                                            Craniata; Veri
Sciurognathi;
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EcoRI fragments
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                                                                                                         Ishii T., Mombaerts
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RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., RA Risen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus."; L. Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

REMBL, AE005905; AAK24330.1; -. REMBL, AE00598; IAYY.

REMBL, AC07881 IAYY.
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01-OCT-2001 (
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
N4-(beta-N-acetylglucosaminyl)-L-asparaginase, putative
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                     SEQUENCE FROM N.A. STRAIN=MAFF303099; MEDLINE=21082930;
                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Phyllobacteriaceae; Mesorhizobium
                                                                                                                                                                                                                                  Hypothetical MLL5838.
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Pfam; PF01112; Asparaginase_2;
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Bacteria; Proteobacteria;
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                                                                                                                              NCBI_TaxID=381;
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al protein ml15838.
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  Nakamura
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PubMed-11214968; ra Y., Sato S., A
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b; Pred. No. 5.1
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o. 5.2;
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  Kato T.,
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01-DEC-2001
01-DEC-2001
01-DEC-2001
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                         Ichimura H., Parra H.-J.;
Genetic Subtypes of HIV Type 1 Based on the v
"Genetic Subtypes of HIV Type 1 Based on the v
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
EMBL; AF410445; AAL10246.1; -.

NON_TER 1 1
                                                                                                                                                                                     SEÓUBNCE FROM N.A.
STRAIN-97CG152;
Taniguchi Y., Takehsia J., Bikano
N'Doundou-N'Kodia M.-Y., M'Pandi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Korade Mirnics Z., Keryanov S., Lovelock J., C
"Cloning of chicken presenilins.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; AY043492; AAK95408.1;
InterPro; IPR001108; Presenilin.
Pfam; PF01080; Presenilin; 1.
PFINTS; PR01072; PRESENILIN.
                                     SEQUENCE
                                                                                                                                                                                                                                                                                     Viruses; Retroid
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q905H6
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Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                         Tat protein (Fragment).
Human immunodeficiency virus type 1.
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STRAIN=E14; TISSUE=BRAIN;
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Gallus.
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8; Conservative
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Neognathae; Galliformes; Phasianidae; Phasiani
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100.0%;
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'Pandi M.,
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Last annotation updat
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Last annotation updat
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0; Mismatches
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Pred. No.
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Score 7;
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DB
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BB
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Pele P., Harada Y., Hayami
                                                                                                                                                                                                                                                                                                         Lentivirus
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Length 19;
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Matches
                                                           01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Putative thioesterase, MMYT OR SCP1.241C
                                                                                                                                                                 Q9ACS2
Q9ACS2;
                       Streptomyces coelicolor. Plasmid SCP1.
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EMBO J. 4:1893-1897(1985).
EMBL; AJ276673; CAB82867.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence analysis reveals similarities betweetermining methylenomycin A resistance in Streptomyces tetracycline resistance in eubacteria.";
Gene 58:229-241(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A3(2);
Bruton C.J., Wietzo
"Genes involved in
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00975; Thioesterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001031; Thioesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chater K.F., Bruton C.J.; "Resistance, regulatory and production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=85284984; PubMed=2992952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-A3(2)
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NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                          206 TPESRAA
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Q9ri465 streptomyce
Q8s699 oryza sativ
Q9sep5 soryhum bic
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Q9hep7 blumeria gr
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Q9uf44 homo sapien
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Q8ylyl ralstonia s
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P89211 tomato bush
P89211 toma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9rrc1 deinococcus
Q8xs36 ralstonia s
Q80824 human t-cel
Q9px29 human t-lym
Q96183 homo sapien
Q9pxy7 human t-lym
Q65226 african swi
Q80974 rhizobium n
Q99749 rhizobium n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  070647 simian t-ly
0930h6 rhizobium m
09xx29 caenorhabdi
09ahf1 agrobacteri
09rrc1 deinococcus
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                                                                                                                          Signal;
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PIR; S06046; S06046.
PIR; D28018; D28018.
HSSP; P11215; LABX.
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J. Biol. Chem. 267:1786-1791(1992).

WITHIN THE ALTERNATIVELY SPLICED CS-1 AND CS-5 REGIONS OF FIBRONECTIN. THEY ARE ALSO RECEPTORS FOR VCAM1. INTEGRIN ALPHA-4/BETA-1 RECOGNIZES THE SEQUENCE O-1-D-S IN VCAM1. INTEGRIN ALPHA-4/BETA-7 IS ALSO A RECEPTOR FOR MADCAM1. IT RECOGNIZES THE SEQUENCE L-D-T IN MADCAM1. ON ACTIVATED ENDOTHELIAL CELLS INTEGRIN VLA-4 TRIGGERS HOMOTYPIC AGREEGATION FOR MOST VLA-4-POSITIVE LEUKOCYTE CELL LINES. IT MAY ALSO PARTICIPATE IN CYTOLYTIC T-CELL INTEGRATIONS WITH TARGET CELLS.
                                                                                                                                                                                         InterPro; IPR000413; Integrin_alpha.
Pfam; PF00357; integrin_A; 1.
Pfam; PF01839; FG-GAP; 5.
PRINTS; PR01185; INTEGRINA.
SMART; SM00191; Int_alpha; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takada Y., Strominger J.L., Hemler M.E.;
"The very late antigen family of heterodimers is part of superfamily of molecules involved in adhesion and embryog proc. Natl. Acad. Sci. U.S.A. 84:3239-3243(1987).
                                                                                                                                          SMART; SMOULY1; LUL_____, PROSITE; PSO0240; INTEGRIN_ALPHA; 1.
PROSITE; PSO0240; INTEGRIN_ALPHA; 1.
                                                                                                                                                                                                                                                                                                                                                                      EMBL; X16983; CAA34852.1; EMBL; L12002; AAB59613.1;
                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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MEDLINE=96256895; PubMed=8643114;
Szabo M.C., McIntyre B.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92112902; PubMed-1730718;
Telxido J., Parker C.M., Kassner P.D., Hemler M.E.;
"Functional and structural analysis of VLA-4 integrin alpha 4 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 598-607, AND PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of two variants of the human integrin alpha 4 subunit.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE INTEGERN ALPHA CHAIN FAMII
SIMILARITY: CONTAINS 7 FG-GAP REPEARS.
DATABASE: NAME-PROW; NOTE-CD guide CD49d entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd49d.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA SUBUNIT CAN SOMETIMES BE CLEAVED INTO TWO NON-COVALENTLY ASSOCIATED FRAGMENTS. ALPHA-4 ASSOCIATES WITH EITHER BETA-1 OR BETA-7.
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INTEGRIN ALPHA-4.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
RG-GAP 1.
FG-GAP 3.
FG-GAP 3.
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SEQUENCE FROM N.A.
STRAIN-$288c / FY1679;
MEDLINE-97197982; PubMed-9046098;
WAND DYCK L., Tettelin H., Purnelle B., Goffeau
Van DYCK L., Tettelin H., Purnelle B., Goffeau
"An 18.3 kb DNA fragment from yeast chromosome
unknown open reading frames, the gene for an As
                                                                                                                                                                                                                                                  YG35_YEAST STANDARD; PRT; 1036 AA. P53273; P53273; O1-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Hypothetical 117.0 kDa protein in ASN2-PHB1 in YGR125W OR G6362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Chlamydia trachomatis.
Bacteria; Chlamydiales;
                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeas Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                             YEAST
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InterPro; IPR0024586; RecB.
InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of an obligate intracellular pathogen of Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stephens R.S., Kalman S., Lammel C.J., For Mitchell W.P., Olinger L., Tatusov R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-D/UW-3/Cx;
MEDLINE-99000809;
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Hydrolase; Nuclease; Exonuclease;
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ALL OF THESE ACTIVITIES REQUIRE CONCOMITANT HYDROLYSIS OF AT
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Saccharomycotina; Saccharomycetes;
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63000D548C0F7A33 CRC64;
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2., Koonin E.
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                  synthase,
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Yeast 13:171-176(1997).
i- SUBCELLULAR LOCATION: Integral memb
-i- SIMILARITY: CONTAINS 1 STAS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00916; Sulfate_transp; Pfam; PF01740; STAS; 1. PROSITE; PS50801; STAS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A.

MEDLINE=92201303; PubMed=1551405;

Rubio M., Nueda A., Vara A., Corbi Lopez A.L.;

"A single mRNA encodes the alpha 150 and alpha alpha subunit of VLA4.";
                                                                                                                                                                TGA4.
HOmo sapiens (Human).
-- 'arvota; Metazoa; Chordata; '
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EMBL; 72910; CAA97136.1; -.
SGD; S003357; YSR125W,
InterPro; IPR002645; STAS.
InterPro; IPR001902; Sulfate_transp.
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                                                                                                                 Takada
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                                                                     JNE-89356603; PubMed-2788572;
da Y., Elices M.J., Crouse C., Hemler M.E.;
primary structure of the alpha 4 subunit of VLA-4:
r integrins and a possible cell-cell adhesion functi
J. 8:1361-1368(1989).
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

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RA Dodson K., Doup L.E., Carry N.S., Gelbart W.M., Glasser K.,

RA Dodson K., Doup L.E., Gary N.S., Gelbart W.M., Glasser K.,

RA Dodson K., Doup L.E., Gary N.S., Gelbart W.M., Glasser K.,

RA Dodson K., J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Nelson D.R., Seache J.M.,

Simbson M., Skusski M.P., Smith T.
                                                                                                                                                                                               EMBL; AE003464; AAF47217.1; -.
EMBL; Y10912; CAA71853.1; ALT_E
FlyBase; FBgn0019886; CG4598.
InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 2.
SMART; SM00054; EFh; 2.
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PROSTTE; PS00018; EF_HAND; 2:
Mitochondrion; Calcium-binding; Repeat.
CA_BIND 700 711 EF-HAND 1 (POTENTIAL).
CA_BIND 783 794 EF-HAND 2 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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Mol. Gen. Genet. 261:64-70(1999).

-i- SUBCELLULAR LOCATION: Mitochondrial.

-i- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING

-i- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN
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15-DEC-1998
16-OCT-2001
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Exodeoxyribonuclease V beta chain (EC 3.1.11.5).
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000805; Glyco_hydro_26 Pfam; PF02156; Glyco_hydro_26; 1. PR1mts; PR00739; GLHYDRLASE26.
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Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannosidic linkages in mannans, galactomannans, glucomannans, and galactoglucomannans.
-!- SIMILARITY: BELONGS TO FAMILY 26 OF GLYCOSYL HYDROLASES.
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RESULT
TRP4_BC
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Colcium perwent cation channel. Probably IS OPERATED BY A CALCIUM FORMAN RECEPTOR-ACTIVATED BY RECEPTOR COMPHAIDLINGSTOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN SHOWN TO BE CALCIUM STORE DEPLETION.

COLUMN TO BE CALCIUM STORE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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P79100;
P79100;
P79100;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Short transient receptor potential channel 4 (TrpC4) (Capacitative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                    EMBO J. 15:6166-6171(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                    Philipp S., Cavalle A., Freichel M., Wissenbach U., Zimmer Trost C., Marquart A., Murakami M., Flockerzi V.; "A mammalian capacitative calcium entry channel homologous Drosophila TRP and TRPL.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOVIN
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TISSUE-Adrenal gla:
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SIMILARITY: BELONGS SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d Adrenal gland;
PubMed=8947038;
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               TO THE TRANSIENT RECEPTOR FAMILY.
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Pred. No.
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PTDTVAHEDYVTTRL -> GRQESVLLLQVGEGGGWEDNRP
YYTKGRNTPRCEDSKHIMI (IN REF. 1).
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QHIDRSDLNRQGPPPTIVEWMILPWVL
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H (IN REF. 1).
O (IN REF. 1).
V (IN REF. 1).
R (IN REF. 1).
O (IN REF. 1).
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No. 3.6e+02;
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RESULT 196
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Best Local S
Matches 5
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P9197; OSW16;

30-MAY-2000 (Rel. 39)

16-OCT-2001 (Rel. 40)

16-OCT-2001 (Rel. 40)

16-CCT-2001 (Rel. 40)

Calcium-binding mitoo

ANON-60DA OR CG4589.
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SEQUENCE
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TRANSMEM
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InterPro; IPR000336; M+channel_nlg.
InterPro; IPR002153; Trans_recep.
InterPro; IPR004729; Trp_CaChannel.
Pfam; PF00023; ank; 2.
Pfam; PF00023; ion_trans; 1.
                       Eukaryota; Metazoa; Arthri
Insecta; Pterygota; Neopta
Muscomorpha; Ephydroidea;
MUSI_TaxID=7227;
                                          Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGR00870; PROSITE; PS50088; ANI PROSITE; PS50297; ANI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce,
SEQUENCE FROM N.A
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ANK repeat;
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                                                                                                                                                                                                                                                                           502 SHLGP
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PS50297; ANK_REP_REGION; 1.
annel; Transmembrane; Ion tr
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617
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                                                                                                                                                                                                  STANDARD;
                                                                                                                     11. 39, Created)
12. 40, Last sequence update)
13. 40, Last annotation update)
14. 40, Last annotation anon-60Da.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at; Alternative splicing.

331 CYTOPLASMIC (POTENTIAL).
352 POTENTIAL.
364 EXTRACELLULAR (POTENTIAL).
385 POTENTIAL.
438 CYTOPLASMIC (POTENTIAL).
459 POTENTIAL.
471 EXTRACELLULAR (POTENTIAL).
492 POTENTIAL.
513 CYTOPLASMIC (POTENTIAL).
513 CYTOPLASMIC (POTENTIAL).
514 POTENTIAL.
514 CYTOPLASMIC (POTENTIAL).
524 EXTRACELLULAR (POTENTIAL).
534 POTENTIAL.
513 CYTOPLASMIC (POTENTIAL).
514 EXTRACELLULAR (POTENTIAL).
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
ANK 1.
ANK 2.
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SIMILARITY)
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Pred. No.
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MISSING (IN ISOFORM
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5. 3.6e+02
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Best Local
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1_RAT
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035119; Q9EQ75; Q9EQ74;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Short transient receptor potential channel 4 (TrpC4) (Trp4)
(Capacitative calcium entry channel 1) (CCE1).
                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
VARSPLIC
VARSPLIC
Funayama M., Goto K., Kondo H.; "Cloning and expression localization of cDNA for rat homolog protein, a possible store-operated calcium (Ca2+) channel.";
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TRANSMEM
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TRANSMEM
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TRANSMEM
                                                                     SEQUENCE FROM N.A. (ISOFORM ALPHA). STRAIN-Wistar Imamichi; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM DOMAIN
                                    MEDLINE-97189270; PubMed-9037541; Funayama M., Goto K., Kondo H.;
                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                  TRPC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGREAMS; TIGRO0870; trp; 1.

PROSITE; PS50088; ANK_REPEAT; 1.

PROSITE; PS50297; ANK_REPEAT; 1.

Ionic channel; Transmembrane; Ion transport; Calcium channel;

RNK repeat; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01097; TRNSRE SMART; SM00248; ANK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004729; Trp_CaChannel.
Pfam; PF00023; ank; 2.
Pfam; PF00520; ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF42135
EMBL; U40983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                500
                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>ب</del>
                                                                                                                                                                                                                                                                                                                                                                                                                SHLGP 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHLGP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF421359; AAL24550.1;
U40983; AAC50630.1; -.;
HGNC:12336; TRPC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000636; M+channel_nlg.
IPR002153; Trans_recep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR002110; ANK.
IPR002111; Cat_channel_TrpL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRNSRECEPTRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            693
870
868
                                                                                                                                             Rodentia;
                                                                                                                                                             Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING
MISSING
MISSING
GAMMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 5;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDS TO ITPR1, ITPR2
ESSENTIAL FOR BINDING
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                         Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-LEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77E4D27C374D660E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IN ISOFORM GAMMA).
(IN ISOFORM DELTA).
(IN ISOFORM BETA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Le
                                                                                                                                           Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D ITPR3.
NHERF PDZ DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                    of TRP
                                                                                                                                             Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
   Pfam; PF00023; ank; 2.

Pfam; PF00520; ion_trans; 1.

PfINTS; PR01097; TRNSRECEPTRP.

SMART; SM00248; ANK; 2.

TIGREAMS; TIGR00870; trp; 1.

PROSITE; PS50088; ANK_REP_REGION; 1.

PROSITE; PS50297; ANK_REP_REGION; 1.

Ionic channel; Transmembrane; Ion tran
VARSPLIC
CONFLICT
CONFLICT
                                                                     SITE
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                      TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang Y.,
Zhu M.X.;
                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                         ANK repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002110; ANK.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR000636; M+channel_nlg.
InterPro; IPR002133; Trans_recep.
InterPro; IPR004129; Trp_CaChannel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB008889; BAA23599.1; -. EMBL; AF288407; AAG21809.1; -. EMBL; AF288408; AAG21810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                          REPEAT
                                                                                                                                                             DOMAIN
                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                         TRANSMEM
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                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain-containing protein, NHERF.";
J. Biol. Chem. 275:37559-37564(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Association of mammalian Trp4 and domain-containing protein, NHERF.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dav
MEDLINE=20545496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brain Res. Mol. Brain Res. 43:259-266(1996).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIO1. Chem. 275:37559-37564(2000).

FUNCTION: THOUGHT TO FORM NON-SELECTIVE A RECEPTOR-ACTIVATED CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE TRANSIENT REC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBFAMILY. SIMILARITY: CONTAINS 2 ANK REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION. SUBUNIT: ISOFORM ALPHA BUT NOT ISOFORM BETA ASSOCIATES INOSITOL-1,4,5-TRIPHOSPHATE RECEPTOR (ITPR). INTERACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB008889;
                                                                                                                                                                                                               330
351
363
384
437
458
470
491
512
 784
11
72
                                                                                                                                                                                                                                                                                                                                                                                           Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٦.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daw1
                                                                                                    t; Alternative splicing.
329 CYTOPLASMIC (
350 POTENTIAL.
362 EXTRACELLULAR
383 POTENTIAL.
436 CYTOPLASMIC (
457 POTENTIAL.
469 EXTRACELLULAR
469 POTENTIAL.
511 CYTOPLASMIC (
532 POTENTIAL.
511 CYTOPLASMIC (
532 POTENTIAL.
512 CYTOPLASMIC (
532 POTENTIAL.
513 CYTOPLASMIC (
532 POTENTIAL.
510 CYTOPLASMIC (
532 POTENTIAL.
511 CYTOPLASMIC (
532 POTENTIAL.
512 POTENTIAL.
513 POTENTIAL.
514 ANK 1.
5170 ANK 2.
5170 ANK 2.
5170 ANK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=10980202;
867
11
76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _Trp_CaChannel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO THE TRANSIENT RECEPTOR FAMILY. STRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trost
MISSING (IN ISOFORM BETA).
N -> D (IN REF. 1).
TALLI -> GLLFSL (IN REF. 1
                                                                                        BINDS TO IT
SIMILARITY)
                                                                       ESSENTIAL FOR BINDING
                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                  POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
EXTRACELLULAR
                                                     (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                            Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c.,
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                                                                                                        ITPR1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA)
                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SHOWN H
                                                                                                                                                                                                                                                                                                                                                                                                            Calcium channel;
                                                                                                        ITPR2 AND ITPR3
 (IN REF. 1).
                                                                       TO NHERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HERE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li M., Ramesh V.,
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AND

BETA;

WITH S

NHERF

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Best Local S
Matches 5
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SMART; SM00240; ANK; 2.
TIGREAM9; TIGRO0870; trp; 1.
PROSITE; PS50088; ANK_REPEAT; FALSE_NEG.
PROSITE; PS50297; ANK_REP_REGION; FALSE_PROSITE; PS50297; ANK_REP_REGION; ANTERPREGION; ANTERPREGION; ANTERPREGION; ANTERPREGION; ANTERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR0003636; M-channel_nlg.
InterPro; IPR002153; Trans_recep.
InterPro; IPR002153; Trans_recap.
InterPro; IPR004729; Trp_Cachannel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
DOMAIN
TRP4_HUMAN STANDARD; PRT; 977 AA. 09UBN4; Q9UIB2; Q9UIB0; Q9UIB1; Q15721; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Short transient receptor potential channel 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
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DOMAIN
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EMBL; AF060117; AAF02200.1; -.
EMBL; AJ006204; CAA06912.1; -.
MGD; MGI:109524; Trrp5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00023; ank; 2.
Pfam; PF00520; ion_trans; 1.
PRINTS; PR01097; TRNSRECEPTRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANK repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ionic
                                                                                                                                                                                                                                                                                                501
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SUBCELLULAR LOCATION: Integral membrane protein (Probable).
TISSUE SPECIFICITY: EXPRESSED IN BRAIN. VERY LOW LEVELS DET
IN LIVER KIDNEY, TESTIS, AND UTERUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS
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SUBUNIT: INTERACTS WITH NHERF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                SHLGP
                                                                                                                                                                                                                                                                                                                                                      SHLGP 5
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100.0%; 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-ARG.
ESSENTIAL FOR BINDING
(BY SIMILARITY).
N-LINKED (GLCNAC...
NF9248168D3D2D62
                                                                                                                                                                                                                                                                                                                                                                                                            Score 5; DB 1
Pred. No. 3.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANK
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CYTOPLASMIC (POTENTIAL).
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      (TrpC4) (trp-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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McKay R.R., Sz
Juengling E.,
"Cloning and e
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Cell 85:661-671(1996).
-I- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATION NON-CETTORITY
                                                              EMBL;
                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21671347; PubMed-11713258; Schaefer M., Plant T.D., Stresow N., & "Functional differences between TRPC4 J. Biol. Chem. 277:3752-3759(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mery L., Magnino F., Schmidt K., Krause K.-H., Dufour J.-F.; "Alternative splice variants of hTrp4 differentially interact with the C-terminal portion of the inositol 1,4,5-trisphosphate receptors."; FEBS Lett. 487:377-383(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRP3
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                 EMBL;
                                                                                                            or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96234226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21099836; PubMed=11163362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               iochem.
                                                                                                                                                                                                                                                                                    SIMILARITY).

SUBCELLULAR LOCATION: Integral membrane protein (Proba ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA (SHOWN HERE), AND GAMMA; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: STRONGLY EXPRESSED IN PLACENTA. EX LOWER LEVELS IN HEARP, PANCREAS, KIDNEY AND BRAIN. ISO WAS FOUND TO BE THE PREDMINANT ISOFORM. ISOFORM BETA
                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE CALCIUM PERMEANT CATION CHANNEL, PROBABLY IS OPERATED BY A PROSPHATIDALINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY), MAY ALSO BE ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.
SUBUNIT: ISOFORM ALPHA BUT ISOFORM BETA ASSOCIATES WITH INOSITOL-1,4,5-TRIPHOSPHATE RECEPTOR (ITPR). INTERACTS WITH NHERE (BY
                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 2 ANK REPEATS
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SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X., Jiang
                                                                                                                                                                                                                                                                              FOUND IN PANCREAS
 AF063822;
AF063823;
AF063824;
AF063825;
AF175406;
AF421358;
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                                                                                                                           requires
                                                                                                         equires a license agreement (See email to license@isb-sib.ch).
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Lueckhoff A., Putney J.W. Jr.;
de xyression of the human transient receptor potential 4
li localization and functional expression of human TRP4 ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351:735-746(2000).
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AAF22927.1;
AAF22928.1;
AAF22929.1;
AAF22930.1;
AAD51736.1;
AAL24549.1;
                                                                                                                                                                                                                                                                 BELONGS
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Peyton M., Boul
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                                                                                                                                                                                                                                                                 RECEPTOR FAMILY. STRPC
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                                                                                                                                                      as its content is
                                                                                                                           http://www.isb-sib
                                                                                                                                       Usage
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                                                                                                                                                                                                                                                                                                               ISOFORM
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16-0CT-2001
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRPC5 OR TRP5.

Oryctolagus cuniculus (Rabbit).

Oryctolagus cuniculus (Chordata; Craniata; Vertebrata; Lu.

Tannmorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01097; TRNSRECEPTRP. SMART; SM00248; ANK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Philipp S., Hambrecht J., Braslavski L., Schroth Murakami M., Cavalle A., Flockerzi V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Capacitative calcium entry channel 2) (CCE2)
TRPC5 OR TRP5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98353453; PubMed=9687496;
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SUBUNIT: INTERACTS WITH NHERF (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein (Probable).
TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN.
SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
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PF00520; ion_trans;
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                                                                                                                                                                                                                                                                                                                                                                       PS50088; ANK_REPEAT; FALSE_NEG.
PS50297; ANK_REP_REGION; FALSE_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR004729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002153;
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CYTOPLASMIC
                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                              POTENTIAL
                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                        POTENTIAL.
EXTRACELLULAR
                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                        POTENTIAL.
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                      Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                       FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CCE2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      974 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed
                                                                                                                                                                                                                                                                                                                                                      Calcium channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrpC5) (Rtrp5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Freichel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
                                                                                                                                                                                                                                                                                                 [3]
SEQUENCE FROM N.A.
MEDLINE=20545496; F
        "trp, a novel mammalian gene family essential for agonist-activat capacitative Ca2+ entry.";
Cell 85:661-671(1996).
-1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE CALCIUM PERMEANT CATION CATION LECOND MESSENGER SYSTEM ACTIVATED BY REPROSEMATIDLYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RESTROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9QXZ9; Q9ROD4; Q9QWT1; Q61059;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
short Transient receptor potential channel 5 (receptor protein 5) (Mirp5) (trp-related protein protein 5)
                                                                                                                                                                                  Philipp S., Hambrecht J., Braslavski
Murakami M., Cavalle A., Flockerzi V.
                                                                                                                                                                                                                                                        "Association of mammalian trp4 and ph domain-containing protein, NHERF."; J. Biol. Chem. 275:37559-37564(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SITE
                                                                                           Birnbaumer
                                                                                                                            SEQUENCE OF 515-637 FROM N.A.
                                                                                                                                                    емво ј.
                                                                                                                                                               cells
                                                                                                                                                                                                           MEDLINE=98353453; PubMed=9687496;
                                                                                                                                                                                                                        TISSUE-Brain
                                                                                                                                                                                                                                 SEQUENCE OF 1-966 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Zhu X., Peyton M., "Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning receptor-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calcium entry channel 2 TRPC5 or TRRP5 OR TRP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                MEDLINE-96234226;
                                                                                                                                                                           "A novel
                                                                                                                                                                                                                                                                                         Zhu M.X.
                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRP5_MOUSE
                                                                                                   thu X., Jiang M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Imoto K., Mori Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98221157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501
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                                                                                                                                                  17:4274-4282(1998).
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5; Conser
                                                                                                                                                                        capacitative calcium entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimizu S.,
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974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       972
                                                                                                                                                                                                                                                                                                                                                                                                         ning and functional characterization of ated TRP Ca2+ channel from mouse brain.' 273:10279-10287(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                    Peyton M.,
                                                                                                                                                                                                                                                                                                     PubMed=10980202;
Chen Z., Trost C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9553080;
S., Wakamori M.,
                                                                                                                 PubMed-8646775;
                                                                                                                                                                                                                                                                                                                                                Boulay B., Birnbaumer B.; and functional expression of the EMBL/GenBank/DDBJ
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111536
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100.0%; Pr
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2) (CCE2).
                                                                                                                                                                                              Braslavski L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (trp-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 5; DB 1
Pred. No. 3.6
0; Mismatches
                                                                                                     Boulay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESSENTIAL FOR BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
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No.
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                                                                                                   G., Hurst
                                                                                                                                                                                                                                                                                                     Flockerzi V., Li M., Ramesh V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     975
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0;
                                                                                                                                                                                               Schroth
                                                                                                                                                                                                                                                                                                                                                                                                                      mouse brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Α.,
                                                                                                                                                                          expressed
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                                                                                                                                                                                                                                                                                                                                                             of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrpC5) (Transient
cein 5) (Capacitative
                                                                                                     R.,
                                                                                                                                                                                                                                                                                                                                                    databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 974
                                                                                                                                                                                                                                                                                                                                                             mouse TRP5.";
                                                                                                                                                                                              G.,
                                                                                                                                                                                                                                                                                C
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                                                                             agonist-activated
                                                                                                     Stefani
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                       RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                a PDZ
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RESULT 190
TRP4_MOUSE
    agonist-dependent vasorelaxation in TRP4-/- mice.";

Nat. Cell Biol. 3:121-127(2001).

-I- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION. TRPC4 DEFICIENT MICE LACK A STORE-OPERATED CALCIUM ENTRY IN ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRP4_MOUSE STANDARD; PRT; 974 AA.

090U05; 090ZC0; 090Z09; 062350;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Short transient receptor potential channel 4 (TrpC4) (Receptor-activated cation channel TRP4) (Capacitative calcium entry channel
                                                                                                                                                                                                                              Freichel M., Suh S.H., Pfeifer A., Schweig U Weissgerber P., Biel M., Philipp S., Freise Hofmann F., Flockerzi V., Nilius B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Association of mammalian trp4 and phospholipase domain-containing protein, NHERF.";
J. Biol. Chem. 275:37559-37564(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qian F., Philipson L.H.;
Submitted (MAR-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                   Drosophila trp and evidence homologues.";
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96003894; PubMed=7575478;
Petersen C.C.H., Berridge M.J., Borgese M.F., Bennett D.L.;
"Putative capacitative calcium entry channels: expression o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRPC4 OR TRRP4
                                                                                                                                                                                                                     "Lack of an endothelial store-operated Ca2+ current impairs
                                                                                                                                                                                                                                                                           MEDLINE=21113116; PubMed=11175743;
                                                                                                                                                                                                                                                                                                                         Biochem. J.
                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 505-642 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS ALPHA AND MEDLINE=20545496; PubMed=10980202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NeuroReport 9:507-515(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oka H., Oba A., Ikenaka K., Kurose "Differential distribution of TRP yrain.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98171352; PubMed=9512398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA)
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M.X.;
SUBUNIT: ISOFORM ALPHA BUT NOT ISOFORM INOSITOL-1,4,5-TRIPHOSPHATE RECEPTOR (INTERACTS WITH NHERF: SUBCELLULAR LOCATION: Integral membrane ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boulay G., Ji
s involved in
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                                                                                                                                                                                                                                                                                                                         311:41-44(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J., Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N., Okada T., Wakamori M., Imoto K., Ikenaka K., Kurosaki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jiang M., Birnbaumer L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                 lum entry channels: expression
for the existence of vertebra
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Sciurognathi; Muridae;
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                membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flockerzi V.,
 ALPHA
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                                          RM BETA
(ITPR)
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 protein (Probable). (SHOWN HERE) AND BETA;
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                                           ASSOCIATES WITH (BY SIMILARITY)
                                                                                                                                                                                                                                                Droogmans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isozymes with a
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Best Local S
Matches
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InterPro; IPR004729; Trp_CaChannel.
Pfam; PF00520; ton_trans; 1.
Pfam; PF00520; ton_trans; 1.
PRINTS; PR01097; TRNSRECEPTRP.
SMART; SM00248; ANK; 2.
TIGREAMS; TIGR00870; trp; 1.
PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                       VARSPLIC
CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                 SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002110; ANK.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR000636; M+channel_nlg.
InterPro; IPR002153; Trans_recep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement
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I- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF011543; AAD110167.1; U50922; AAC05179.1; U50922; AAC05179.1; U50921; AAC05178.1; U50921; AAC05178.1; AF019663; AAD10168.1; AAC0667; AAC0518.1; U50667; AAC0518.1; U5067; AAC0518.1; U50667; AAC0518.1; U50667; AAC0518.1; U50667; AAC0518.1; U5067; 
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                                                                                                                                    Score 5; I
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MISSING (IN ISOFORM BETA).
E -> K (IN REF. 3).
R -> L (IN REF. 3).
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ESSENTIAL FOR BINDING TO NHERF PDZ
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2D0BB2F235F5F8D1 CRC64;
                                                                                                                Mismatches
                                                                                                                                 DB 1; Lo
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RESULT 191 TRP5_RABIT

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RESULT 189
TRP5_HUAN
ID TRP5_H
AC 09UL62
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT Short
GN TRPC5
OS Homo s
OC Eukary
OC Mammal
OX NCBI_T
RN [1]
RN [2]
RR SEQUEN
RC TISSUE
RX MEDLIN
RA SOSSey
RA Hane E
RT Molec
RT Pomolc
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  Genomics [2]
                                                                                                                                                                                              TRP5_HUMAN STANDARD; PRT; 973 AA.

99UL62; 075233; 09Y514;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Short transient receptor potential channel 5
TRPC5 OR TRP5.

Homo sapiens (Human).
                                         TISSUE-Fetal brain;
MEDLINE-99425273; PubMed=10493832;
MEDLINE-99425273; PubMed=10493832;
Sossey-Alaoui K., Lyon J.A., Jones L., Abidi F.E., Hartung A.J.,
Hane B., Schwartz C.E., Stevenson R.E., Srivastava A.K.;
"Molecular cloning and characterization of TRPC5 (HTRP5), the human homologue of a mouse brain receptor-activated capacitative Ca(2+)
                                entry channel."
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000967; Znf_NEX1.
InterPro; IPR001841; Znf_ring.
Pfam; PF01422; zf-NR-X1; 5.
Pfam; PF01424; R3H; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andre B., Iraqui Houssaini I., Urrestarazu L.A., Vissers Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO DROSOPHILA SHUTTLE CRAFT PROTEIN (STC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00393; R3H;
SMART; SM00184; RING;
SMART; SM00438; ZnF_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
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                                                                                                                               EQUENCE FROM N.A.
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M00438; ZNF_NFX; 7.
PS00518; ZF_RING_1;
PS50089; ZF_RING_2;
                 60:330-340(1999)
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Pred. No. 3.6
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7 X APPROXIMATE
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No. 3.6e+02;
0;
                                                                                                                                                                                                                           (TrpC5) (Htrp-5) (Htrp5).
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DOMAIN
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
FUNCTION: THOUGHT TO FORM A RECEPTOR ACTIVATED BY A PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.
SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY).
SUBGUNIT: INTERACTS WITH NHERE (BY SIMILARITY).
SUBGUNIT: INTERACTS WITH NHERE (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein (Probable).
                                                                                                                                                                                                                                                                                                                                                                          pfam; PF000023; ank; 2.
Pfam; PF00520; ion_trans; 1.
PRINTS; PR01097; TRNSRECEPTRP.
SMART; SM00248; ANK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF054568; AAF00002.1; -. EMBL; AC005191; AAC24563.1; -. EMBL; AL049563; CAB44737.1; -.
                                                                                                                                                                                         TRANSMEM
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                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                ANK repeat;
                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50088; ANK_REPEAT; FAL: PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGR00870;
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002110; ANK.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR000315; M+channel_nlg.
InterPro; IPR002153; Trans_recep.
InterPro; IPR004729; Trp_Cachannel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
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SIMILARITY: BELONGS
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                           Similarity
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                            Conservative
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491
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                                                                                                                                                                                                                                                                                                                 Glycoprotein
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                                      100.0%;
                                                   33.3%;
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                           0;
                           Score 5; DB:; Pred. No. 3.6
0; Mismatches
                                                                         ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
1; FBC8CBF17BE42166 CRC64;
                                                                                                                             ANK
                                                                                                                                        CYTOPLASMIC ANK 1.
                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                    POTENTIAL.
CYTOPLASMIC
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                                      DB 1; Les
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                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                              (POTENTIAL)
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                                                  Length 973;
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719

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KINL_LEICH
ID KINL_L
AC P46865
AC P16865
DT 01-NOV
DT 01-NOV
DT 01-OCT
DE Kinesi
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UVRA_PASMU
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                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conser
          01-NOV-1995 ()
01-NOV-1995 ()
01-OCT-1996 ()
Kinesin-like )
                                                    KINL_LEICH
P46865;
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ZN_FING
ZN_FING
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p57979;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last seq
16-0CT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UVRA OR PM1951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Pm70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21145866; PubMed-11248100;
                                                                                                                                                                                                                                                             DNA-binding;
                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                               TIGRFAMS;
                                                                                                                                                                                                                                                                                                         ProDom;
                                                                                                                                                                                                                                                                                                                   Pfam; PF00005; ABC_tran;
                                                                                                                                                                                                                                                                                                                            InterPro; IPR003439; ABC_transportr.
InterPro; IPR004602; UvrA.
                                                                                                                                                                                                                                                                                                                                                   EMBL; AE006231; AAK04035.1; -
                                                                                                                     719
                                                                                                                                                                                                                                                   AP_BIND
                                                                                                                                   10 PESRA 14
                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
                                                                                                                                                                                                                                                                         response;
                                                                                                                    PESRA 723
                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                       PD000006; ABC_transportr;
                                                                                                                                                                                                                                                                    PS00211; ABC_TRANSPORTER; 2.
onse; Excision nuclease; DNA repair; ATP-binding; Repeat;
                                                                                                                                                                                                                                                                                              TIGR00630; uvra;
                                                                                                                                                                                                        740
943 AA;
          (Rel. 32, Creatéd)
(Rel. 32, Last sequence update)
(Rel. 34, Last annotation update)
e protein K39 (Fragment).
                                                                                                                                                                                                                           zinc-finger;
31 38
640 647
253 280
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253
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                                                                 STANDARD;
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104186
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ATP (POTENTIAL).
ATP (POTENTIAL).
C4-TYPE.
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                                                                                                                                                                         Score 5;
Pred. No.
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                                                                 PRT;
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YNC3_YEAST
ID YNC3_YAC
AC P53971
DT 01-OCT
DT 15-JUN
DE Hypoth
GN YNL022
OS Sacche
OC Eukary
OC Sacche
OX NCBI_1
RN [1]
RP SEQUEL
RA Hilbe;
RL Submi:
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                                                                                                                                                                                                                                         RESULT 188
                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                    YNC3_YEAST STANDARD; PRT; 965 AA. P53971; 91-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Hypothetical 108.5 kDa protein in UME3-HDA1 in YNL023C OR N2812.
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NP_BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=MHOM/BR/82 / Isolate BA-2;
MEDLINE=93133867; PubMed=8421715;
                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
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Pfam; PF00225; kinesin; 1.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L07879; AAA29254.1; HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leishmania chagasi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=44271;
 Duesterhoeft A., Floeth M., Hilbert H., Moestl D.; Submitted (MAY-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Microtubules; ATP-binding; Colled coll; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania chagasi that detects specific American visceral leishmaniasis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burns J.M. Jr., Shreffler W.G.,
                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Molecular characterization of a kinesin-related
                                                                                                                                                                                                                                                                                 478 ESRAA 482
                                                                                                                                                                                                                                                                                                            11 ESRAA 15
                                                                                                                                                                                                                                                                                                                                        Similarity 5; Conserv
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129
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742
781
820
859
898
937
>955
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100.0%; Pi
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                                                                                                                                                                                                                                                                                                                                      33.3%; Score 5; DB
100.0%; Pred. No. 3.
live 0; Mismatches
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  EMBL/GenBank/DDBJ databases
                             Fritz C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINESIN-MOTOR (BY SIMILARITY).
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
7 x 39 AA APPROXIMATE TANDEM RI
                                                                                                                                                                                                                                                                                                                                                                                                                         (PARTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Benson D.R., Ghalib H.W.,
                                                                                                                                                                                                                                                                                                                                                                                               8CA76815BE84C6E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                  DB 1; Lc..,
NO. 3.5e+02;
0;
                              Heuss-Neitzel D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
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                                                                                                                                        intergenic region
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RESULT 185

UVRA_ECOLI
ID PO7671

AC P07671

AC Escher

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Best Local S
Matches 5
                               Nucleic [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UVRA_ECOLI STANDARD; PRT; 940 AA P07671; P76788; O1-APR-1988 (Rel. 07, Created) O1-APR-1988 (Rel. 07, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Excinuclease ABC subunit A. UVRA OR DINE OR B4058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: The ABC excision nuclease is a DNA repair enzyme that catalyzes the excision reaction of UV-damaged nucleotide segments producing oligomers having the modified base(S). UVrA is an ATPase and a DNA-binding protein that preferentially binds singlestranded or UV-irradiated double-stranded DNA (By similarity).
-i- SUBUNIT: Consists of three subunits; uvrA, uvrB and uvrC.
-i- SUBCELLULAR IJCATION: CYCOplasmic (By similarity).
-i- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
                                                                                                                                                     MEDLINE=94089392; PubMed=8265357;
Blattner F.R., Burland V.D., Plunkett G.
                                                                                                                                                                                                                                                                              "Sequences of Escherichia coli uvrA potential ATP binding sites."; J. Biol. Chem. 261:4895-4901(1986).
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=86168204; PubMed=3007478;
Husain I., van Huten B., Thomas D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; Zinc-finger; NP_BIND 31 38 NP_BIND 640 647 ZN_FING 253 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRRAMS; TIGRRO0630; uvra; 1.
TIGRRAMS; TIGRRO0630; uvra; 1.
PROSITE; PS00211; ABC_TRANSPORTER;
SOS response; Excision nuclease; D:
  SEQUENCE OF 1-25 FROM N.A.
                                                                         "Analysis of the Escherichia coli genome. region from 89.2 to 92.8 minutes.";
                                                                                                                              Daniels D.L.;
                                                                                                                                                                                                          STRAIN-K12
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00005; ABC_tran; 2.
ProDom; PD000006; ABC_transportr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003439; ABC_transportr.
InterPro; IPR004602; UvrA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use
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                                                    Acids
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940
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                                                    Res.
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                                                 o 92.8 minutes.";
21:5408-5417(1993)
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ATP (POTENTIAL).
ATP (POTENTIAL).
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W; A20C90C935A0ACEB
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                                                                                                                                                                                                                                                                                                                                   gene
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0;
                                                                                                                                                     III,
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                                                                                                 IV. DNA sequence of
                                                                                                                                                                                                                                                                                                                                   protein reveal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae;
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Query Match
Best Local
 Matches
                                                                                                                                                                                                                                                                        EMBL; M13495; AAA24754.1; -. EMBL; U00006; AAC43152.1; -. EMBL; AE000479; AAC77028.1; -. EMBL; X01621; CAA25764.1; -. EMBL; J01721; AAA24753.1; -. PIR; A2869; BVECUA.
                                                     NP_BIND
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SEQUENCE
                                                                                                                                                                                        Pfam; PF00005; ABC_tran; 2.
ProDom; PD000006; ABC_transportr;
                                                                                                                                                                                                                       ECO2DBASE; H124.0; 6TH EDITION. ECOGENE; EG11061; uVAB. INTERPRO1439; ABC_transportr. InterPro; IPR004602; UVrA.
                                                                                                                                                                                                                                                                                                                                                                         entitles requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Navaratnam S., Myles G.M., Strange R.W., "Evidence from extended X-ray absorption secific mutagenesis for zinc fingers in coli".
                                                                                                                                                       SOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
MEDLINE=91208117; PubMed=1826851;
Myles G.M., Sancar A.;
"Isolation and characterization of functional domains of UvrA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "In vivo regulation of the uvrA gene: promoter regions.";
Nucleic Acids Res. 11:5795-5810(1983)
                                                                                                                                                                               TIGRFAMS; TIGRO0630; uvra;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89380205;
                                                                                                                                        DNA-binding;
                                                                                                                                                                  PROSITE; PS00211; ABC_TRANSPORTER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 30:3834-3840(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sancar A., Sancar G.B., Rupp W.D., Li
"LexA protein inhibits transcription
vitro ":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-83299251; PubMed-6310514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRA IS AN ATPASE AND A DNA-BINDING PROTEIN THAT PREFERENTIALLY BINDS SINGLE-STRANDED OR UV-IRRADIATED DOUBLE-STRANDED DNA.
SUBUNIT: CONSISTS OF THREE SUBUNITS; UVRA, UVRB AND UVRG.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
MISCELLANEOUS: BINDS ABOUT 2 ZINC ATOMS/MOLECULE.
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298:96-98(1982).
Similarity
5; Conser
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253
740
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 Conservative
                                                                                                                             Zinc-finger;
31 38
                                                                                                                                       Excision nuclease; DNA inc-finger; Complete p
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              33.3%;
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the uvrA gene: role of the '-10' a
                                                      WW;
              Score 5; pred. No
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                                                                  ATP.
C4-TYPE.
C4-TYPE.
C->A,H,S:
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fine structure a
UvrA protein of
              1; Le .5e+02;
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E. coli uvrA gene
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                           Length 940,
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16-OCT-2001
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                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS0041; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
            the human MSH4 gene.";
Genomics 44:188-194(1997)
                                    Paquis-Flucklinger V., Santucci-E
Turc-Carel C., Desnuelle C.;
"Cloning and expression analysis
                                                                             SEQUENCE FROM N.A. MEDLINE-97446137; PubMed-9299235;
                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1997) to
                                                                                                                                                                                      Muts protein
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O15457;
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                                                                                                                                    Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol.
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5; Conserv
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nilarity 100.0%;
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1 337 KINESIN-MOTOR (BY
8 741 COILED COIL.
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ATP (POTENTIAL).
A: 2E2475195F674C02 CRC64;
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                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
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Pfam; PF01624; MutS_N; 1.

ProDom; PD001263; MutS_C; 1.

ProDom; M00534; MUTSac; 1.

SMART; SM00534; MUTSac; 1.

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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyi Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe 1 Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinayawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:87 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasses D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpt Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpt Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Popodaca J., Anantharaman T.S., Lin J., Yen G., Schwai Welch R.A., Blattner F.R.;
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STRAIN=0157:H7 / E
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MEDLINE-21156231; PubMed-11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
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SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
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hwartz D.C.,
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Tobe T.,
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DOMAIN 158
NP_BIND 164
BINDING 185
ACT_SITE 269
DOMAIN 568
DOMAIN 668
DOMAIN 698
DOMAIN 753
MUTAGEN 185
MUTAGEN 192
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NCBI_TaxID=10116;
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                                              "Activation of the JNK pathway
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SMART; SM00221; STYKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00108; PROTEIN_KINASE_DOM;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR004040; STY_pkinase.
InterPro; IPR002299; Ser_thr_pkin
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     Oncogene 12:641-650(1996)
                                                                                                  SEQUENCE FROM N.A. MEDLINE-96226099;
                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                 (MAPK-upstream kinase) (MUK).
MAP3K12 OR MUK.
                                                                                                                                                                                                                                                                                                                                  Mitogen-activated
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                               MEKK and
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4. Osada S., Spyrou G., Ohno S.,
5. Spyrou G., Ohno S.,
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7. Spyrou G., Ohno S.,
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E->A: NO CHANGE.
V -> A (IN REF 2).
KL -> NV (IN REF. 2).
S -> T (IN REF. 2).
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Neurospora crassa. Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora. NCBI_TaxID=5141;

Steinberg G., Schliwa M.;
"The Neurospora organelle motor: a distant kinesin with unconventional properties.";

relative

of

conventional

MEDLINE=96157894; PubMed=8589459 Steinberg G., Schliwa M.;

STRAIN-74A;

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(Rel. 33, 10) (Rel. 38, 10) (Rel. 40, 10) (Rel. 40, 10)

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                                                                                                                                                                                                                 Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00221; STYKC; 1.
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InterPro; IPR002290; Ser_thr_pkinase.
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PTM: Autophosphorylated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: May be an activator of the JNK/SAPK pathway. Phosphorylates beta-casein, histone 1 and myelin basic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR:
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                      Similarity 5; Conser
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ATP (BY SIMILARITY).
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52AD964006BAE149
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Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Caphano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Erritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galieron N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NATURE 390:249-256(1997).

NATURE 390:249-256(1997).

-I- FUNCTION: CELL WALL HYDROLASE NOT INVOLVED IN CELL AUTOLYSIS.

HYDROLYZES THE BETA-1,4 GLYCAN BOND BETWEEN THE N-

APPRVICULOSAMINYL AND THE N-ACETYLMURAMOYL RESIDUES IN THE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rashid M.H., Mori M., Sekiguchi J.; "Glucosaminidase of Bacillus subtilis: cloning, regulation, structure and biochemical characterization.";
                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-slb.or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98044033;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96036197;
                                                                                                                                          SubtiList;
                          InterPro; IPR002901; Amidase_4.
InterPro; IPR003646; SH3_bac.
Pfam; PF01832; Amidase_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        residue remains attached to the protein; the rest of the Oligosaccharide is released intact. SUBUNIT: HOMODIMER. SUBCELLULAR LOCATION: Secreted. SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN.

CATALYTIC ACTIVITY: Endohydrolysis of the di-N-acetylchitobiosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unit in high-mannose glycopeptides and glycoproteins containing the -[Man(GlcNAc)2]Asn-structure. One N-acetyl-D-glucosamine residue remains attached to the protein; the rest of the oligosaccharide is released intact.
                                                                                                                                                                         U02562;
D45048;
Z99122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                          BG10455; lytD.
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Bertero M.G., Bessieres P., Bolotin A., Borche
                                                                                                                                                                         AAA67857.1; -.; BAA08089.1; -.; CAB15595.1; -.
Amidase_4
/: LYZ2; 1
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Best Local
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kinase) (DLK)
MAP3K12 OR ZPK.
                                                                                                                                                                                                                                                                                                                               J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
CHAIN
                                                                                                                                     STRAIN-CD-1; TISSUE-Brain;
STRAIN-CD-1; TISSUE-Brain;
MEDLINE-95074107; pubMed-7983011;
Holzman L.B., Merritt S.E., Fan G.;
Holzman L.B., Merritt S.E., Fan G.;
"Identification, molecular cloning, and characterization of dual leucine zipper bearing kinase. A novel serine/threonine protein that defines a second subfamily of mixed lineage kinases.";
J. Biol. Chem. 269:30808-30817(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mitogen-activated protein kinase kinase kinase 12 (EC Leucine-zipper protein kinase) (ZPK) (Dual leucine zipper)
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REPEAT
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DOMAIN
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Mata M., Merritt S.E., Fan G., Yu G.G., Holzman L.B.;
"Characterization of dual leucine zipper-bearing kinase,
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ICR X Swiss Webster; TISSUE-Brain;
MEDLINE-96365388; PubMed-8769565;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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16-OCT-2001 (Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                          DNA Cell Biol. 15:631-642(1996)
                                                                                                                                                                                                                                                                     Blouin R., Beaudoin J., Bergeron P., "Cell-specific expression of the ZPK
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M3KC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                    PHOSPHORYLATION, AND MUTAGENESIS OF LYS-185 AND GLU-192
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                                                    COFACTOR: Magnesium.
SUBCELLULAR LOCATION: Cytoplasmic and membrane associated.
TISSUE SPECIFICITY: Expressed in brain, kidney, lung, heart, testis, gastrointestinal tract, stomach, liver and pancreas.
Within the nervous system, predominantly expressed in neuron
associated.
SIMILARITY:
                   enriched in synaptic terminer. Autophosphorylated on under basal conditions and
                                                                                                                CATALYTIC ACTIVITY:
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880
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Pred. No
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Sciurognathi; Muridae
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o. 3.3e+02;
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n adult mouse
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                                                                                                                phosphoprotein
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                                                                  MEDLINE-21154917; PubMed=11230166; Wilemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl Wilemann S., Weil B., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner Mewes H.-W., Korn B., Klein M., Poustka A.; Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDIJNS=21601154; PubMed=11735225;

Jaworski C.J., Moreira E., Li A., Lee I

A family of 12 human genes containing
Genomics 78:185-196(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and characterization of human oxyst related protein-5 (ORP-5).";
Submitted (AUG-2001) to the EMBL/GenBank/nnn-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9HOX9; O9BZBO; Q9P1Z4;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Oxysterol binding protein-related protein 5 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00169; PH; 1.
Pfam; PF01237; Oxysterol_BP;
SMART; SM00233; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01013; OSBP; 1. PROSITE; PS50003; PH_DOMAIN;
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OSBPL5 OR ORP5 OR KIAA1534.
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DOMAIN 126 243
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  SEQUENCE OF 1-61 FROM N.A
                                                       Genome
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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InterPro; IPR001849; PH.
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ilarity 100.0%;
Conservative
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Primates;
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Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                              Lee R., Rodriguez I.R.; ining oxysterol-binding
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5. 3.3e+02;
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RESULT 179
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P39848;
01-FEB-1995
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                                                                                                                                                                                                                                              Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00169; PH; 1.
Pfam; PF01237; Oxysterol_BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Prediction of the coding sequences of The complete sequences of 100 new cDN for large proteins in vitro."; DNA RES. 7:143-150(2000).
-i- SIMILARITY: BELLONGS TO THE OSBP F-i- SIMILARITY: CONTAINS 1 PH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lehto M., Laitinen S., Chinetti G., Johansson Staels B., Ikonen E., Olkkonen V.M.; "The OSBP-related protein family in humans."; J. Lipid Res. 42:1203-1213(2001).
                                                        MEDLINE=95020588; PubMed=7934877;
Margot P., Maueel C., Karamata D.
                                                                                                                                                                                                                                                                                                                                      Beta-N-acetylglucosaminidase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01013; OSBP; 1. PROSITE; PS50003; PH_DOMAIN;
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                                                                                                                       STRAIN=168;
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             LYTD OR CWLG
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DOMAIN 126 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew;
                                                                                                                                                                                                               NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 15-879 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21376257; PubMed-11483621; Lehto M., Laitinen S., Chinetti G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 5; Conserv
, Maueel C., Karamata D.;
of the N-acetylglucosaminidase,
hydrolase not involved in vegeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001849;
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15
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AAL40666.1; -...
CAB66852.1; -...
AAG53417.1; -...
BAA96058.1; -...
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100.0%; Pr
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; 7EF06544347CC60A CRC64;
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                                                                                                                                                                                                                                              Bacillaceae;
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es of unidentified human genes. XV:
cDNA clones from brain which code
idase, a Bacillus subtilis vegetative cell autolysis.
                                                                                                                                                                                                                                                                                                                                                                                                  update;
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r (EC 3.
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Q12852;
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DOMAIN 208

DOMAIN 489

DOMAIN 609

DOMAIN 710
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between
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AP3K12 OR Zrn.
HOMO Sapiens (Human).
Homo sapiens (Human).
Herota; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitogen-activated protein kinase kinase kinase
(Leucine-zipper protein kinase) (ZPK).
MAP3K12 OR ZPK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00660; BAND_41_1; PROSITE; PS00661; BAND_41_2; PROSITE; PS50057; BAND_41_3;
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                                                                                                                                                                                                                                                                 Reddy U.R., Pleasure D.;
"Cloning of a novel putative protein kinase having domain from human brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this st
entities requires a
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                                                                                                                                                                                                                                                    Biochem.
                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Teratocarcinoma;
MEDLINE=94311945; PubMed=8037767;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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SMART; SM00295; B41; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 PESRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 PESRA 14
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                                                            CATALYTIC ACTIVITY: AT COFACTOR: Magnesium. SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASS SPECTROMETRY: MW-17199.3; METHOD-Electrospray; RANGE-709-858 SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
                                                                                                                                                                              Chem. Biophys. Res. Commun. 202:613-620(1994).
FUNCTION: May be an activator of the JNK/SAPK pathway.
Phosphorylates beta-casein, histone 1 and myelin basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alternative splicing
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5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-profit institutions we have a usage by and this statement is not removed. Usage by and this statement is not removed. Usage by and this statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. It is no
   SPECIFICITY: Highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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707
858
95990
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HYDROPHILIC.
SPECTRIN--ACTIN-BINDING.
CARBOXYL-TERMINAL (CTD).
CARBOXYL-TERMINAL (CTC64.
                                                                                                                           +
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Pred. No.
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                                                                  membrane-associated
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                                                                                                                                                                                     protein
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ORP5_MOUSE
ID ORP5_M
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Best Local S
Matches
                                    MEDLINE-2051929; PubMed-11063728; Engemann S., Stroedicke M., Paulsen M. Lane N., Reik W., Walter J.; "Sequence and functional comparison in implications for a novel imprinting ce Hum. Mol. Genet. 9:2691-2706(2000).

-i- SIMILARITY: BELONGS TO THE OSBP F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation; I
DOMAIN 125
NP_BIND 131
BINDING 152
ACT_SITE 236
DOMAIN 720
SEQUENCE 859 AA
                                                                                                                                                                                                                           O9ER64: Q99NF5;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Oxysterol binding protein-related protein 5 ((ORP-5) (Oxystyrol-binding protein homologue)
OSBPL5 OR OSBP2 OR OBPH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license.
                        Hum. Mol. Genet. 9:2691-2706(2000).
-!- SIMILARITY: BELONGS TO THE OSBP F
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
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PROSITE; PS00108;
PROSITE; PS50011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00221; STYKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U07358; AAA67343.1; -. HSSP; P12931; 1FMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                STRAIN-129/SV;
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004040; STY_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
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MIM; 600447; -.
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                                                                                                                                                SEQUENCE
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InterPro; IPR004040; STY_pkinase.
                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase;
                                                                                                                                                                                                                                                                                                                                                                                            65 PESRA
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SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                            33.3%; So lilarity 100.0%; I Conservative 0;
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366
139
152
236
668
725
AA; 93188 MW
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ATP (BY SIMILARITY).
BY SIMILARITY.
POLY-PRO.
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0; Mismatches
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0E5209792C5C6F05 CRC64;
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Sciurognathi; Muridae;
                                                              in the
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                                      FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FALSE_NEG
                                                                                                       Franck O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; I
1.2e+02
                                                                 and
                                                                             Beckwith-Wiedemann
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1).
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                                                                 extended
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                                                                                                        Reinhardt
                                                                                                                                                                                      Euteleostomi; Murinae; Mus
                                                               iemann region:
imprinting.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001944; GH_35.
InterPro; IPR000922; Gal_lectin.
Pfam; PF01101; Glycc_hydro_35; 1.
Pfam; PF02140; Gal_Lectin; 1.
PRINTS; PR00742; GLHYDRLASE35.
PRODOM; PD005612; Gal_lectin; 1.
PROSITE; PS01182; GAL_SCAYL_HYDROL_F35; 1.
PROSITE; PS50228; SUEL_LECTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q60563;
01-NOV-1997
01-NOV-1997
16-OCT-2001
J. Cell Sci. 107:2749-2760(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                       Synaptonemal complex protein 1 (SCP-1 protein) synaptic protein) (Fragment). SCP1 OR SYN1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
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                                                                                                               MEDLINE=95181577; PubMed=7876343;
Dobson M.J., Pearlman R.E., Karai
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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                                                                                            Moens P.B.;
                                                                                                                                                                                                                                                                                                                                                                                           Mesocricetus auratus (Golden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCP1_MESAU
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Schuch W., Seymour G
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                     Mesocricetus
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                                                          Synaptonemal complex proteins: occurrence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
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43
835
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93336 MW;
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                                                                                                               Karaiskakis A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 5;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                           hamster).
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PROTON DONOR (POTENTIAL).
NUCLEOPHILE (POTENTIAL).
94C9685F95C4A646 CRC64;
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                                                                                                                                                                                                                                                                                                                             Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Le .1e+02;
                                                                                                                                                                                                                                                                                                                                 Muridae;
                                                                                                               Spyropoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Meiotic chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-reducing beta-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                 Cricetinae;
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                                                                                                                     в.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
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Best Local :
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L32978; AAC42039.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
806 STPES 810
                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: MAJOR COMPONENT OF THE TRANSVERSE FILAMENTS OF SYNAPTONEMAL COMPLEXES (SCS), FORMED BETWEEN HOMOLOGOUS CHROMOSOMES DURING MEIOTIC PROPHASE (BY SIMILARITY). HAS SPECIFIC DNA BINDING CAPABILITY.

SUBCELLULAR LOCATION: NUCLEAR. IN TRIPARTITE SEGMENTS OF SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS IS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEXES IS FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS IS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX IS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX IN THE SYNAPSHORY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. T DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNAPTONEMAL
                                                   STPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                    Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                   12
                                                                                                                                                                                                                 845
                                                                                                          Conservative
                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Meiosis;
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                                                                                                                                                                                                                                           672
556
756
838
                                                                                                                                                                                                                 99401 MW;
                                                                                                                                 33.3%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                         Cell division; Phosphorylation;
                                                                                                       0,
                                                                                                                              Score 5;
Pred. No
                                                                                                                                                                                                           COILED COIL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL
NUCLEAR LOCALIZATION SIGNAL
ARG/LYS-RICH (BASIC).
; D7F28873C824C6A8 CRC64;
                                                                                                       Mismatches
                                                                                                                                   No.
                                                                                                                                 DB 1;
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                                                                                                          0
                                                                                                                                                        Length 845;
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                                                                                                    Gaps
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RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                               41_MOUSE
P48193;
01-FEB-1996
01-FEB-1996
15-JUN-2002
Protein 4.1
MEDLINE-21325946; PubMed-11432737;
Scott C., Phillips G.W., Baines A.J.;
*Properties of the C-terminal domain of 4.1 proteins.*;
Eur. J. Biochem. 268:3709-3717(2001).
-i- FUNCTION: Protein 4.1 is a major structural element of the erythrocyte membrane skeleton. It plays a key role in regulating membrane physical properties of mechanical stability and
                                                                                                                                                                     J. Biol. Chem. 2
                                                                                                                                                                                                         basis
                                                                                                                                                                                                                                                            Huang J.-P.,
                                                                                                                                                                                                                                                                                                    STRAIN-BALB/c
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                 SEQUENCE OF 709-713, AND CHARACTERIZATION OF
                                                                                                                                                                                                                                                                               MEDLINE=93155238;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                              EPB41 OR EPB4.1
                                                                                                                                                                                                     Genomic structure of the locus encoding pasis for complex combinational patterns
                                                                                                                                                                                                                                               Cang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
(Band 4.1) (P4.1) (4.1R).
                                                                                                                                                                                                                                                              Tang
                                                                                                                                                                     a splicing.";
268:3758-3766(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                              PubMed=8429050;
C.-J.C., Kou G.
                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                                     ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                              G.-H.,
                                                                                                                                                                                                                                                                                                                     SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            858
                                                                                                                                                                                                                                                              Marchesi V.T.,
                                                                                                                                                                                                         protein 4.1. Structural of tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                   CARBOXY-TERMINAL DOMAIN
                                                                                                                                                                                                                                                                Benz
                                                                                                                                                                                                                                                              E.J.
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RESULT 172
BGAL_ASPOF
ID BGAL_A
AC P45582
DT Q1-NOV
                                                                                                                                                                                                             SOLUTION COUNTRY AND COUNTRY A
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                                                                                                                                                     Query Match
Best Local S
Matches
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between
_ASPOF STANDARD;
BGAL_ASPOF STANDARD;
P45582;
Q1-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROY entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
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DOMAIN
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DOMAIN
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PIR; S16328; S16328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000676; NaH_Exchngr.
InterPro; IPR004709; NaH_exchang3
Pfam; PF00999; Na_H_Exchanger; 1.
                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                               TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMs; TIGR00840; b_cpa1; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSDUCTION: Integral membrane protein.
SUBCELLUAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: KIDNEY AND INTESTINE.
PTM: PHOSPHORYLATED (POSSIBLE).
SIMILARITY: BELONGS TO THE MA(+)/H(+) EXCHANGER FAMILY.
CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
                                                                                                                         TPESR 13
                                                                                                 TPESR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X59935; CAA42558.1; -.
X61504; CAA43721.1; -.
X56536; CAA39881.1; -.
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                                                                                                                                                      Similarity
5; Conserv
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                                                                                                 72
                                                                                                                                                                                                             Conservative
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406
410
430
430
500
500
816
75
370
                                                                                                                                                33.3%; Er
100.0%; Pr
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                                                                                                                                                                                                                                       CYTOPLASMIC (PÓTENTIAL).

**LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

V -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M4 (POTENTIAL)
CYTOPLASMIC (F
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                                                                                                                                                                                                                                                                                                                                       M8 (POTENTIAL)
CYTOPLASMIC (P
                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POM7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                             EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                          M9 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M5A (POTENTIAL
                                                                                                                                                                                                            -> A (IN REF. 2).
-> E (IN REF. 2).
336738D267F7F436 CRC64;
                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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                              832
                                                                                                                                                                   DB 1; L, 3.1e+02
                              B
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                                                                                                                                                                                Length 816
                                                                                                                                                      Indels
                                                                                                                                                     0;
                                                                                                                                                     Gaps
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BGAL_LYCES
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                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
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ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asparagus.
NCBI_TaxID=4686;
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                                                                                                                                                                                                            BGAL_LYCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                       NCBI_TaxID-4081;
                                                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                                                                          7 RSTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European
                                                                                                                                                                                                                                                                                  RSTPE
                                                                                                                                                                                                                                                                                                                                                                                           26
741
183
252
832 /
                                                                                                                                                                                                                                                                                56
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InterPro; IPR0001944; GH_35.
InterPro; IPR000922; Gal_Lectin.
Pfam; PF01301; Glyco_hydro_35; 1.
Pfam; PF02140; Gal_Lectin; 1.
PR.NTS; PR00742; GLHYDRLASE35.
PRODOM; PD005612; Gal_lectin; 1.
PROSITE; PS01182; G1YCOSYL_HYDROL.IPROSITE; PS01182; G1YCOSYL_HYDROL.IPROSITE; PS01228; SUEL_LECTIN; 1.
                                                                                                                                                           p48980;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 31, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Beta-galactosidase precursor (EC 3.2.1.23) (Lactase).
Beta-galactosidase precursor (EC 3.2.1.23) (Lactase).
Asparagus officinalis (Garden asparagus).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epsermatophyta; Magnollophyta; Lilliopsida; Asparagales; Asparagaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A., AND STRAIN=cv. Ailsa Craig; MEDLINE=95357407; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
5; Conserv
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S01182; GLYCOSYL_HYDROL_F35;
S50228; SUEL_LECTIN; 1.
Glycosidase; Signal.
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       PubMed-7630937;
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                                     TISSUE-Pericarp;
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SUEL-TYPE LECTIN.
PROTON DONOR (POTENTIAL).
NUCLEOPHILE (POTENTIAL).
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5. 3.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer Genet. Cytogenet. 120:37-43(2000).

(i-i-FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SOLUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
                                                   TRANSMEM
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                                      DOMAIN
                                                                 DOMAIN
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                                                                                           DOMAIN
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                                                                                                                                           PRINTS; PR01084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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                                                                                                                                                                   InterPro; IPR000676; NaH_Exchngr.
InterPro; IPR004709; NaH_exchang?
                                                                                                                                                                                                                     L; AF146438;
L; AF146439;
A31311; A31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DERIVATIVES AND ACTIVATED IN A COOPERATIVE FASHION BY INTRACELLULAR H+. FULLY ACTIVE AT ACIDIC PH, THE ANTIPORTER IS VARTUALLY TURNED OFF AT NEUTRAL PH. IN QUIESCENT CELLS UPON GROWIN FACTOR STIMULATION, THE APPARENT AFFINITY FOR INTERNAL H+ IS INCREASED, RESULTING IN A PERSISTENT RISE IN CYTOPLASMIC PH. SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY. CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Interacts with tescalcin.
SUBCELLULAR LOCATION: Integral membrane |
TISSUE SPECIFICITY: KIDNEY AND INTESTINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: PHOSPHORYLATED (POSSIBLE).
MISCELLANEOUS: INHIBITED BY AMILORIDE AND 5-AMINO-SUBSTITUTED
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AF146437;
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AF146435;
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AF141352;
AF141353;
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AF146430;
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AF146432;
AF146433;
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S68616;
                                                                                                                                                      PF00999; Na_H_Exchanger;
                                                                                                                                                                                                         HGNC:11071;
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16
36
108
128
130
150
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                                                                                                               Glycoprotein;
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AAF21353 1

AAF21353 1

AAF21354 1

AAF21355 1

AAF21357 1

AAF21357 1

AAF21359 1

AAF25593 1

AAF25594 1

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AAF25595 1

AAF25596 1

AAF25596 1

AAF25598 1
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AAF21353.1
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AAF25599.1
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ls of leukemia patients: A comparison with
                                                                                                                                          NAHEXCHNGR
                                                                                                      Phosphorylation
 15
107
127
127
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149
154
                                                                                                                                                                                                         SLC9A1.
                                                                                                                                                      NaH_exchang3.
Exchanger; 1.
                    CYTOPLASMIC (POTENTIAL).

M1 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

M2 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

M3 (POTENTIAL).
                                                                                                               Transport; Antiport; Sodium transport;
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GROWTH
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RESULT 171
NAH1_RAH1_R
AC P23791
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DT 01-NOV
DT 01-NOV
DT 15-JUN
GN SLC9A1
OS OFFCTC
OC EMARMA1
ON NOBL_1
RN (1)
RP SEQUEN
RC STRAIN
RX MEDLII
RA TSE C.
RR MONTE
RC TISSUI
RR EMBO (
RT WOLLE
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Best Local
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                                                                                                                                                                                                   MEDIANE-2006447; PubMed=1661611;
MEDIANE-2006447; PubMed=1661611;
Hildebrandt F., Pizzonia J.H., Reilly R.F., Reboucas N.A.,
Sardet C., Pouyssegur J., Slayman C.W., Aronson P.S., Igar
                                                                                                                                                                                   Sardet C., Pouyssegur J., Slaym "Cloning, sequence, and tissue exchanger transcript.", Biochim. Biophys. Acta 1129:105
                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAH1_RABIT
P23791;
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CARBOHYD
                                                                                             MEDLINE-91138752; PubMed-1704856; Fliegel L., Sardet C., Pouyssegur J., "Identification of the protein and cD
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TRANSMEM
                                                                                                                                         SEQUENCE OF 472-816 FROM N.A. STRAIN-New Zealand white; TIS
                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                             Tse C.-M., Ma A.I., Yang V.W., Watson A.J.M., Levine S., Montrose M.H., Potter J., Sardet C., Pouyssegur J., Donowitz "Molecular cloning and expression of a cDNA encoding the rabb villus cell basolateral membrane Na+/H+ exchanger.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger 1) (NHE-1).
                                                                                                                                                                                                                                                                        TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-New Zealand white; TISSUE-Ileal villus; MEDLINE-91293066; PubMed-1712287;
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S Lett. 279:25-29(1991).

S Lett. 279:25-29(1991).

S Lett. 279:25-29(1991).

FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD CONTINUE TON CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  Yang V.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.3%;
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                                                                                                                                         TISSUE-Heart muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M9 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

M10 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ч7
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                                                                                              cDNA of
                                                                                                             Barr
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3.1e+02;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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                                                                                                the cardiac Na+/H+
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                                                                                                                                                                                                               nson P.S., Igarashi P.;
of a rabbit renal Na+/H+
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rabbit ileal
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Best Local S
Matches 5
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InterPro; IPRO05121; Fdx-AntiCB.
InterPro; IPR004532; Pher_bact.
InterPro; IPR004532; Pher_bind.
Pfam; PP01588; tRNA_bind; 1.
Pfam; PF03147; FDX-ACB; 1.
Pfam; PF03483; B3_4; 1.
Pfam; PF03484; B5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Preprotein translocase secA subunit.
SECA OR MPN210 OR MP621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The surple by non-profit institutions as long modified and this statement is not removed
                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plagens H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECA_MYCPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma
                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae."
                                                                                                                                                                                                                                                                                                                                                                                                     "Complete sequence analysis of the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285
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                                                                                                                                                                                                             FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH THE SECY/SEC SUBUNITS. SECA HAS A CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF ATP TO THE TRANSFER OF PRE-SECRETORY PERIFLASMIC AND OUTER MEMBRANE PROTEINS ACROSS THE MEMBRANE (BY SIMILARITY).

SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS WHICH COMPRISE SECA, SECB, SECE, SECE, SECG AND SECY
                                                                                                                                     (BY SIMILARITY).
SIMILARITY: BELONGS TO
                                                                                                                                                                               (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF
                       SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBI outset
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STPES
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AP002547; BAA98801.1;
CP0154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE001644; AAD18733.1;
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Firmicutes; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR005146; B3_4. IPR005147; B5.
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577
792 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                Res.
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577
87732 MW;
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etase; Protein biosynthesis;
                                                                                                                                       THE SECA FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 5; |
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          റെ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> A (IN REF. 3).
-> Y (IN REF. 1).
852C86BF0F07486F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasmataceae; Mycoplasma
  removed.
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NI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   808
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3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REF. 3).
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    Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                 [F]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                 MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   드
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    Ьy
                                                                                                                                                                                                                                                                                                             WITH THE SECY/SECE
HE HYDROLYSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                            В.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .-c.,
    and
                                                                     EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding;
                                                                     a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma
    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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    commercial
                         20 S
                                           its
                         way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUN-2002 (Rel. 41, Last anotation update)
Sodium/hydrogen exchanger 1 (Na(+)/H(+) excha
antiporter, amiloride-sensitive) (APNH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAH1_HUMAN
P19634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000059; AAB96269.1; ... InterPro; IPR001650; Helicase_C. InterPro; IPR000185; SecA. Pfam; PF00271; helicase_C; 1. Pfam; PF01043; SecA_protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                    MEDLINE-91293066; PubMed-1712287; Tse C.-M., Ma A.I., Yang V.W., Watson A.J.M., Levine Montrose M.H., Potter J., Sardet C., Pouyssegur J., I "Molecular cloning and expression of a cDNA encoding villus cell basolateral membrane Na+/H+ exchanger."; EMBO J. 10:1957-1967(1991).
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-Kidney;
MEDLINE=90140739; PubMed=2154036;
Sardet C., Counillon L., Franchi A., Po
"Growth factors induce phosphorylation
glycoprotein of 110 kD.";
Science 247:723-726(1990).
                                   Mol.
                                               Fliegel L., Dyck J.R., Wang H., Fong C., Haworth R.S. "Cloning and analysis of the human myocardial Na+/H+
                                                                                                                                                                                                                                                                                                                    Sardet C., Franchi A., Pouyssegur J.; "Molecular cloning, primary structure, and e growth factor-activatable Na+/H+ antiporter. Cell 56:271-280(1989).
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiporter, amiloride-se
SLC9A1 OR NHE1 OR APNH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
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Protein transport; ATP-binding; Membrane; Translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00906;
SEQUENCE FROM N.A. MEDLINE-20375279;
                                                                     MEDLINE=94111706; PubMed=8283968;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                               REVISIONS
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89106219; PubMed-2536298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                     rissuE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255
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                                     Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 808 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
 PubMed=10913675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.3%; >--
100.0%; Pr
                                  125:137-143(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₩;
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%; Pred. No. 3e+
0; Mismatches
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; E768F0B8915F892F
                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                             Pouyssegur J.;
on of the Na+/H+ antiporter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; I
5. 3e+02;
                                                                                                                                                                                                                                                                                                                                              and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                             Donowitz
                                                exchanger.";
                                                                                                                                                the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NHE-1) (Na+/H+
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
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RESULT 167
CADI_HUMAN
ID CADI_HOMAN
AC CAGA
AC TIGA
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Best Local S
Matches 5
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Q13634;
15-JUL-1998
15-JUL-1998
16-OCT-2001
                                              Signal
SIGNAL
PROPEP
                                                                                                                 PROSITE; PS00232; CADHERIN_1; PROSITE; PS50268; CADHERIN_2; Cell adhesion; Glycoprotein: "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of human cadherin-14, a novel neurally specific type II cadherin, by protein interaction cloning.";

J. Biol. Chem. 272:5236-5240(1997).

-I. FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

-I. FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

-I. FUNCTION: CADHERINS ARE CALCIUM SEELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES.
                                                                                                                                                                                                                              InterPro; IPR002126; Cadherin.
InterPro; IPR000233; Cadherin_C_term
Pfam; PF00028; cadherin; 5.
Pfam; PF01049; Cadherin_C_term; 1.
                                                                                                                                                                                                                                                                                                                                                EMBL; U59325; AAB02933.1;
HSSP; P15116; 1NCJ.
Genew; HGNC:1757; CDH18.
                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                          PRINTS; PR00205; CADHE SMART; SM00112; CA; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cadherin-18 pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000201; DNApol_viral_N.
InterPro; IPR000477; RVYse.
Pfam; PF00078; rvt; 1.
Pfam; PF00242; DNA_pol_viral_N; 1.
Pfam; PF00336; DNA_pol_viral_C; 1.
    DOMAIN
                                                                                                                                                                                                                                                                                                                                    мім; 603019; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97184182; PubMed=9030594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodom; PD000814; DNApol_viral_C; 1.
Transferase; RNA-directed DNA polymerase; DNA-directed DNA Hydrolase; Nuclease; Endonuclease; DNA replication; DNA-bin SEQUENCE 788 AA; 89378 MW; F482FB578D75BF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 PESRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 PESRA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359
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                                                                                                               Glycoprotein;
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Primates;
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100.0%; P
tive 0;
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Pred. No.
POTENTIAL.
CADHERIN-18.
EXTRACELLULAR (POTENTIAL).
                                                                                                                    Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.isb-sib.ch/announce/
                                                                                                                 Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
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RESULT
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Best Local
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                                               "Comparison of whole genome sequences of Chlamydia pneumon from Japan and CWLO29 from USA."; Nucleic Acids Res. 28:2311-2314(2000).

-I CAPALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) - diphosphate + L-phenylalanyl-tRNA(Phe).

-I SUBUNIT: TETRAMER OF TWO ALPHA AND TWO prom.

SIMILARITY).
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYFE_CHLPN STANDARD; PRT; 792 AA.

0927W0; Q9K2D4; Q9JSD3;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)

phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)

tRNA ligase beta chain) (PheRS).

PHET OR CPN0594 OR CP0154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
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                                   -!- SUBCELLULAR LOCATION: Cytoplasmic -!- SIMILARITY: BELONGS TO THE PHENYL
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. tra Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia pneumoniae (Chlamydophila pneumoniae). Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHLPN
                                                                                                                                                                                    STRAIN-J138
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CWL029;
                                                                                                                                                                                                                                    "Genome sequences of Chlamydia trachomatis
pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                      MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                       CHAIN FAMILY. SUBFAMILY
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CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 4.
CADHERIN 61.CNAC.
N-LINKED (GLCNAC.
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Pred. No.
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                                     PHENYLALANYL-TRNA
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5. 3e+02;
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                                     SYNTHETASE
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                                                                                                                                   pneumoniae J138
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(POTENTIAL).
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DPOL_HPBDC STANDARD; PRT; 787 AA.

P30028;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
P protein [Includes: DNA-directed DNA polymerase (EC 2.7.7.7); RNA-directed DNA polymerase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K6PF_ASPNG
P78985;
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SEQUENCE FROM N.A. MEDLINE-91045091; Tong S., Mattes F.
                                                                                                     Duck hepatitis B
Viruses; Retroid
NCBI_TaxID=31510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0476; PHERCTKINASE.
PRODOM; PD000707; Ppfruckinase; 2.
PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 2.
Transferase; Kinase; Glycolysis; Repeat.
SEQUENCE 783 AA; 85759 MW; 7BE3F6B553F06304 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CBS 120.49 / N400;
de Graaff L.H., Everse S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus niger.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Asperg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 279690; CAB01923.1;
HSSP; P00512; 3PFK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000023; Ppfruckinase.
Pfam; PF00365; PFK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Visser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5061;
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5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.3%; Silarity 100.0%; Conservative 0;
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     Ŧ
                                                                                                                                  virus (st
l viruses;
     PubMed=2235506;
., Teubner K., Blum
                                                                                                                                  (strain China) (DHBV).
es; Hepadnaviridae; Avihepadnavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 5; DB 1; Pred. No. 3e+0; Mismatches
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). 3e+02;
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DPOL_HPBDB
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Matches 5
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17192;
101-NUG-1990 (Rel. 15, Created)
101-NUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 protein [Includes: DNA-directed DNA polymerase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                          Uchida M., Esumi M., Shikata T.;
"Molecular cloning and sequence analysis of duck hepatitis genomes of a new variant isolated from Shanghai ducks.";
Virology 173:600-606(1989).
-i- CATALLTIC ACTIVITY: N deoxynucleoside triphosphate = N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00242; DNA_pol_viral_N; 1.
Pfam; PF00336; DNA_pol_viral_C; 1.
ProDom; PD000814; DNApol_viral_C; 1.
Transferase; RNA-directed DNA polymerase; DNA-directed DNA polymerase; Hydrolase; Nuclease; Endonuclease; DNA replication; DNA-binding.
SEQUENCE 787 AA; 89214 MW; 1A99D7A656665180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR001462; DNApol_viral_C.
InterPro: IPR000201; DNApol_viral_N.
InterPro: IPR000477; RVTse.
Pfam; PF00078; rvt; 1.
         EMBL; M32990; AAA45754.1; PIR; A33746; JDVLBD.
                                                                                                                                                                                                                                                                                                                                                                     Duck hepatitis B virus (brown Shanghai duck isolate S5) (DHBV).
Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
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-!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete nucleotide sequence of a Chinese duck hepatitis B virus.
nucleic Acids Res. 18:6139-6139(1990).
-i- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosp
+ [DNA](N).
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=90085807; PubMed=2596031;
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10439;
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CATALYTIC ACTIVITY:
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                                                                                                                                                                                              Endonucleolytic cleavage
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0; Mismatches
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b. 3e+02;
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ase H (EC 3.1.;
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                                                                                                                                      collaboration
                                                                                                                                                                                                                                                                            virus
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Best Local S
Matches
                                 TISSUE-Fetal liver;
MEDLINE-21177478; PubMed-11280991;
Zhang C.G., Xing G.C., Wei H.D., Y
                                                                                                                                     SEQUENCE FROM N.A.

MEDLINB-20439481; PubMed-10985348;

Salehi A.H., Roux P.P., Kubu C.J., Zeindler C., Bhakar A.,

Tannis L.-L., Verdi J.M., Barker P.A.;

"NRAGE, a novel MAGE protein, interacts with the p75 neurotrophin receptor and facilitates nerve growth factor dependent apoptosis.";
                                                                                                                                                                                                  Genomics [2]
                                                                                                                                                                                                                                                                                                                                   MGD1_HUMAN STANDARD; PRT; 778 AA 09Y5V3; Q9UF36; Q9HBT4; Q9HBS2; 16-OCT-2001 (Rel. 40, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                          TISSUE-Testis;
Blum H., Bauer
                                                                                                                                                                                                        MEDLINE-99339980; PubMed-10409427; Pold M., Zhou J., Chen G.L., Hall J.M., Vescio Fold M., Zhou J., Chen G.L., unorthodox member of "Identification of a new, unorthodox member of Genomics 59:161-167(1999).
                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                               MAGEDI OR NRACE
                                                                SEQUENCE OF 396-778 FROM
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                           "A new melanoma
                                                                                                             SEQUENCE OF 304-778 FROM N.A.
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                                                                                                                                                                                                                                                                                                              MAGED1 OR NRAGE
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         Chuan Hsueh
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                                                                                                                                 27:279-288(2000).
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d (DEC-1999) to
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775
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                         antigen-encoding gene
       28:197-203(2001)
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                                                                                 Mewes H.-W., Gassenhuber J., Wiemann the EMBL/GenBank/DDBJ databases.
                                                                1 N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAGE.
Q -> R (IN REF. 3).
CIL -> WIP (IN REF. 1).
LETELCL -> IGDEAVS (IN REF. 1
WS -> GP (IN REF. 3).
W; 2E554B7B365512E1 CRC64;
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Pred. No
                                                                                                                                                                                                                                                                                Craniata; Vertebrata; | Catarrhini; Hominidae;
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                                     Yu Y.T.,
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                           subfamily
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                                   He
                                  F.C.;
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                                                                                                                                                                                                               R.A., Berenson J.R.;
the MAGE gene family.";
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                           chromosome
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Query Match
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Matches 5
                                             REPEAT
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PROSITE; PS50838; MAGE; 1.

PROSITE: Multigene family;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kubu C.J., Goldhawk D.G., Barker P.A., Verdi J.M.;
"Identification of the translational initiation codon in human
                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION OF THE TRANSLATIONAL INITIATION CODON MEDLINE=20541720; PubMed=11087672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UBIQUITOUSLY EXPRESSED.
SIMILARITY: CONTAINS 1 MAGE DOMAIN.
CAUTION: REF.1 differs from that shown due to seve:
that resulted in a N-terminally truncated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
TISSUE SPECIFICITY: EXPRESSED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          progression, and facilitates p75NTR-mediated apoptosis. May act a regulator of the function of DLX family members. SUBUNIT: Interacts with the p75 neurotrophine receptor. SUBCELLULAR LOCATION: Cytoplasmic. Expression shifts from the cytoplasm to the plasma membrane upon stimulation with NGF (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Involved in the apoptotic response after nerve factor (NGF) binding in neuronal cells. Binds p75NTR and antagonizes its association with TrkA, inhibits cell cycl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOTH MULTIPLE MYELOMA PATIENTS AND
                                                                                                                                                                                                                                                                                                                                                                                                     AF124440; AAD31421.1; ALT_FRAME
AF217963; AAG09704.1; -.
AL133628; CAB63752.1; -.
AF132205; AAG35551.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                            HGNC:6813; MAGED1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
   Similarity
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    Conservative
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33.3%; >---
100.0%; Pr
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                                               86150 MW;
   Score 5; DB 1; Pred. No. 2.9
0; Mismatches
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MAGE.
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                                               OF8BEC7155326FCC CRC64;
                                                                                          (IMPERFECT).
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             1; Le
.9e+02;
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Best Local
                               MGD1_RAT STANDARD; PRT; 775 AA. 09ES73; Q9QX92; Q9JHZ6; 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Melanoma-associated antigen D1 (MAGE-D1 antigen) receptor-interacting MAGE homolog) (Sertoli cell related gene-1) (SNERG-1).
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or send an email to license@isb-sib.ch).
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TISSUE SPECIFICITY: Ubiquitously except for the spleen. Expressed chondrogenic cell lines and also
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AK017275; BAB30666.1; -.
AK013231; BAB38729.1; ALT_INIT
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TE; PS50838; MAGE; 1.
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                     OR NRAGE
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22 X 6 AA TANDEM REPEATS OF W-[PQ]-X-P-X-
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Pred, No.
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224B82470816835A CRC64;
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o. 2.9e+02;
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Hennuy B., Reiter E., Cornet A., Bruyninx M., Daukandt M., Houssa N'Guyen V.-H., Closset J., Hennen G.;
"A novel messenger ribonucleic acid homologous to human MAGE-D is strongly expressed in rat Sertoli cells and weakly in Leydig cells and is regulated by follitropin, lutropin, and prolactin.";
Endocrinology 141:3821-3831(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Sprague-Dawley; TISSUE-Neural crest; MEDLINE-20439481; PubMed-10985348; Salehi A.H., Roux P.P., Kubu C.J., Zeindler C. Tannis L.-L., Verdi J.M., Barker P.A.; "NRAGE, a novel MAGE protein, interacts with receptor and facilitates nerve growth factor receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Testis;
MEDLINE=20466167; PubMed=11014239;
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[2]
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 178-775 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Rattus norvegicus mRNA for SNERG-1 protein, partial CDS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 206-775 FROM N.A.
                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic. Expression shifts from the cytoplasm to the plasma membrane upon stimulation with NGF. TISSUE SPECIFICITY: Ubiquitous and in the seminiferous tubules expressed in sertol1 cells but not in germ cells. Expression decreases in all tissues with increased age and is detectable of the content of the cells of the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             progression, and facilitates p75NTR-mediated apoptosis. May a regulator of the function of DLX family members. SUBUNIT: INTERACTS WITH DLX5, DLX7 AND MSX2 AND FORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Involved in the apoptotic response after nerve factor (NGF) binding in neuronal cells. Binds p75NTR and antagonizes its association with TrkA, inhibits cell cycles.
                                                                             FRAMESHIFT IN POSITION 726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMOMULTIMERS (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases.
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This SWISS-PROT entry is copyright. It is produced through a clotween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT Antigen; DOMAIN InterPro; IPR002190; MA: Pfam; PF01454; MAGE; 3. PROSITE; PS50838; MAGE; EMBL; AF217964; AAG09705.1; EMBL; AJ133038; CAB65381.1; EMBL; AF274043; AAF75283.1; or send an email to license@isb-sib.ch). entities requires a license agreement (See http://www.isb-sib.ch/announce/ Multigene 293 299 305 329 335 341 353 304 310 310 340 346 352 family; MAGE. ALT_FRAME 8765432HX о Х AA TANDEM REPEATS OF W-[PQ]-X-P-Xrestrictions on for outstation no

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'Best Local
    CHAIN
ACT_SITE
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., M Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nha Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                         Pfam; PF00933; Glyco_hydro_3; 1.
Pfam; PF01915; Glyco_hydro_3_C; 1.
PROSITE; PS00775; GLYCOSYL_HYDROL_F3; 1.
                                                                                                                                                                                                                                         StyGene; SG10604; bglx. InterPro; IPR002772; GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-LT2 / SGSC1412 / ATCC 70072
MEDLINE-21534948; PubMed-11677609;
McClelland M., Sanderson K.E., Spi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Periplasmic beta-glucosidase precursor (EC 3.2.1.21)
[Crellobiase] (Beta-D-glucoside glucohydrolase) (T-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q56078;
01-NOV-1997
                                                                                                SIGNAL
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                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as modified and this statement is not removed. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucose residues with release of beta-D-glucose.
-!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001).
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Q56078;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of Salmonella enterica serovar Typhimurium
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287 I
83460 MW;
                                                                                                                                                                                                                                         GH_3C.
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100.0%;
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priplasmic; Signal; Complete prote
POTENTIAL.
PERIPLASMIC BETA-GLUCOSIDASE.
BY SIMILARITY.
R -> L (IN REF. 1).
EA -> KP (IN PEP 1)
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(T-cell inhibitor).
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RESULT 161

MGDL_MOUSE

AC 09QYH6; Q991

AC 09QYH6; Q991

AC 09QYH6; Q991

DT 15-JUN-2002

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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I.,
RA Sakai K., Okido T., Furuno M., Aono H., Beldarelli R., Barsh G.,
Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Kamiya M., Lee N.H.,
Rakai K., Okido T., Furuno M., Hume D.A., Kamiya M., Lee N.H.,
Rakai K., Okido T., Mashima J., Mazzarelli J., Mombaerts P.,
Rakai K., Sato K., Scohenbach C., Seya T., Shibata Y., Storch K.-F.,
Rakai K., Sato K., Scohenbach C., Seya T., Shibata Y., Storch K.-F.,
Rakai K., Sato K., Scohenbach C., Seya T., Shibata Y., Storch K.-F.,
Rakai K., Sato K., Scohenbach C., Seya T., Shibata Y., Storch K.-F.,
Rakai K., Sato K., Scohenbach C., Seya T., Shibata Y., Storch K.-F.,
Rakai K., Sato K., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Melanoma-associated antigen D1 (MAGE-D1 antigen) (Neurotrophin receptor-interacting MAGE homolog) (Dlxin-1).
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CONFLICT
                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21265065; PubMed=11084035; Masuda Y., Sasaki A., Shibuya H., Uen Masuda Y., Sasaki A., Shibuya H., Uen "Dixin-1, a novel protein that binds transcriptional function.";
J. Biol. Chem. 276:5331-5338(2001).
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Mammalia; Eutheria;
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Mus musculus (Mouse).
Chordata;
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"Ten new murine members
                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21085660; PubMed=11217851;
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Auguler P.H., Chomez
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                                                                                                                                                  FUNCTION: Involved in the apoptotic response after nerve growth factor (NGF) binding in neuronal cells. Binds p75NTR and antagonizes its association with TrkA, inhibits cell cycle
                                                            progression, and facilitates p75NTR-mediated apoptosis. a regulator of the function of DLX family members (By structure in the function of DLX family members (By structure).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shinagawa A., Shibata K.,
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V -> F (IN REF. 1).
E -> K (IN REF. 1).
E -> K (IN REF. 1).
C7C767E6CAC96786 (
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No.
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5. 2.9e+02;
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                                                                                                                                                                                                                                                                                    cDNA collection.";
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Fukuda S.,
manaka I.,
Saito R.,
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LOCATION: Cytoplasmic.

Expression shifts from

the

similarity).

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InterPro; IPR002110; ANK.
InterPro; IPR001164; hRIP_like.
Pfam; pr00023; ank; 3.
Pfam; pr00412; ArfGap; 1.
PRINTS; pR00405; REVINTRACTIG.
SMART; SM00248; ANK; 3.
SMART; SM00248; ANK; 3.
SMART; SM00105; ArfGap; 1.
PROSITE; PS50089; ANK_REPEAT; 1.
PROSITE; PS50097; ANK_REP_REGION
PROSITE; PS50115; ARFGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Premont R.T., Claing A., Vitale N., Perry S.J., Lefkowitz R.:
"The GIT family of ADP-ribosylation factor GTPase-activating
Functional diversity of GIT2 through alternative splicing.";
J. Biol. Chem. 275:22373-22380(2000).
                        REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                This SWI
between
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                                                                                                             DOMAIN
ZN_FING
                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.; "Prediction of the coding sequences of unidentified human The coding sequences of 40 new genes (KIAA0121-KIAA0160) of analysis of cDNA clones from human cell line KG-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROMEDLINE-9612
                                                                                                                                                  GTPase activation;
                                                                                                                                                                                                                                                                                       Genew; HGNC:4273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21149839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                     Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH PAXILLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                 short, 3/C-, 4/BC-, 5/E-, 6/CD-, 7/DE-, 8
by alternative splicing. Many more seems
skipping of internal exons.
SIMILARITY: CONTAINS 1 ARF-GAP DOMAIN.
SIMILARITY: CONTAINS 3 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: At least 9 isoforms; 1 (short, 3/C-, 4/BC-, 5/E-, 6/CD-, 7/DE-, 8/BE-,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Interacts with G protein-coupled Associates with paxillin. Also interacts w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: GTPase-activating
                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor family.
                                                                                                                                                                                                                                                                                                 D63482; BAA09769.1; -
BC001379; AAH01379.1;
                                                                                                                                                                                                                                                                                                                        AF124491; AAD28047.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
96127530; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2:167-174(1995).
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              11
132
166
199
466
472
334
415
                                                                                                                                     splicing
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PubMed=8590280;
                                                                                                                                                              ANK_REP_REGION;
ARFGAP; 1.
                                                                                                                                                                                                                                                                                        GIT2
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              124
124
161
161
195
228
271
471
414
464
                                                                                                                                                 Repeat;
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                                                                                                                                                 ANK repeat;
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            ARF-GAP.
C4-TYPE.
ANK 1.
ANK 2.
ANK 3.
QTLQSE-
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-> LGKDAN (IN GIN ISOFORM ) (IN ISOFORM ) (IN ISOFORM ) (IN ISOFORM ) (IN ISOFORM )
                                                                                                                                                 Zinc-finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                              . Usage by and for commercial http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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BE-, 9/AE-; are
           M 2).
M 9).
M 4 AND ISOFORM 0
M 3, ISOFORM 4 AN
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                                                             ISOFORM
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                                                            2).
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RESULT 159
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Best Local (
Matches
                                                                                                                                                                                                                                                                             Blattner F.R., Plunkett G. III, Bloch C.A. Riley M., Collado-Vides J., Glasner J.D., Gregor J., Davis N.W., Kirkpatrick H.A., G. Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
SEQUENCE
         EcoGene; EG12013; bg1X.
InterPro; IPR002772; GH_3C.
InterPro; IPR001762; GH_3N.
InterPro; IPR001762; GH_3N.
Pfam; PF01933; Glyco_hydro_3; 1.
PRINTS; PR00133; GLHYDRLASE3.
                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P333b3;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Periplasmic beta-glucosidase precursor (EC 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BGLX_ECOLI P33363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC VARSPLIC
                                                                                                                                                                                                                                                            "The complete genome sequence of Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-K12 / MG1655; MEDLINE-97426617; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang
                                                                           EMBL; U15049; AAB38487.1; -.
EMBL; U00007; AAA60495.1; ALT_INIT.
EMBL; AE000302; AAC75193.1; -.
                                                                                                                                                                                                                             <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-1993)
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Church G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586 STPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                               CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing lucose residues with release of beta-D-glucose. SUBCELLULAR LOCATION: Periplasmic. SIMILARITY: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                          X
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5; Conserv
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Luoh S., God
d (SEP-1994)
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759
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 GLYCOSYL_HYDROL_F3;
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84542
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577
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                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN ISOFORM 6 AND ISOFORM 7, MISSING (IN ISOFORM 5, ISOFORM 7, ISOFORM 8 AND ISOFORM 9).

V -> M (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reilly
                                                                                                                                                                                                                                                                                                                                                                                                 G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                         Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                   Jaehn
                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 759 . 2.9e+02;
                                                                                                                                                                                                                                                                                             .A., Perna N.T., Burland V
., Rode C.K., Mayhew G.F.,
, Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                   L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Henzel W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2.1.21) (Gentiobiase)
                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
                                                                                                                                                                                                                                                                                                                                                                             databases
                                                                                                                                                                                                                                                   non-reducing
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                                                                                                                                                                     restrictions
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                                                                                                                                                                                  collaboration -
                                                                                                                                                                                                                                                    beta-D-
                                                                                                                                                                                 outstation
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В
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                                                                                                                                                                         InterPro, IPRUo...
InterPro, IPRUo...
Pfam; PF00168; C2; 1.
Pfam; PF00175; PLA2_B; 1.
R SMART; SM00239; C2; 1.
OR SMART; SM00022; PLAC; 1.
OR PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
OR PROSITE; PS50004; C2_DOMAIN_2; 1.
OR PROSITE; PS50004; C2_DOMAIN_2; 1.
OR PROSITE; PS50004; C2_DOMAIN_3
OR PHOSPHOLIPID BINDING (PROBABICAL DATE)
OR PHOSPHORYLATION (BY MAPK) ('OR PHOSPHORYL
                                                                                                                                                                                                             Matches
                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE INFLAMMATORY RESPONSE.

-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acylglycerophosphocholine + a fatty acid anion.
-!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)0 =
glycerophosphocholine + a fatty acid anion.
-!- ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ATP, EGF,
THROWBRIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC. TRANSLOCATES TO MEMBRANE
VESICLES IN A CALCIUM-DEPENDENT FASHION (BY SIMILARITY).
-!- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID
MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE
ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF
CYTOSOLIC CA2+ (BY SIMILARITY).
-!- PTM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE (BY
SIMILARITY): CONTAINS 1 C2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phospholipase A2, a regulatory Ca(2+)-dependent lipid-binding domain and a Ca(2+)-independent catalytic domain.";

J. Biol. Chem. 269:18239-18249(1994).

-i- FUNCTION: SELECTIVELY HYDROLYZES ARACHIDONYL PHOSPHOLIPIDS IN THE SN-2 POSITION RELEASING ARACHIDONIC ACID. TOGETHER WITH ITS LYSOPHOSPHOLIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---
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Cytosolic phospholipase A2 (CPLA2) [Includes: Phospholipase A2
(EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase
(EC 3.1.1.5)]
PLA264A OR PLA264 OR CPLA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZFIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           +
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Eukaryota; Metazoa; Chordata;
Actinopterygii, Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nalefski E.A., Sultzman L.A., Martin D.M., Kriz R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Delineation of two functionally distinct domains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knopf J.L., Clark J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94299545; PubMed=8027085;
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  47
                                                    9
                                                  TPESR 13
  TPESR 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZDB-GENE-990415-45; cpla2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U10330; AAA53229.1; -. P47712; 1BCI.
                                                                                                      Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-profit institutions as long as its content
                                                                                                      Conservative
                                                                                                                               33.3%;
100.0%;
                                                                                                      0
                                                                                                                          Score 5;
Pred. No
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
                                                                                                    red. No. 2.8
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                               . DB
                                                                                                                               1; Le
.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage by and
                                                                                                                                                      Length 741;
                                                                                                                                                                                                                                                                                                                  (PROBABLE).
                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytosolic
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RESULT 157
YKN9_YEAST
ID YKN9_YEAST
AC P36124;
DT 01-JUN-1994
DT 01-JUN-2002
DE Hypothetica.
GN YKN029C.
OS Saccharomyc.
OC Eukaryota;
OC Saccharomyc.
OX NCBL_TaxID=
RP SEQUENCE FR
RA Urrestarazu
RL Submitted (
CC -!- SIMILAR
CC -!
RESULT 158
GIT2_H
GIT2_H
AC Q14161
DT 01-NOV
DT 16-OCT
DT 15-JUN
DE ARF GT
DE Intera
GN GIT2 O
OCS Homo s
OC Eukary
OC Mammall
OX NCB1_T
RN [1]
RP SEQUEN
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                                                                                                                                                                                                                                                                                             _HUMAN
_HUMAN STANDARD; PRT; 759 AA
Q14161; Q9Y5V2; Q9BV91;
Q1.NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
ARF GTPase-activating protein GIT2 (G prote
interactor 2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P36124;
01-JUN-1994
01-JUN-1994
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Urrestarazu L.A., Jauniaux J.-C.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO YEAST YJL105W AND S.POMBE SPAC22E12.11C.
-!- SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS 1 SET DOMAIN.
SEQUENCE FROM N.A. (ISOFORMS 1 TO 9), MEDLINE=20357364; PubMed=10896954;
                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                  GIT2 OR KIAA0148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50280; SET; 1.
PROSITE; PS01359; ZF_PHD_1; 1.
PROSITE; PS50016; ZF_PHD_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00249; PHD; 1.
SMART; SM00317; SET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00628; PHD; Pfam; PF00856; SET;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S38101; S38101.
SGD; S0001737; YKR029
InterPro; IPR001214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          movilies requires a license agreement (See http://www.isb-sib.ch/announce/
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes
                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z28254; CAA82101.1; -.
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117 166
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. 29, Last sequence upd
. 41, Last annotation u
. 41, sequence in SAP19(
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100.0%; Pr
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85479 MW;
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6 PHD-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SET
                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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SAP190-SP014 intergenic region.
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                                       AND
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protein-coupled receptor kinase-
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o. 2.8e+02;
                                       CHARACTERIZATION
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InterPro; IPR003987; ICAM_VCAM-1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003508; Ig_C2.
InterPro; IPR003600; Ig_like.
InterPro; IPR003989; VCAM-1.
Pfam; PF0047; ig; 6.
PRINTS; PR01472; ICAMVCAM1.
PRINTS; PR01474; VCAM1.
SMART; SM00410; IG_like; 2.
SMART; SM00410; IG_like; 2.
SMART; SM00410; IG_like; 2.
SMART; SM00408; IGC2; 3.
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between
the Euro
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DOMAIN
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EMBL; M30257; AAA51917.1; ALT_TERM.
EMBL; M73255; AAA61270.1; -.
EMBL; M60335; AAA61269.1; -.
PIR; A33758; A33758.
PIR; A39755; A39755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PDB; 1VCA; 15-SEP-95.
PDB; 1VSC; 20-JUN-96.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDUCTION: BY CYTOKINES (E.G. IL-1, TNF-ALPHA).

PTM: STALOGLYCOPROTEIN.

DISEASE: MAY PLAY AN IMPORTANT ROLE IN THE GENESIS OF
ARTHEROSCLEROSIS AND RHEUMATOID ARTHRITIS.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN LIKE C2-TYPE DOWNSTANDARIANS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOWNTARRY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOWNTABASE: NAME-PROW; NOTE-CD guide CD106 entry;

MAWA-"http://www.nobi.nlm.nlh.gov/prow/cd/cd106.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN LEUKOCYTE-ENDOTHELIAL CELL ADHESION. INTERACTS WITH THE BETA-1 INTEGRIN VLA4 ON LEUKOCYTES, AND MEDIATES BOTH ADHESION AND SIGNAL TRANSDUCTION. THE VCAMI/VLA4 INTERACTION MAY PLAY A PATHOPHYSIOLOGIC ROLE BOTH IN IMMUNE RESPONSES AND IN LEUKOCYTE EMIGRATION TO SITES OF INFLAMMATION.

SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type I sofforms; A LONG FORM (SHOWN ALTERNATIVE PRODUCTS; AT LEAST 2 ISOFFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EXPRESSED ON INFLAMED VASCULAR ENDOTHELIUM, AS WELL AS ON MACROPHAE-LIKE AND DENDRITIC CELL TYPES IN BOTH NORMAL AND TATELAMED TISSUES OF THE STREET 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A41288;
B41288;
S11476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no war
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FUNCTION: IMPORTANT IN CELL-CELL RECOGNITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND INFLAMED TISSUE
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B41288.
S11476.
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739
698
720
739
106
202
202
287
379
496
675
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPICASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 5.
IG-LIKE C2-TYPE DOMAIN 6.
IG-LIKE C2-TYPE DOMAIN 7.
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                                                                                                                                                                                                                                                                  VASCULAR CELL
                                                                                                                                                                                                                                                                                                                     3D-structure
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RESULT 156
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BSG2_DROME
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P11929;
01-OCT-1989 (Rel. 1
01-OCT-1989 (Rel. 1
01-MAR-1992 (Rel. 2
PA24_BRARE
P50392;
01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

MCBI_TaxID=7227;
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MEDLINE-87174755; PubMed-3104878;

Boyer P.D., Mahoney P.A., Lengyel J.A.;

"Molecular characterization of bsg25D: "
                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                      PIR; A26572; A26572.
FlyBase; FBgn0000228; Bsg25D
                                                                                                                                                                                                                                                                   EMBL; X04896; CAA28582.1; -.
                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.";
Nucleic Acids Res. 15:2309-2325(1987).
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                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                              between
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5; Conserv
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5; Conser
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ilarity 100.0%;
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SEQUENCE FROM N.A.
Miyata T., Inagi R., Yasuda '
"Homo sapiens meg-3 mRNA, co'
"Homo sapiens may-1999) to the
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                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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Mammalia; Eutheria; Primates;
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
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PRINTS; PR00742; GLHYDRLASE35.
PROSITE; PS01182; GLYCOSYL_HYDROL_F35;
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AL137555; CAB70809.1;
BC001979; AAH01979.1;
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  179 P
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PROTON DONOR (POTENTIAL).
NUCLEOPHILE (POTENTIAL).
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-> L (IN REF. 3).
38E1C24CF737F3DB CRC64;
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Best Local (
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Cybulsky M.I., Fries J.W.U., Williams A.J., Sultan P.,
Byers M., Shows T., Gimbrone M.T., Collins T.;
"Gene structure, chromosomal location, and basis for al
splicing of the human VCAMI gene.";
Proc. Natl. Acad. Sci. U.S.A. 88:7859-7863(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90090619; PubMed-2688898; MEDLINE-90090619 C., Tizard R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGAM1 OR LALL,
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Eukaryota; Metheria; Primates;
                                   Browning B., Osborn L.;
"The crystal structure of an N-terminal two-domain fragment vascular cell adhesion molecule 1 (VCAM-1); a cyclic peptide
                                                                                    X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) MEDLINE=95296382; PubMed=7539925;
                                                                                                                                   Jones E.Y., Harlos K., Bottomley M.J., Robinson R.C.,
Edwards R.M., Clements J.M., Dudgeon T.J., Stuart D.I.
"Crystal structure of an integrin-binding fragment of
adhesion molecule-1 at 1.8-A resolution.";
                                                                                                                                                                                    x-ray Crystallography (1.8 angstroms) MEDLINE-95147978; PubMed-7531291;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=91201302; PubMed=1707873;

Hession C., Tizard R., Vassallo C., Schiffer S.B.,

Chi-Rosso G., Luhowskyj S., Lobb R., Osborn L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Osborn L., Hession C., Tiza
Chi-Rosso G., Lobb R.;
"Direct expression cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Umbilical vein;
MEDLINB=91016951; PubMed=1699207;
Polte T., Newman W., Gopal T.V.;
"Full length vascular cell adhesion mo."
Nucleic Acids Res. 18:5901-5901(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, I
15-JUN-2002 (Rel. 41, I
Vascular cell adhesion
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                                                                       Wang J.-H., Pepinsky R.B., Stehle
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VCAM1 OR L1CAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P19320;
01-NOV-1990
                                                                                                                         Nature
                                                                                                                                                                                                                                      "Cloning of an alternate form of vascular cell adhesion (VCAM1).";
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 59:1203-1211(1989).
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(Rel. 16,
(Rel. 41,
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100.0%; Pr
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al protein that binds
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  92:5714-5718(1995)
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T.,
                        VCAM-1-alpha 4 integrin
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                                                                       Liu J.-H., Karpusas
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RESULT 151
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AC 000662
DT 01-APR
DT 15-JUN
DE PUTAT1
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Best Loc
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Putative beta-galactosidase precursor (EC 3
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                                                                       Dianthus caryophyllus (Carnation) (Clove pink).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.
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Prodom; PD000448; NA_Ntiral_symport; 2.
PROSITE; PS00610; NA_NEUROTRAN_SYMP_1;
PROSITE; PS00754; NA_NEUROTRAN_SYMP_2;
PROSITE; PS50267; NA_NEUROTRAN_SYMP_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: L06434; AAB24776.1; -.
EMBL: S68944; AAC60673.1; -.
PIR: S27043; S27043.
InterPro; IDR000175; Na/ntran_symport.
Pfam: PF00209; SNF; 1.
SEQUENCE FROM N.A.
STRAIN-cv. White Sim; TISSUE-Peta
MEDLINE-91329738; PubMed-1868223;
Raghothama K.G., Lawton K.A., Gol
"Characterization of an ethylene-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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5; Conserv
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an email to license@isb-sib.ch).
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100.0%; Prv
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12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (PO
N-LINKED (GLCNAC. . .) (PO
Y -> C (IN REF. 2).
G -> S (IN REF. 2).
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8 (POTENTIAL).
9 (POTENTIAL).
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4 (POTENTIAL).
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3 (POTENTIAL)
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            Goldsbrough P
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-> S (IN REF. 2).
C676048COA6BDF7C CRC64;
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red. No. 2.8
Mismatches
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(EC 3.2.1.23)

    Transmembrane; Glycoprotein;

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                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                 Plant
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Beta-galactosidase precursor (EC 3.2.1.23) (Lactase)
galactosidase) (Exo-(1-->4)-beta-D-galactanase).
Malus domestica (Apple) (Malus sylvestris).
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                          Ross
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Granny Smith; TISSUE=F MEDLINE=95083752; PubMed=7991682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                  *Apple beta-galactosidase. Activity against cell wall polysaccharides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56
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                                                                                                                                                     characterization of a related CDNA clone."; int Physiol. 106:521-528(1994).

FUNCTION: Involved in cell wall degradation. De polysaccharides containing beta-(1-->4) linked as an exo-(1-->4)-beta-D-galactanase.

CATALYTIC ACTIVITY: Hydrolysis of terminal, non galactose residues in beta-D-galactosides.

SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HY
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SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES
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IPR001944; GH_35.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Smith; TISSUE=Fruit cortical tissue;
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  (See
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                                                                                                                                                                                                           non-reducing
                                                                                                                                                               HYDROLASES
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                                                                                                                                                                                                                                                      galactans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eudicots;
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RESULT 149
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Matches
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
ARF GTPase-activating protein GIT2 (G protein coupled receptor kinase-interactor 2) (Tyrosine-phosphorylated protein CAT-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02518; HATPASE_C; 1.
PRINTS; PR00775; HEATSHOCK90.
SMART; SM00387; HATPASE_C; 1.
PROSITE; PS00228; HSP90; 1.
Chaperone; ATP-binding; Heat shock.
                                                                                                                                                                        -i- FUNCTION: GTPase-activating protein for the factor family (By similarity).
-i- SUBUNIT: Interacts with G protein-coupled Associates with paxillin. Also interacts of factors (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=99357767; PubMed=10428811;
Bagrodia S., Bailey D., Lenard Z.,
Taylor S.J., Cerione R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Requena J.M.;
Submitted (APR-2002) to
-i- FUNCTION: MOLECULAR
                                                                                                                                                                                                                                                                                               proteins.";
J. Biol. Chem. 274:22393-22400(1999).
                                                                                                                                                                                                                                                                                                                                                     regulatory region on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P07900;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         œ
                                                                         PTM. Tyrosine-phosphorylated when co-expressed focal adhesion kinase Fak and Src. STMILARITY: CONTAINS 1 ARF-CAP DOMAIN. SIMILARITY: CONTAINS 3 ANK REPEATS.
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SIMILARITY: BELONGS TO
                            SWISS-PROT entry is
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P07900; 1YER.
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5; Conser
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     Swiss Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
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copyright. It is produced through a collaboration tute of Bioinformatics and the EMBL outstation -
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O THE HEAT SHOCK PROTEIN 90 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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o. 2.7e+02;
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p21-activated
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ACTIVITY
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ed kinase-binding
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Best Local
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Pfam; PF01412; ArfGap; 1.

PRINTS: PR00405; REVINTRACTING.

SMART; SM00248; ANK; 1.

SMART; SM00105; ArfGap; 1.

PROSITE; PS50088; ANK_REP_REGION; 1.

PROSITE; PS50297; ANK_REP_REGION; 1.

PROSITE; PS50215; ARFGAP; 1.
                                                                                                                                  GABAergic and glutamatergic neurons in the rat J. Neurochem. 62:445-455(1994).
-i- FUNCTION: NOT YET KNOWN, ORPHAN TRANSPORTER
                                                                                                                                                                                 "Characterization of an atypical member of the Na+/Cl(-)-dependent transporter family: chromosomal localization and distribution in GABAergic and glutamatergic neurons in the rat brain.";
                                                                                                                                                                                                                                                MEDLINE=94125086; PubMed=8294906;
el Mestikawy S., Giros B., Pohl M.,
Seldin M.F., Caron M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZN_FING
REPEAT
                            -
                                                                   -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CEREBELLUM AN
                                                                                                                                                                                                                                                                                                                                                                   "A rat brain cDNA encoding the unusual structure.";
FEBS Lett. 315:114-118(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93114444; PubMed=8093354;
Liu Q.-R., Mandiyan S., Lopez-Corcuera B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orphan sodium-
NTT4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUI-1993 (Rel. 26, Created)
01-JUI-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Orphan sodium- and chloride-dependent neurotransmitter transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FISSUE-Brain;
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CORTEX.
- SIMILARITY:
FAMILY (SNF)
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                         BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Repeat; ANK repeat; 1
124 ARF-GAP.
34 C4-TYPE.
161 ANK 1.
195 ANK 2.
228 ANK 3.
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                            THE
                                                                                                                                                                                                                                                                                                                                                                                                               pez-Corcuera B., Nelson H., Nelson N.;
the neurotransmitter transporter with
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                         SODIUM: NEUROTRANSMITTER SYMPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BEA1C5D74182D8CA CRC64;
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                                                                      CEREBELLUM AND
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RP SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RR SEQUENCE FROM N.A.

RR SEQUENCE FROM N.A.

REDLINE-97313371; PubMed-9169875;

RX MEDLINE-97313371; PubMed-9169875;

RX MEDLINE-97313371; PubMed-9169875;

RA Bussey H., Storms R.K., Ahmed A., Albermann K., Benes V.,

RA Bussey H., Storms R.K., Ahmed A., Albermann K., Benes V.,

RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,

RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,

RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,

RA Chung E., Churcher C.M., Coster F., Davis E., Davis R.W.,

RA Dietrich F.S., Delius H., DiPaolo T., Dubbis E., Duesterhoeft A.,

RA Duncan M., Floeth M., Fortin N., Friesen J.D., Filtz C., Goffeau A.,

RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,

RA Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,

RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,

RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,

RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,

RA Komp C., Kurdi O., Lashkari D., Mewes H.-W., Mirtipati S., Moesti D.,
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Best Local S
Matches 5
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Pfam; PF02318; RPH3A_effector; 1.

PRINTS; PR00369; C2DOMAIN

PRINTS; PR00399; SYNAPTOTAGMN.

SMART; SM00239; C2; 2.

PROSITE; PS00499; C2_DOMAIN_1; 2.

PROSITE; PS50004; C2_DOMAIN_2; 2.

PROSITE; PS50178; ZF_FYVE; 1.
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DOMAIN
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P37838;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Nucleolar protein NOP4 (Nucleolar prot
NOP4 OR NOP77 OR YPL043W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _YEAST
                                                                                                                                                                                                                                                                        Berges T., Petfalski E., Tollervey D., Hurt E.C.; 
"Synthetic lethality with fibrillarin identifies 
protein required for pre-rRNA processing and modi 
EMBO J. 13:3136-3148(1994).
                                                                                                                                                                                                                                                                                                                                                                                          EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-94313993; PubMed-8039505;
Sun C., Woolford J.L. Jr.;
"The yeast NOP4 gene product is a
required for pre-rRNA processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacclaromycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000008; C2.
InterPro; IPR002149; LRI.
InterPro; IPR003315; RPH3A_effector.
InterPro; IPR001555; Synaptotagmin.
InterPro; IPR000306; Znf_FYVE.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-94313994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synapse;
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280
384
542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                         PubMed-8039506;
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364
488
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                                                                                                                                                                                                                                                                                                                                                                                                                    product is an essential nucleolar protein A processing and accumulation of 60S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.3%;
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FYVE-TYPE.

PRO-RICH.

C2 DOMAIN 1.

C2 DOMAIN 2.

C2 DOMAIN 2.
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Pred. No. 2.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sport; Zinc-finger; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                            modification.";
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RESULT 148
HS83_LEIIN
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Best Local S
Matches 5
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EMBL; X76245; CAA53824.1; -.
EMBL; U4030; AAB68177.1; -.
PIR; S46365; S46365.
PIR; S45178; S45178.
HSSP; P09651; 1HA1.
SGD; S0005964; NOP4.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                 15-DEC-1998
15-JUN-2002
15-JUN-2002
SEQUENCE FROM N.A.

STRAIN-LEM 75 / Zymodeme 1;

STRAIN-P97123362; PubMed-8971277;

MEDILINE-97126362; PubMed-8971277;

Angel S.O., Requena J.M., Soto M., Criado D., Alonso "During canine leishmaniasis a protein belonging to heat-shock protein family elicits a strong humoral racta Trop. 62:45-56(1996).
                                                                                                                                                                                                      HS83_LEIIN
Q25293;
                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
SEQUENCE
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DOMAIN
DOMAIN
DOMAIN
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"The nucleotide sequence of Saccharomyces cerevisiae chromosome Nature 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                   Leishmania infantum.
Eukaryota; Euglenozoa;
CCBI_TaxID=5671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- FUNCTION: REQUIRED FOR 60S RIBOSOMAL SUBUNIT S INVOLVED IN THE PROCESSING OF 27S RRNA TO PROD -I- SUBUNIT: INTERACTS WITH NOPL -I- SUBCELLULAR LOCATION: Nuclear; nucleolar.-I- SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS
                                                                                                                                          HSP83-
                                                                                                                                                     Heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00360; RRM; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00076; rrm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosome
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                                                                                                                                                                                                                                                                                117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biogenesis; Nuclear
                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                    685
                                                                                                                                                   (Rel. 37, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
protein 83-1 (HSP 83).
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147
290
462
241
308
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225
383
612
617
267
308
77825
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100.0%; Pr
0;
                                                                                                                Kinetoplastida;
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%; Pred. No. 2.6
0; Mismatches
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RNA-BINDING
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RNA-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                   -> A.
61261815EA3DEE5C CRC64;
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There are no rescritory as its content long as its content long and rescritory.
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                                                                                                                 Trypanosomatidae; Leishmania.
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(RRM)
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                                                                                                                                                                                                                                                                                                                                                                                                          (ACIDIC).
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               humoral response.";
                                       Alonso
                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                        Length 685
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                             the 83-kDa
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tent is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    processing
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Voss H.,
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RESULT 145
RP3A_MOJAE
RP3A_MOJAE
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ID3A_MOJE
ID3A_MOJAE
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                    InterPro; IPROC
InterPro; IPROC
InterPro; IPROC
InterPro; IPROC
InterPro; IPROC
Pfam; PFOO168;
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01-FEB-1996 (Rel. 33, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a centre of the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and content of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                entities requires a license agreement
                                                                                                                                InterPro;
                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95122445; PubMed=7822236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-606 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Cloning of a mouse Rabphilin-3A expressed in hormone-secreting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inagaki N., Mizuta M., Seino S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RP3A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: PROTEIN TRANSPORT, PROBABLY INVOLVED WITH RAS-RELATED PROTEIN RAB-3A IN SYNAPTIC VESICLE TRAFFIC AND/OR SYNAPTIC VESICLE FUSION. COULD PLAY A ROLE IN NEUROTRANSMITTER RELEASE BY
                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 2 C2 DOMAINS. SIMILARITY: CONTAINS 1 FYVE-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGULATING MEMBRANE FLOW IN THE NERVE SUBUNIT: MONOMER.
TISSUE SPECIFICITY: SPECIFICALLY EXPRI
                                                                                                                                                         MGI:102788;
                                                                                                                                                                           D29965; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00515;
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                                                            IPR000008; C2.
IPR002149; LRI.
IPR003315; RPH3A_effector.
IPR001565; Synaptotagmin.
                                             IPR000306;
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  RPH3A_effector; 1
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Rodentia;
                                          Synaptotagmin.
Znf_FYVE.
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COILED COIL (POTENTIAL).
GLU-RICH (ACIDIC).
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Pred. No
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Sciurognathi; Muridae; Murinae;
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o. 2.6e+02;
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RESULT 146
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                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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           EMBL; U12571;
                                                                                                                                                                                                                                           the small G protein Rab3A rabphilin-3A.";
                                                                                                                                                                                                                                                                                                                                                  Li C., Takei K., Geppert M., Daniell L., Stenius K., Ch
Jahn R., de Camilli P., Suedhof T.C.;
"Synaptic targeting of rabbhilin-3A, a synaptic vesicle
Ca2+/phospholipid-binding protein, depends on rab3A/3C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Mammalia; Eutheria;
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01-FEB-1996 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00499; C2_DOMAIN_1; PROSITE; PS50004; C2_DOMAIN_2; PROSITE; PS50178; ZF_FYVE; 1.
                                                                                                                                                                                                                                                                              Ostermeier C., Brunger A.T
                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-95033210; PubMed-7946335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
Eukaryota; Metazoa; Cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rabphilin-3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                    "Structural basis of Rab effector
                                                                                                                                                                                                                                                                                           MEDLINE=99148269; PubMed=10025402;
                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                          Neuron 13:885-898(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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                                                                                                                              SUBUNIT: MONOMER.
TISSUE SPECIFICATY: SPECIFICALLY EXPRESSED IN
SIMILARITY: CONTAINS 2 C2 DOMAINS.
SIMILARITY: CONTAINS 1 FYVE-TYPE ZINC FINGER.
                                                                                                                                                                              FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED WITH RAS-RE PROTEIN RAB-3A IN SYNAPTIC VESICLE TRAFFIC AND/OR SYNAPTIC VESICLE FUSION. COULD PLAY A ROLE IN NEUROTRANSMITTER RELERBULATING MEMBRANE FLOW IN THE NERVE TERMINAL.
                                                                                                                                                                                                                                 96:363-374(1999).
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RAB P2
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complexed with the ef
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C2 DOMAIN 1.
C2 DOMAIN 2.
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FYVE-TYPE.
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REPEAT
                                                                                                                                                                                                                                        STRAIR-Sprague-Dawley: TISSUE-Liver;
STRAIR-Sprague-Dawley: TISSUE-Liver;
MEDLINE-95331313; PubMed-7607247;
Fan H., Josic D., Lim Y.P., Reutter W.;
"CDNA cloning and tissue-specific regulation of expression of calcium-binding protein 65/67. Identification as a homologue annexin VI.";
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
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                                                                              CALCIUM AND PHOSPHOLIPID.

CASICILANEOUS: SEEMS TO BIND ONE CALCIUM I SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

SIMILARITY: CONTAINS 8 ANNEXIN REPEATS.
                                                                                                                                                          J. Biochem. 230:741-751(1995).
FUNCTION: MAY ASSOCIATE WITH CD21.
CA(2+) FROM INTRACELLULAR STORES.
DOMAIN: A pair of annexin repeats n
                      SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSTPE 11
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MGI:88255; Anxa6.
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5; Conserv
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ANNEXIN 3.
ANNEXIN 5.
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ANNEXIN 8.
ANNEXIN 8.
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Sciurognathi; Muridae;
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Annexin;
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                                        This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 NASP_RABIT P27123;
                                                                                                                               Welch J.E., Zimmerman L.J., Joseph D.R., O'Rand M.G.;

"Characterization of a sperm-specific nuclear autoantigenic protein.

"Complete sequence and homology with the xenopus protein, N1/N2.";

Biol. Reprod. 43:59-568(1990).

-!- FUNCTION: MAY PLAY A ROLE IN REGULATING THE EARLY EVENTS OF SPERMATOGENESIS BY BINDING NEWLY SYNTHESIZED HISTONES VARIANTS AI TRANSPORTING THEM TO THE NUCLEUS.

-!- SUBCELLULAR LOCATION: NUCLEUS.

-!- SUBCELLULAR LOCATION: NUCLEUS.

-!- SIBILARITY: WITH XENOPUS HISTONE-BINDING PROTEIN N1/N2.
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01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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or send an email 1
                    EMBL; M37893; AAA31423.1;
                                                                                                                                                                                                                                                   STRAIN-New Zealand white; TISSUE-Testis; MEDLINE-91145522; PubMed-2289010;
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ANNEXIN 3.
ANNEXIN 4.
ANNEXIN 5.
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ANNEXIN 6.
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Annexin VI (Lipocortin VI) (P68) (P70) (Protein III)
(67 kDa calelectrin) (Calphobindin-II) (CPB-II).
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MEDLLNE=96336697; PubMed=8709144;
Benz J., Bergner A., Hofmann A., Deman
Huber R., Voges D.;
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protein from human placenta.";
J. Biochem. 107:43-50(1990).
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Yoshizaki H., Mizoguchi T., Arai
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MEDLINE-88124902; PubMed-2963335;
Suedhof T.C., Slaughter C.A., Leznicki I., Barjon
"Human 67-kDa calelectrin contains a duplication of the contains of the contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Primary structure of the human, membrane-associated protein p68 a novel member of a protein family."; EMBO J. 7:21-27(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-2001) to the EMBL/GenBank/DDBJ
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ween the Swiss Institute ... There are ... European Bioinformatics Institute. There are ... European Bioinformatics Institutens as long as its content is in the summer of this statement is not removed. Usage by and for commercial iffied and this statement is not removed. Usage by and for commercial rities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                            DOMAIN: A pair of annexin repeats may form on calcium and phospholipid.

PTM: PHOSPHORYLATED IN RESPONSE TO GROWTH FACMISCELLANBOUS: SEEMS TO BIND ONE CALCIUM ION SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

SIMILARITY: CONTAINS 8 ANNEXIN REPEATS.
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Natl. Acad. Sci. U.S.A. 85:664-668(1988)
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ens R.J., Totty N.F.,
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AC P14824;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 14, Last sequence)
DT 15-JUN-2002 (Rel. 14, Last annotation update)
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DNA replication; DNA-binding; Helicase; Primosome; Zinc-finger; Metal-binding; Complete proteome.
ZN_FING 371 383 C4-TYPE (POTENTIAL).
ZN_FING 399 414 C4-TYPE (POTENTIAL).
SEQUENCE 651 AA; 69923 MW; 06CFE91D208C7043 CRC64;
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Nature 404:502-506(2000).

-I- FUNCTION: This protein is involved in the repair of mismatches in DNA. It is required for dam-dependent methyl-directed DNA mismatch repair. May act as a "molecular matchmaker", a protein that promotes the formation of a stable complex between two or more DNA-binding proteins in an ATP-dependent manner without itself being part of a final effector complex (By similarity).

-I- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., HO Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Train of Neisseria Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9JTS2:
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA mismatch repair protein mutL.
                                                                                                                                   InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR002099; DNA_mis_repair.
Pfam; PF01119; DNA_mis_repair; 1.
Pfam; PF02518; HATPase_C; 1.
TIGREAMS; TIGR00585; mutl; 1.
                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no use by non-profit institutions as long as its commodified and this statement is not removed. Usage by entitles requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis (se
Bacteria; Proteobacteria;
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                                                        PS00058; DNA_MISMATCH_REPAIR_1; FALSE_NEG
ir; Complete proteome.
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MEDLINE-2015755; PubMed-10710307;

Eisen J.A., Ketchum K.A., Heod D.W., Deden J.F., Dodson R.J.,

Eisen J.A., Ketchum K.A., Hood D.W., Peder J.F., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,

Nelson W.C., Gwinn M.L., White O., Fleischmann R.D., Dougherty B.A.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,

Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

Cotton M.D., Utterback T.R., Khouri H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Plzza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                        InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR002099; DNA_mis_repair;
Pfam; PF011119; DNA_mis_repair; 1.
Pfam; PF02518; HATPase_C; 1.
                                                                                                                                                                                                                                                          EMBL; AE002493; AAF41803.1; HSSP; P23367; 1BKN.
TIGR; NMB1442; -
                                                                                                                                                                                                                                                                                                                    entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no resta
                                                                                                                                                     Pfam; PF02518; HATPASE_C; 1.
TIGRRAMS; TIGR00585; mutl; 1.
PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:1809-1815(2000)
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Bacteria; Proteobacteria;
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                                                                                                                                             DNA repair;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
                                ESRAA 15
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412
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658 AA; 71646 MW;
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Mismatches
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EMBL outstation

Institute of Bioinformatics and the

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RESULT 137

VP74_NPVOP

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01-NOV-1997
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CONFLICT
CONFLICT
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MEDLINE=97271300; PubMed=9126251;
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PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.

Multigene family; G-protein coupled receptor;

Developmental protein; Glycoprotein; Signal.
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or send an email to license@isb-sib.ch).
                         NCBI_TaxID=164623;
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Pfam; PF01534; Frizzled; 2.
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(Rel.
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RESULT 138
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Q9CCQ3;
16-OCT-2001
                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruct use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                      "Massive gene decay in the leprosy bacillus.";

Nature 409:1007-1011(2001).

-i- FUNCTION: RECOGNIZES A SPECIFIC HAIRPIN SEQUENCE ON PHIX SSDNA;

THIS STRUCTURE IS THEN RECOGNIZED AND BOUND BY PROTEINS PRIB AN

PRIC. FORMATION OF THE PRIMOSOME PROCEEDS WITH THE SUBSEQUENT

PRIC. FORMATION OF THE PRIMOSOME PROCEEDS WITH THE SUBSEQUENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Virology 229:381-399(1997).
-!- FUNCTION: ESSENTIAL FOR VIRULENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-TN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1769;
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                                                                                                                                                                                                                                   ACTIONS OF DNAB, DNAC, DNAT AND PRIMASE. PRIA THEN FUNCTIONS HELICASE WITHIN THE PRIMOSOME (BY SIMILARITY). SIMILARITY: BELONGS TO THE HELICASE FAMILY. PRIA SUBFAMILY. CAUTION: COMPARED TO OTHER BACTERIAL PRIA, IT HAS A VERY DIVE
                                                                                                                                                                                                            HELICASE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 40, Creact, (Rel. 40, Last sequence update) (Rel. 41, Last annotation update recommal protein N' (Replication)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor Y).
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MBL outstation -
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InterPro; IPR000539; Frizzled.
InterPro; IPR00024; Fz_domain.
InterPro; IPR000832; GPCR_secretin.
Pfan; PF01392; Fz; 1.
Pfam; PF01534; Frizzled; 1.
PRINTS; PR00489; FRIZZLED.
SMART; SN0063; FRI; 1.
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PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.

Multigene family; G-protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99324245; PubMed-10395542;
Sheldahl L.C., Park M., Malbon C.C., Moon R.T.;
"Protein kinase C is differentially stimulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Two homologs of the Drosophila polarity expressed in mammalian tissues.":
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                        Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUPLING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93094228; PubMed-1334084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Sprague-Dawley; TISSUE-Osteosarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             target genes.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Widely expressed. Most abund liver, uterus, ovary and heart. Lower levels see intestine. Extremely low in calvaria, mammary glanterstine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Receptor for What proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of What target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for What-mediated inactivation of GSK-3 kinase. Both pathways seem to require the control of the control of GSK-3 kinase. Both pathways seem the canonical pathway has pkc seems to be required to what was the control of GSK-3 kinase. Both pathways seem the control of GSK-3 kinase seem the control of GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Wnt/beta-catenin signaling DOMAIN: The fz domain is involv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at lower levels in adult.

DOMAIN: Lys-Thr-X-X-X-Trp motif is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: Expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues. Activation by Wat8 induces expression of beta-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TO BETA-CATENIN
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m. 267:25202-25207(1992)
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   EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

2 (POTENTIAL).

3 (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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                                                                                                                                                                                                             (POTENTIAL).
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brain and
and testis.
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Best Local S
Matches
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070421; 008974;

15-JUN-2002 (Rel. 41, C

15-JUN-2002 (Rel. 41, L

15-JUN-2002 (Rel. 41, L
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CARBOHYD
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TRANSMEM
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TRANSMEM
                                                                                                                                                                 Johnson M.A., Greenberg N.M.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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SITE
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                               TISSUE-Prostate;
                                                                                                                                                                                                                                                                                                                                Xu L., Tan L., Goldring M.B., Olsen "Expression of frizzled genes in mountrix Biol. 20:147-151(2001).
                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6; TISSUE=Embryo;
MEDLINE=21233588; PubMed=11334716;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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                                                                                       SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: Expressed in chondrocytes. DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the
                     SIMILARITY: CONTAINS 1 FRIZZLED
                                            similarity).
SIMILARITY:
                                                                 the Wnt/beta-catenin signaling pathway (By similarity) DOMAIN: The fz domain is involved in binding with Wnt
                                                                                                                        tissues
                                                                                                                                               to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity
                                                                                                                                    information
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                                                                                                                                   during tissue morphogenesis
                                            BELONGS
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Rodentia;
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100.0%;
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Last sequence up
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5 (POTENTIAL).
CYTOPLASMIC (PC
6 (POTENTIAL).
EXTRACELLULAR (
7 (POTENTIAL).
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Pred. No.
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LYS-THR-X-X-X-TRP
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Sciurognathi; Muridae;
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use costochondral chondrocytes.";
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                      (FZ) DOMAIN
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pfam; pF000047; ig; 1.

SMART; SM00181; EGF; 1.

SMART; SM00408; IGC2; 1.

SMO0408; IGC2; 1.

PROSITE; pS00022; EGF 1; 1.

pROSITE; PS01186; EGF-2; FALSE_NEG.
EGF-1ike domain; Glycoprotein; Immunc
                                                                                                                                                                                                                                                                                                                                                                                                                                                V70K_TYMV
P10357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                   MEDIINE-88289359; PubMed=3399388; Morch M.D., Boyer J.C., Haenni A.L.; Morch M.D., Boyer J.C., Haenni A.L.; Poverlapping open reading frames revealed by comp sequencing of turnip yellow mosaic virus genomic Nucleic Acids Res. 16:6157-6173(1988).
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InterPro;
   EMBL; X07441;
                                                                  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                          69 kDa protein.
Turnip yellow mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage;
NCBI_TaxID-12154;
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01-AUG-1992 (Rel. 23, Last seg
01-AUG-1992 (Rel. 23, Last ann
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IPR003006;
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 CAA30321.1; ALT_SEQ
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100.0%;
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                                                                                                                                                                    TO 70 kDa PROTEIN FROM OTHER TYMOVIRUSES
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POTENTIAL.
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IG-LIKE C2-TY
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Best Local :
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Best Local
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InterPro; IPR004935; Tymo_45_70kDa.
Pfam; PF03251; Tymo_45kd_70kd; 1.
Pfam; PF03251; ABA; 69195 MW; 9B01
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial contents a license agreement (See http://www.isbailcohappounced.)
SEQUENCE FROM N.A
                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Frizzled 1 precursor (Frizzled-1) (Fz-1) (rFz1).
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X16378; CAA34414.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic RNA sequence of turnip yellow mosaic cDNA-based clone with verified infectivity."; Plant Mol. Biol. 18:403-406(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 kDa protein.
Turnip yellow mosaic virus (isolate TYMC).
Viruses; ssRNA positive-strand viruses, no.
NCBI_TaxID-31751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P28478;
01-DEC-1992
                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                 PIR; S19150; S19150
InterPro; IPR004935
                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - i- SIMILARITY: TO 65 TO 70 kDa PROTEIN FROM OTHER TYMOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dreher T.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92119261; PubMed=1731998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1992 (Rel.
01-DEC-1992 (Rel.
                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472
                                                                                                                                                                                                                                           472
                                                                                                                                                                                                135
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                                                                                                                                                                                                                                          TPESR
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                                                                                                                                                                                                                                                                                                                                              S19150; S19150.
Pro; IPR004935; Tymo_45_70kDa.
Pr03251; Tymo_45kd_70kd; 1.
PF03251; Tymo_45kd_70kd; 0DF0
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5; Conserv
                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bransom K.L
                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24, Created)
24, Last sequence update)
24, Last annotation updat
                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                          33.3%; 50.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.3%; suc
100.0%; Pr
.... 0;
                                                                                                                                                                                                                                                                                                s; Score 5; DB 1; Pred. No. 2.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 5;
Pred. No.
                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                      1.
0DF0C64E8ECBC6DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9B01CE5ADFCEAC77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                      641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           628
                                                                                                                                                                                                                                                                                                             DB 1; Le
o. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                0;
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                                          Rattus
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RESULT 131

IF48_HUMAN
ID P23588
AC P23588
AC P23588
DT 01-NOV
DT 01-OCT
DE EURARY
GN EIF48
OS HOMO S
OC EURARY
OC MAMMALL
OX NCBLT
RN MEDLIN
RX MEDLIN
RX MEDLIN
RX MEDLIN
RY CHARAC
RX MEDLIN
RA METHOT
RT TEGION
RA METHOT
RT CONSET
RT TAPE T
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Best Local S
Matches 5
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PROSITE; PS00
Hypothetical
NP_BIND 1
NP_BIND 4
SEQUENCE 61
                                                                                                                                                                                                                                                                                                                                            Methot N., Song M.S., Sonenberg N.;

"A region rich in aspartic acid, arginine, tyrosine, and glycine (DRYG) mediates eukaryotic initiation factor 4B (eIF4B) self-association and interaction with eIF3.";

Mol. Cell. Biol. 16:5328-5334(1996).

"HOLICON: REQUIRED FOR THE BINDING OF MRNA TO RIBOSOMES. FUNCTIONS IN CLOSE ASSOCIATION WITH EIF4-F AND EIF4-A. BINDS NEAR THE 5'-TERMINAL CAP OF MRNA IN PRESENCE OF EIF4-FAND ATP. PROMOTES THE ATPASE ACTIVITY AND THE ATP-DEPENDENT RNA UNWINDING ACTIVITY OF BOTH EIF4-A AND EIF4-F.

SUBJUNT: SELF-ASSOCIATES AND INTERACTS WITH EIF3 pl70 SUBJUNTT.

--- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94187701; PubMed-8139536;
Methot N., Pause A., Hershey J.W., Sonenberg N.;
"The translation initiation factor eIF-4B contains an RNA-binding region that is distinct and independent from its ribonucleoprotein consensus sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
EMBO J. 9
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SI
MEDLINE-90360989; PubMed-2390971;
MILDUR S.C., Hershey J.W.B., Dav.
"Cloning and expression of eukary
"Cloning and expression identifies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION. MEDLINE-96413282;
                                                      Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IF4B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203
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                              ; X55733; CAA39265.1;
S12566; S12566.
W; HGNC:3285; EIF4B.
603928; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell. Biol.
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                           603928;
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD000006;
                                                                                                                                                      s requires a license agreement (S an email to license@isb-sib.ch).
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     IPR000504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114
428
610 AA;
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llarity 100.0%;
Conservative
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435
68377 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14:2307-2316(1994).
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ABC_TRANSporter; 1.
ein; ATP-binding; Transport;
121
ATP (POTENTIAL).
435
ATP (POTENTIAL).
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=8816444;
RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .W.B., Davies M.V., Kelleher K., Kaufman R.J.; of eukaryotic initiation factor 4B cDNA: identifies a common RNA recognition motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹
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b; Pred. No. 2.4
0; Mismatches
                                                                                                                                                                          agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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hes 0;
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RESULT 132
VEIN_DROME
В
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Best I
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                                                                                                                                                                                   SPI, SUGGESTING A MOLECULAR INTERDEPENDENCE. REQUIRED FOR THE
DEVELOPMENT OF INTERVEINS CELLS.

-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
PRODUCED BY ALTERNATIVE SPLICING.
-!- DEVELOPMENTAL STRIPES THAT ARE BROUGHT TO THE MIDLINE AS
CASTRULATION PROCEEDS. IN THE GERM-BAND RETRACTION STAGE,
EXPRESSION IS SEEN IN THE GERM-BAND RETRACTION STAGE,
EXPRESSION IS SEEN IN THE AND EPIDERMIS. AT LATE BLASTODERM,
EXPRESSION IS SEEN IN THE AND EPIDERMIS. AT LATE BLASTODERM,
EXPRESSION IS SEEN IN THE AND EPIDERMIS. AT LATE BLASTODERM,
EXPRESSION IS SEEN IN THE AND EPIDERMIS. AT LATE BLASTODER,
EXPRESSION IS SEEN IN THE AND EPIDERMIS. AT LATE BLASTODER,
EXPRESSION IS DECAYS IN ALL ECTODERMAL COBES,
AND AROUND THE STOMODEUM THROUGHOUT EMBRYO DEVELOPMENT. IN LATE
EMBRYOS, EXPRESSION DECAYS IN ALL ECTODERMAL CELLS AND APPEARS IN
THE SEGMENTAL MUSCLES AND THE GUT WALL. IN THE LARVA, EXPRESSION
OCCURS IN THE DORSAL METATHORACIC DISC, THE EYE-ANTENNAL DISC AND
THE VENTRAL THORACIS DISC. FOUND IN THE INTERVEIN IN THE PUPA.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Imaginal disks, and Embryo;

MEDLINE-96421972; PubMed-8824589;

Schnepp B.C., Grumbling G.B., Donaldson T.D., Simcox A.A.;

Yein is a novel component in the Drosophila epidermal growth factor receptor pathway with similarity to the neuregulins.";

Genes Dev. 10:2302-2313(1996).

-i- PUNCTION: LICAND FOR THE EGFR RECEPTOR. SEEMS TO PLAY A ROLE IN THE GLOBAL PROLIFERATION OF WING DISC CELLS AND THE LARVAL PATTERNING. SHOWS A STRONG SYNERGISTIC GENETIC INTERACTION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
             EMBL;
                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Vein protein precursor (Epidermal growth fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEIN_DROME Q94918;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
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Best Local :
                                                                                                                                                                                                                                                   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamur; Miyajina N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
Yamada M., Yasuda M., Yasuda M., Nakazaki N., Nakazaki N., Naruo K., Naruo K., Nakazaki N., Naruo K., Naruo K., Nakazaki N., Naruo K., Nar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ASPRS).
ASPS OR
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P73851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat Aspartyl-trnA synthetase (EC 6.1.1.12) (Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biosci. Biotechnol. Blochem. 60:717-720(1996).

- CATALYTIC ACTIVITY: Hydrolysis of alpha-(1-×4)-D-glucosidic linkage in 4-alpha-D-{(1-×4)-alpha-D-glucanosyl}(n) trehalose yield trehalose and alpha-(1-×4)-D-glucan.

- PATHWAY: Trehalose biosynthesis.
- SIMILARITY: BECONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restitute by non-profit institutions as long as its content and the content and the content and the content and the content as the content and the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97061201; PubMed=8905231; Kaneko T., Sato S., Kotani H., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synechocystis sp. (strain Bacteria; Cyanobacteria; C
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MEDLINE=96219094; PubMed=8829547;
Maruta K., Hattori K., Nakada T., Kubota M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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InterPro; IPR004193; Isoamylase_N.
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                                             CATALYTIC ACTIVITY: ATP + L-aspartate diphosphate + L-asparty1-tRNA(Asp). SUBUNIT: HOMODIMER (BY SIMILARITY). SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: BELONGS TO CLASS-II AMINOZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR SLR1720.
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PF02922; isoamylase_N; ]
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Chroococcales;
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STRAIN=S28c /
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                                         EMBL; U18796; AAB64571.1; SGD; S0000838; YER036C.
                                                                                                           or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi;
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last septence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Probable ATP-dependent transporter YER036C.
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PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase;
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Pfam; PF02938; GAD; 1.
PRINTS; PR01042; TRNASYNTHAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
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                                                                                                         and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                              non-profit institutions as long
                      IPR003439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002312; tRNA-synt_asp. IPR004365; tRNA_anti.
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IPR004115; GAD_dom.
IPR004364; tRNA-synt_2.
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NP_BIND 147

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SEQUENCE 593 AA;
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01-NOV-1997
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GTP-binding
CGP-1
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A newly formed telomere in Ascaris
position effect on a nearby gene.",
MOI. Cell. Biol. 16:130-134(1996).
--I- SIMILARITY: BRIONCE TO THE
                                                                                                                                                                                                                                                                                                                                                          SYD_MYCTU STANDARD; PRT; 594 AA Q50649; 01-NOV-1997 (Rel. 35, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Asparty1-trna synthetase (EC 6.1.1.12) (Asp
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Ha Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holl Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy J. Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Mycobacterium tuberculosis, 
Bacteria; Actinobacteria; /
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InterPro; IPR004161; EFTU_D2.
InterPro; IPR000795; EF_GTPbind.
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                                                                                                                                         MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                            STRAIN-H37RV;
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                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      Actinomycetales;
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PF03143; GTP_EFTU_D3;
PF03144; GTP_EFTU_D2;
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5; Conser
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Corynebacterineae; Mycobacteriaceae;
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Pred. No. 2.3e+02;
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InterPro; IPR004524; AspS_bact.
InterPro; IPR004115; Gab_dom.
InterPro; IPR004364; tRNA-synt_2.
InterPro; IPR004364; tRNA-synt_asp.
InterPro; IPR004365; tRNA-synt_asp.
InterPro; IPR004365; tRNA_anti.
Pfam; PF00152; tRNA-synt_2; 2.
Pfam; PF00152; tRNA-synt_2; 2.
Pfam; PF00136; tRNA-synt_2; 2.
Pfam; PF02938; Gab; 1.
Pfam; PF02938; Gab; 1.
PRNASYNTHASP.
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HSSP; P36419; 1E
TIGR; MT2648; -.
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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg

Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula

Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aminoacyl-tRNA:
Complete proteor
SEQUENCE 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TREZ_RHISP STANDARD; PRT; 596 AA.

(53238;
(502T-2001 (Rel. 40, Created))
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Malto-oligosyltrehalose trrehalohydrolase (EC 3.2.1.141) (MT)
alpha-D-{(1->4)-alpha-D-glucano}trehalose trehalohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS;
PROSITE; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatist the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commez entitles requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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[2]
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                        Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 277724; CAB01271.1;
     Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TubercuList; Rv2572c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole genome comparison of Mycobacterium tuberculosis clinical
                                                                                                                                                                                                                                                                                                                                                                                                  169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSTPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TIGR00459; aspS_bact; 1.
PS50862; AA_TRNA_LIGASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteome.
594 AA;
  sp. (strain M-1
Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                  173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                           (strain M-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetase; Protein biosynthesis; Ligase;
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     alpha
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; Mismatches
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     subdivision;
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     Rhizobiaceae group;
                                                                                                                                 3.2.1.141) (MTHase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
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Query Match
Best Local S
Matches 5
                                                                                                                                                                    InterPro; IPR002106; AAtrNA_ligaseII.
InterPro; IPR004524; AspS_bact.
InterPro; IPR004515; GAD_dom.
InterPro; IPR004364; trNA-synt_2.
InterPro; IPR002312; trNA-synt_asp.
InterPro; IPR004365; trNA_anti.
Pfam; PF00152; trNA-synt_2; 2.
Pfam; PF01336; trNA_anti; 1.
Pfam; PF02938; GAD; 1.
                                                                                                                                                                                                                                                                                                                             EMBL; ALDOSSEL,
PIR; S42047; S42047.
HSSP; P36419; 1EFW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simmon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Squarell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                      Complete proteome SEQUENCE 589 AA
                                                                                                                      TIGRFAMS; TIGR00459; asps_bact; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Massive gene decay in the leprosy bacillus.", Nature 409:1007-1011(2001).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate + tR
                                                                                                      Aminoacyl-tRNA synthetase;
                                                                                                                                                       PRINTS; PR01042;
                                                                                                                                                                                                                                                                                                                        Leproma; ML0501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium leprae antigen T5." Infect. Immun. 63:4682-4685(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last annotation update)
Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)
(AspRS) (Antigen T5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular characterization and T-cell-stimulatory capacity of Mycobacterium leprae antigen T5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ottenhoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wieles B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=96071886; PubMed=7591123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinomycetales;
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diphosphate + L-aspartyl-trna(Asp).
SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OR ML0501
                                                                                                                                                                                                                                                                                                                                                                                                             X77655; CAA54735.1; -. S82268; AAC27132.1; -.
                                                                                                                                                                                                                                                                                                                                                                           AL023591; CAA19094.1; -. AL583918; CAC30009.1; -.
 Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spierings
     Conservative
                                                                      A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR MLCB1259.19
                                                                                                                                                       TRNASYNTHASP
                                                                      64630 MW;
                   100.0%;
                                                                                                                                                                                                                                                                                                           AAtRNA_ligaseII.
                                     33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 van
                                                                                                    Protein biosynthesis; Ligase;
Score 5; DB;; Pred. No. 2.3
   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Noort J.,
                                                                    6B0EA0675367031C CRC64;
                 DB 1; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Naafs B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tRNA(Asp) =
                               Length 589
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   Indels
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                                                                                                      ATP-binding;
 0;
Gaps
 0;
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CGP1_CAEEL
ID CGP1_C
AC Q18905
                                                                                                                                                                                                                    RESULT 125
FTSZ_BARBA
                                                                                           В
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                                             RESULT 126
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                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                       Matches
CGP1_CAEEL
Q18905;
                                                                                                                                                                                                                 Cell division;
NP_BIND 107
SEQUENCE 592
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                            PRINTS, PRO0423; CELLDVISFTSZ.
TIGREAMS; TIGRO0065; ftsz; 1.
PROSITE; PS01134; FTSZ_1; 1.
PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Padmalayam I., Anderson B., Kron M., Kelly T., Baumstark E Padmalayam I., Anderson B., Kron M., Kelly T., Baumstark E The T5-kilodalton antigen of Bartonella bacilliformis is structural homolog of the cell division protein ftsz.";
J. Bacteriol. 179:4545-4552(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36,
15-DEC-1998 (Rel. 37,
15-JUN-2002 (Rel. 41,
Cell division protein
                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF007266; AAC15082.1; HSSP; Q57816; 1FSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases -:- FUNCTION: This protein is essential to the cell-divi
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000158; FtsZ.
InterPro; IPR003008; Tubulin_FtsZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
Bartonellaceae; Bartonell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTSZ_BARBA O31314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bartonella bacilliformis.
                                                                                           557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166
                                                                                                                        5 PHRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: This protein is essential to the cell-division process. It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity). SUBUNIT: Aggregates to form a ring-like structure (By similarity). SUBCELLULAR LOCATION: Cytoplasmic. Assembles at the inner surface of the cytoplasmic membrane (By similarity).

SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                           PHRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSTPE 170
                                                                                                                                                                                                                                                                                                                           PF00091; tubulin;
                                                                                                                                                       Similarity 5; Conserv
                                                                                                                        9
                                                                                                                                                                                                                    592 AA;
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                 n; Septation; GTP-binding.
107 115 GTP (POTENTIAL)
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ormatics Institute. There are no restinstitutions as long as its content attement is not removed. Usage by an income.
                                                                                                                                                                                                                    63503 MW;
                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
annotation update)
(75 kDa antigen).
                                                                                                                                                       0;
                                                                                                                                                                       Score 5;
Pred. No.
                PRT;
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                                                                                                                                                       Mismatches
                 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 592
                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                     Length 592;
                                                                                                                                                                                                                    CRC64;
                                                                                                                                                       Indels
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                                                                                                                                                     Gaps
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RESULT 122
SYD_THEMA
ID SYD_TH
AC QSYLTA
DT 30-MAY
DT 30-MAY
DT 16-OC2
DE ASPARI
GN ASPS
GN AS
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X MEDLINE-99287316; PubMed-10360571;

A Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J. Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett A McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett A Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richard Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., Whi A Heidelberg J., Smith H.O., Venter J.C., Fraser C.M., "Evidence for lateral gene transfer between Archaea and Bacte genome sequence of Thermotoga maritima.";

T genome sequence of Thermotoga maritima.";

L Nature 399:323-329(1999).

C -1 CATALYTIC ACTIVITY: ATP + L-aspartate + tRNA(Asp) - AMP + diphosphate + L-aspartyl-tRNA(Asp).
                                                                 InterPro; IPR004524; AspS_bact.
InterPro; IPR004115; GAD_dom.
InterPro; IPR004364; tRNA-synt_2.
InterPro; IPR002312; tRNA-synt_asp.
InterPro; IPR002312; tRNA_anti.
Pfam; PF00152; tRNA-synt_2; 2.
Pfam; PF01316; tRNA_anti; 1.
Pfam; PF01316; tRNA_anti; 1.
Pfam; PF01316; tRNA_SYNTHASP.
PRINTS; PR01042; TRNASYNTHASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYD_THEMA STANDARD,
SYD_THEMA STANDARD,
G9XIF4;
G9XIF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor; Tra
Zinc-finger.
DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license(15b-slb.ch).
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Bacteria; Thermotogae; Thermotogae (class); Thermotogales; Thermotogaceae; Thermotoga.

NCBI_TaxID=2336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001796; AAD36510.1; HSSP; P36419; 1EFW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
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SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EE European Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TM1441;
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5; Conservative
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   TIGR00459;
PS50862; AA
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59; aspS_bact; 1.
AA_TRNA_LIGASE_II;
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C4-TYPE.
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Pred. No.
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). 2.2e+02;
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, Richardson D.,
J.A., White O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration -
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RESULT 124
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  SYD_MYCLE STAN
P36429; P95671;
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O1-JUN-1994 (Rel. 2
                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002299; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
PROSITE; PS00100; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Badcock K., Churcher C., Barrell B.G., Rajandream M.A.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KM8S_YE
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SEQUENCE 579 AA; 66495 MW; 84195147100B9A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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STRAIN=S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Transferase; Serine/threonine-protein kinase;
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66219 MW;
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SMART; SM00370; LRR; 2.
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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008770;
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15-JUL-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003591; Li
Pfam; PF00560; LRR; 13
Pfam; PF01463; LRRCT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                             Platelet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000372; InterPro; IPR003592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001611;
InterPro; IPR000483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z69594; CAA93440.1; -.
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Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10116;
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1998 (Rel. 36,
2001 (Rel. 40,
t glycoprotein
                                                                                                                                                                                                                                                                                                         00369; LRR_TYP; 10.
Transmembrane; Glycoprotein; Blood coagulation;
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ch repeat;
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Last annotation updat
V precursor (GPV) (CD
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CYTOPLASMIC
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Best Local :
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NH22_CAEEL
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EMBL;
HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Bogan A., Maina C.V., Yamamoto K., Cohen F., Sluder A.E.;
"Caenorhabditis elegans nuclear receptor sequences exhibit biophysical compatibility with the ligand-binding domain fold.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ORPHAN NUCLEAR RECEPTOR.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q09587; Q9GTI4; Q9GTI5;
01-FEB-1996 (Rel. 33, Created)
15-DEC-1998 (Rel. 37; Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nuclear hormone receptor family member nhr-22
NHR-22 OR KO6A1.4.
                                                                                                                                                                                                                                                                                                                       modified and this statement
                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                     entities requires a license agreement
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100.0%; Pr
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Pfam; PF00105; zf-C4; 3. ProDom; PD000035; Znf_C4steroid; Pfam; PF00104; hormone_rec; Pfam; PF00105; zf-C4; 3.

HOLI;

WormPep; K06Al.4; CE18017.
InterPro; IPR000536; Hormone_rec_lig
InterPro; IPR001628; Znf_C4steroid.

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HEMA_IAJAP
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21-JUL-1986 (R
16-OCT-2001 (R
Hemagglutinin
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF00509; Hemagglutinin;
PRINTS; PR00329; HEMAGGLUTN12.
Probom; PD000225; Hemagglutn;
Envelope protein; Hemagglutinii
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MEDLINE-81030852; PubMed-7421990;

Gething M.-J., Bye J., Skehel J.J., Waterfield M.;

"Cloning and DNA sequence of double-stranded copies of haemagglutinin genes from H2 and H3 strains elucidates antigenic shift and drift in
                                                                                                                                                        SEQUENCE
                                                                                                                                                                            CARBOHYD
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HSSP; P03437; 1HTM.
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Influenza A viruses; Influenzavirus
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InterPro; IPR001364; Hemagglutn.
1. The management of the second s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human influenza virus.";
Nature 287:301-306(1980)
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Viruses; ssRNA negative-strand viruses; Or
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CELL RECEPTORS AND FOR INITIATING INFECTION
SUBUNIT: HOMOTRIMER, EACH OF THE MONOMERS IS FORMED BY TWO
(HAI AND HA2) LINKED BY A DISULFIDE BOND.
SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                  RSTPE 11
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(Rel. 01, Last sequence update)
(Rel. 40, Last annotation updat
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HA2 chain].
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2D (GLCNAC . . ) (POTENTIAL).

ED (GLCNAC . . ) (POTENTIAL).
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RESULT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions are long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The yeast halotolerance determinant Halp is an inhibitory subut the Ppzlp Ser/Thr protein phosphatase.";
Proc. Natl. Acad. Sci. U.S.A. 95:7357-7352(1998).
PRIOTICALLY EXPRESSED DURING LATE G1. ALSO MODULATES THE EXPRESSION OF THE ENAI ATPASE. INTERACTS WITH THE C-TERMINAL DOMAIN OF THE SERINE-THREONINE PROTEIN PHOSPHATASE PPZ1 AND JONAL OF THE SERINE-THREONINE PRZI.

AS AN INHIBITORY SUBURIT OF PPZ1.
PROC. NATL. ACAD. SCI. CALLES SISZ/HALJ AND TO YEAST YKLO88W. STR. ACAD. SCI. CALLES SISZ/HALJ AND TO YEAST YKLO88W.
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MEDLINE-95220693; PubMed-7705654;

di Como C.J., Bose R., Arndt K.T.;

"Overexpression of SIS2, which contains an extremely acidic region, increases the expression of SWI4, CLN1 and CLN2 in sit4 mutants.";
                                                                                                                                                                                                                                                                                      EMBL; U01878; AAA80000.1;
EMBL; Z28297; CAA82151.1;
PIR; S38149; S38149.
                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       de Nadal E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ferrando A., Kron S.J., Rios G., Fi
"Regulation of cation transport in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics 139:95-107(1995).
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                                                                                                           SEQUENCE
                                                                                                                                                          Protein phosphatase
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S0001780; SIS
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Cell. Biol. 15:5470-5481(1995).
                                                                       Pro; IPKUUSUS,
PF02441; Flavoprotein; 1.
PF02441; Flavoprotein; 1.
in phosphatase inhibitor; Nuclear protein.
in phosphatase inhibitor; Nuclear protein.
A96 553 ASP/GLU-RICH (HIGHLY ACIDIC)
IN 496 553 ASP/GLU-RICH (HIGHLY ACIDIC)
IN 62478 MW; 19A9A475145DA7AB CRC64;
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                              Similarity
                                                                                                                                                                                                            1780; SIS2.
IPR003382; Flavoprotein.
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                           Score 5;
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RESULT 116
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Best Local
                PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid;
SMART; SM00430; HOLI; 1.
                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Nuclear receptor ROR-gamma (Nuclear receptor ROR-gamma)
                                                                                 Pfam; PF00105; zf-C4;
                                                                                                                       InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                   MIM; 602943;
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Eukaryota; Metazoa; Chordata;
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; Z54141;
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                                                                                                PF00104; hormone_rec;
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AC; T02749; -.
HGNC:10260; RORC.
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CAA90837.1;
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                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Å
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RESULT 117
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DOMAIN
                                                                                                                    between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
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ZN_FING
ZN_FING
SEQUENCE
                            Cytoskeleton;
NON_TER
                                                       Pfam; PF00169; PH; SMART; SM00233; PH;
                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                 EMBL; BC003984; AAH03984.1;
                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                              PROSITE;
                                                                         InterPro; IPR001849;
                                                                                                                                                                                                                                                                                                                  TISSUE-Mammary gland;
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                  TARA.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                          Protein Tara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 RSTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                            dimer (By similarity).
SIMILARITY: CONTAINS 1 PH DOMAIN.
                                                                                                                                                                                            II (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic; localized to F-actin in periodic pattern (By similarity).
DOMAIN: Contains at least 2 actin-binding sites per coiled-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
5; Conser
                                              PS50003; PH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261
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  (Trio-associated repeat on actin) (Fragment)
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                                   Actin-binding;
ΑA;
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                                                     PH;
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Rodentia;
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C4-TYPE.
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Pred. No.
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LIGAND-BINDING (POTENTIAL)
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NUCLEAR REC
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _PSEFL STANDARD; PRT; 50
Q51772;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up)
15-JUN-2002 (Rel. 41, Last annotation)
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Pfam; PP00096; zf-C2H2; 7.
Pfam; PP01352; KRAB; 1.
SMART; SM00349; KRAB; 1.
SMART; SM00355; Znf_C2H2; 7.
                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   "The sequence of the mer operon of pMER327/419 and transposon ends pMER327/419, 330 and 05."; Gene 146:73-78(1994).
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DOMAIN
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MEDLINE=94341572; PubMed-8063107;
Hobman J., Kholodii G., Nikiforov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein;
NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid
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                                                                                                                                                                                                           MISCELLANEOUS: THE ACTIVE SITE IS A SIMILARITY: BELONGS TO THE PYRIDINE OXIDOREDUCTASES CLASS-1. SIMILARITY: CONTAINS 1 HMA DOMAIN.
                                                                                                                                                                                                                                                                                                                     COFACTOR: FAD.
                                                                                                                                                                                                                                                                                                                                FUNCTION: RESISTANCE TO HG(2+) IN BACTERIA APPEARS TO BE GOVERNI BY A SPECIALIZED SYSTEM WHICH INCLUDES MERCURIC REDUCTASE. MERA PROTEIN IS RESPONSIBLE FOR VOLATILIZING MERCURY AS HG(0). CATALYTIC ACTIVITY: Hg + NADP(+) + H(+) = Hg(2+) + NADPH.
                                                                                                                                                                                                                                                                                               SUBUNIT: HOMODIMER (BY SIMILARITY).
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    x73112;
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PS50805; KRAB; 1.
PS00028; ZINC_FINGER_C2H2_1; 7.
PS500157; ZINC_FINGER_C2H2_2; 7.
PS10157; ZINC_FINGER_C2H2_2; 7.
Ption regulation; DNA-binding; Zinc-finger; Metal-binding;
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    CAA51542.1;
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    Last annotation update)
    (EC 1.16.1.1) (Hg(II) reductase).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nikiforov V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ritchie D.A.,
                                                             oved. Usage by and for (See http://www.isb-sib.
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InterPro;
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DISULFID
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                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
Low-affinity Fe(II) transport protein
FET4 OR YMR319C OR YM9924.11C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00070; pyr_redox; Pfam; PF00403; HMA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95014434; PubMed=7929320; Seguence FROM N.A.
MEDLINE=95014434; PubMed=7929320; PubMed=792900; PubMed=792900; PubMed=792900; PubMed=792900; PubMed=7929000; PubMed=7929000; PubMed=7929000; PubMed=7929000; PubMed=7929
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PROSITE; PS01047; HMA_1; 1.
PROSITE; PS50846; HMA_2; 1.
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            or send an email
                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                              FET4 gene encodes the low affinity
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR00411; PNDRDTASEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00076; PYRIDINE_REDOX_1; 1. resistance; Oxidoreductase; Flavoprotein; Redox-active center; Metal-binding; Plasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000815; Hg_reductase.
IPR001100; Pyr_redox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR004099;
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. 269:26092-26099(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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REDOX-ACTIVE.
FAD (FLAVIN PART) (BY SIMI HG(2+) (POTENTIAL).
HG(2+) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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RESULT 112
NAB2_MOUSE
ID NAB2_M
AC Q61127
DT 16-OCT
DT 18SUE
RX MEDLIN
RA MILBRA
RT WAB2,
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Best Local S
Matches
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Q61127;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).

MEDLINE-97271553; PubMed-9126479;

Svaren J., Apel E.D., Simburger K.S., Jenkins N.A., Gilbert D.J.,

Copeland N.A., Milbrandt J.;

"The Nab2 and Stat6 genes share a common transcription termination and the state of the stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics 41:33-39(1997).
-!- FUNCTION: ACTS AS A TRANSCRIPTIONAL REPRESSOR FOR ZINC FINGER TRANSCRIPTION FACTORS EGR1 AND EGR2. ISOFORM 2 LACKS REPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sydren J., Sevetson B.R., Milbrandt J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "NAB2, a corepressor of NGFI-A (Egr-1) and Krox20, is induced proliferative and differentiative stimuli."; mol. Cell. Biol. 16:3545-3553(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NGFI-A binding protein 2 (EGR-1 binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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SMART; SM00432; MADS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                       INDUCTION: BY SERUM STIMULATION.

DOMAIN: THE NAB CONSERVED DOMAIN 1 (NCD1) INTEI
INHIBITORY DOMAIN AND MEDIATES MULTIMERIZATION
DOMAIN: THE NAB CONSERVED DOMAIN 2 (NCD2) IS NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABILITY: HOMOMULTIMERIS MAY ASSOCIATE WITH EGRI SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR. ISOFORM 2 IS NOT
                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING. PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN AND THYMUS, AND LOWER LEVELS IN SPLEEN, KIDNEY, HEART AND TESTIS. ISOFORM 1 IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE NUCLEUS
                                                                                                                                                                                                                                                                  ABUNDANT IN THYMUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISOFORMS 1 AND
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ARG/LYS-RICH (BASIC).
SER/THR-RICH.
GLN/HIS-RICH.
                                                                                                                                                                                                                                                                                                          IN TESTIS,
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TRANSCRIPTIONAL REPRESSION

NAB FAMILY

HSSP; P08046; 1A1H.

HGNC:13154;

IPR001909; KRAB

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RESULT 113
ZNOB.HOMAN
ID ZNOB.H
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01-AUG-1990
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Zinc finger
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VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-9016993; PubMed-2106481;
Lania L., Donti E., Pannuti A., Pascucci A.,
Feliciello I., la Mantia G., Lanfrancone L.,
"cDNA isolation, expression analysis, and chr
two human zinc finger genes.";
Genomics 6:333-340(1990).
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                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR
-i- SUBCELULIAR LOCATION: NUCLEAR (Probable).
-i- TISSUE SPECIFICITY: UBIQUITOUSLY PRESENT IN MANY
OF DIFFERENT EMBRYOLOGICAL DERIVATION.
-i- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C21
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DOMAIN
                                                                                                                EMBL; M29581; AAA61314.1;
                                                                                                                                                              or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
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MISSING (IN ISOFORM 2).
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RA Wood V. Gwilliam R., Rajandream M.A. Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
Annes K., Jones M., Leather S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
Annes K., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones M., Leather S., Stevens K.,
RA Holroyd S., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Guller S., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Woodward J., Volckaert G., Aert R., Squares S., Stevens K.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Holler S., Rajger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Ra Gere P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Charles S., McCambie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe.";
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Matches 5
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Q10150;
Q1-0CT-1996
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last anotation update)
Hypothetical protein ClD4.03c in chromosome I
SPACID4.03C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetae
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InterPro; IPR004291; Transposase_25; 1.
Pfam: PF03050; Transposase_25; 1.
Hypothetical protein; Plasmid.
SEQUENCE 511 AA; 56701 MW; BB67F
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-!- SIMILARITY: TO Y4AQ, Y4HP AND Y4QI.
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Nature 387:394-401(1997).
-!- SIMILARITY: TO A NUMBER OF ORF OF VARIABLE SIZE IN R.MELILOTI AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomycetaceae;
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Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB67F48B9EDE9601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               red. No. 2e-
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 111
                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEFA_XENLA STANDARD; PRT; 516 AA. 003414; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) Myocyte-specific enhancer factor 2A homolog (11ke protein 2) (SL-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                       EMBL; Z19123; CAA79530.1; HSSP; P11831; 1SRS.
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein. SEQUENCE 513 AA; 58003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z69239; CAA93212.1; -.
InterPro; IPR004353; Yeast73DUF
Pfam; PF03164; DUF254; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        MEDLINE=93099873; PubMed=1281451; Chambers A.E., Kotecha S., Towers
                                                                                                                                                                                                                                                                                                                                                  TISSUE=Neurula;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01546; YEAST73DUF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 RSTPE
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100.0%; Pr
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; I
5. 2e+02;
                                                                    . Usage by and for http://www.isb-sib.
                                                                                                                                                                                                                                                                                                            genes in the early embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Serum response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 513
                                                                                                                                                                      EARLY NEURULA.
                                                                                                                                                                       TRANSCRIPTION
                                                                                                           restrictions
                                                                                                                        EMBL
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                                                                                                                                                                                                                                                           CELL TYPES
                                                                                                                        a collaboration
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TRANSFAC;

IPR002100; TF_MADSbox

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'RESULT 108
'MURE_BORBU
|ID MURE_B
AC 051219
|AT 15-DEC
|DT 15-DEC
|DT 15-JUN
DP-N-
DE (EC 6.
|DE diamin
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RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA HO P.L., Hohelsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madelira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
RA Machado M.A., Matrins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Manok C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Monok C.F.M., Niracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Monoh D.H., Nagai M.A., Nascimento A.L.T.C., Netto L.E.S.,
RA Monoh A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E.,
RA Quaggio R.B., Tode Sa R.G., Santelli R.V., Sawasaki H.E.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA da Silva A.C.R., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA da Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Zago M.A., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
"The genome sequence of the plant pathogen xylella fastidiosa.";
C. -- (CC.-+ TERNALUTI) ATP + L-lysine + trnA(Lys) = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
(EC 6.3.2.13) (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-
diaminopimelate-adding enzyme) (UDP-MurNAc-tripeptide synthetase).
MURE OR BB0201.
                                                                                                                                                                                                                                                                                                                            MURE_BORBU
051219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002106; AAtRNA_ligaseII.
InterPro; IPR004364; tRNA-synt_2.
InterPro; IPR002313; tRNA-synt_lys_2.
InterPro; IPR004365; tRNA_anti.
Pfam; PF00152; tRNA-synt_2; 1.
Pfam; PF00153; tRNA_anti; 1.
Pfam; PF01336; tRNA_anti; 1.
Pfam; PF01336; tRNA_anti; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
       Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
                                    Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003947; AAF83922.1; HSSP; P14825; 1E10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   + L-1ysyl-tRNA(Lys).
SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPESR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPESR 13
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR00982; TRNASYNTHLYS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.3%;
llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57531 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 5; DB 1; Pred. No. 2e+0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B194E13ED1ECC6D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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Y4JD_RHISN
ID Y4JD_RA
AC P55504
DT 01-NOV
DT 01-NOV
DT 01-NOV
DE Hypoth
GN Y4JD.
OS Rhizob
OG Plasmi
OC Bacter
OC Rhizob
OX NCBI_T
RN (1)
RP SEQUEN
RX MEDLIN
RA Freibe
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Best Local
                                                                                                                                                                                                                                                                                                        01-NOV-1997
01-NOV-1997
01-NOV-1997
SEQUENCE FROM N.A.
MEDLINE-97305956; PubMed-9163424;
                                                                                                                                                                                                                                                                                                                                                                                          Y4JD_RHISN
P55504;
                                                                                                                                                                        Plasmid sym pNGR234a.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.
NP_BIND 118 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000713; Mur_ligase. InterPro; IPR004101; Mur_ligase_C. Pfam; PF01225; Mur_ligase; 1. Pfam; PF02875; Mur_ligase_C; 1. TIGRPAMS; TIGR01085; murE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               Rhizobium sp.
                                                                                                                                                                                                                                                                                     Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weldman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Gairking S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith H.O., Venter J.C.; "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001130; AAC66588.1; -.
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MEDLINE=98065943; PubMed=9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 STPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate + meso-2,6-dlaminoheptanedioate = ADP + phosphat-UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diaminoheptanedioate.
PATHWAY: Peptidoglycan biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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100.0%; Pr
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                   Bairoch A.,
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c. 2e+02;
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Broughton W.J.,

Rosenthal

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RESULT
SCRY_KL
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DT 01
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Best Local S
Matches 5
                                   Y_KLEPN
SCRY_KLEPN
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EMBL; M65016; AAA28481.1; -.
EMBL; M61958; AAA28830.2; -.
EMBL; M93149; AAA28732.1; -.
EMBL; AE003637; AAF53209.1; -.
PIR; B41277; B41277;
PIR; B41277; B41277
P27218;
01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
                                                                                                                                                                                                                                             DNA_BIND
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
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ProDom; PD000010; Homeobox; 1.
ProDom; PD000583; POU_domain;
SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T01901; -: F1yBase; FBgn0004394; pdm2.
InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU_domain.
Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                            CONFLICT
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                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                 382
                                                                                                                                                                                                                                                                                                                                  Activator;
                                                                                                                                                                                                                                                                                                                                               Homeobox;
                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AN EARLY ROLE IN SPECIFIC ECTODERMAL CELLS, AND A SUBSEQUENT IN THE EMBRYONIC NERVOUS SYSTEM.

SUBCELLULAR LOCATION: NUCLEAR:
TISSUE SPECIFICITY: NEUROBLASTS AND SENSORY ELEMENTS.
DEVELOPMENTAL STAGE: EXPRESSED PRIMARILY DURING THE FIRST HALE EMBRYOGENESIS. INITIAL EXPRESSED PRIMARILY DURING THE MASTODERM STAGETHEN IN ECTODERMAL STRIPES DURING GERMBAND EXTENSION. BROAD EXPRESSION IN THE NEUROPECTODERM FOLLOWED BY LIMITATION TO DISSUBSETS OF CMS CELLS, AND EXPRESSION IN SPECIFIC PMS NEURONS SUPPORT CELLS.

SUPPORT CELLS. BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                STPES
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                                                                                                                       STPES 12
                                                                                                                                                Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           PS50071;
                                                                                                                                                                                                                                                                                                                                                                                PS00027; HOMEOBO
PS00035; POU_1;
                                                                                                                                                                                                                                                                                                                                                                      PS00465;
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                                                                                                                                                                                                498 AA;
                                                                                                                                                Conservative
                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                         HOMEOBOX_2;
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450
221
224
248
447
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79
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Created)
Last sequ
                                                                                                                                                                                                                                                                                                                                          Transcription regulation;
 sequence
                                                                                                                                                                                         M -> S (IN REF. 4).
K -> N (IN REF. 4).
POA -> RRL (IN REF. 2).
MISSING (IN REF. 2).
MS 60e17Ae776603974 CRC64;
                                                                                                                                              0;
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                                                                                                                                                                                                                                                       V -> GA (IN REF. RH -> AR (IN REF.
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                                                                                                                                                                                                                                                                                                                                         Nuclear protein;
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STAGE,
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RESULT 107
SYK_XYLFA
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Best Local S
Matches 5
Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Canargo A.A., Camargo I.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dlas-Neto E., Docena C., El-Dorry H.,
                                                                        MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
SIGNAL
                                                                                          STRAIN-9a5c
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                Xylella fastidiosa
                                                                                                                                                                                       16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
Lysyl-trna synthetase
                                                                                                                                                                                                                              Q9PEB6;
16-OCT-2001
                                                                                                                                                                                                                                                     SYK_XYLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003192; Po Pfam; PF02264; LamB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; x57401; CAA40657.1; PIR; S15194; S15194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=1033-5P14 / MEDLINE=91312133; F
                                                                                                                                                   Bacteria;
                                                                                                                                                                             LYSS OR XF1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Microbiol. 5:941-950(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A sugar-specific porin, ScrY, is involved enteric bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCRY.
                                                                                                                             NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P22340; 1A0T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klebsiella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Porin for sucrose uptake.
SUBUNIT: HOMOTRIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: THE C-TERMINUS HELPS TO ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEMBRANE
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55650
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                                                                                                                                                                                   Last sequence update)
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(EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS).
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                                                                                                                                                  gamma subdivision; Xanthomonas group;
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THE PORIN
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Bacteriol.

171:3926-3932(1989)

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RESULT 105
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A Boistard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux S.,
A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
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A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
A Renard C., Thebault P., Vandenbol M., Weidner S., Masuy M., Caller P., Weidner S., Masuy M., Weidner S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                              Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                               PDM2_DROME STANDARD; PRT; 498 AA P31369; Q24430; Q9YK70; O1-JUL-1993 (Rel. 26, Created) O1-JUL-1993 (Rel. 26, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                        DROME
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InterPro; IPR000924; Glu_trNA-synt_lc.
InterPro; IPR001412; trNA-synt_lc;
Pfam; PF00749; trNA-synt_lc; 1.
PRINTS; PR00987; TRNASYNTHGLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGREAMS; TIGR00464; gltX_bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding;
  SEQUENCE FROM N.A
                                                                                                                                                                                                         POU domain protein
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HSSP; P27000; 1GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M27221; AAC35209.1; -. EMBL; AL591792; CAC47482.1; -.
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100.0%;
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0; Mismatches
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"KWSKS" REGION.
ATP (BY SIMILARITY).
ATSSING (IN REF. 1).
K -> KQ (IN REF. 2).
K -> KQ (IN REF. 2).
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b. 1.9e+02;
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RA Borkova D., Buchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Bustchan M.R., Bouck J., Brokstein P., Brottier P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Dodson K.J., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gana P., Harris M., RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McDherson D., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Rainert K., Remington K., Saunders R., D.C., Scheeler F., Shen H., RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Dang S., Yao Q.A., Pan S., Pollard J., Puri V., Reese M.G., RA Wang Z.-Y., Barrillong R. Schon K.S., Nusskern D.R., Pacleb J., RA Wang S.-Yao Q.A., Weinstock G.M., Weinsenbach J., RA Wang S.-Yao Q.A., Weinstock G.M., Weissenbach J., RA Wang S.-Yao Q.A., Pan S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Pelson C.R., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfeiffer B.D., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkhan M.P., Benok F., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92357775; PubMed=1496003;
Prakash K., Fang X.D., Engelberg D., Behal A., Parker C.
"dOct2, a Drosophila Oct transcription factor that funct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
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Dick T., Yang X., Yeo S., Chia W.;
"Two closely linked Drosophila POU domain genes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lloyd A., Sakonju S.; "Characterization of two Drosophila oct-1 and oct-2, and the regulation Mech. Dev. 36:87-102(1991).
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"Isolation of a family of Drosophila POU
early development.";
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HSSP; P27000;
TIGR; HI0274;
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MEDLINE-95350630; PubMed-7542800;

Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Eleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Gocayne J.D.,

Scott J.D., Shiritey R., Liu L.-T., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

"Whole-genome random sequencing and assembly of Haemophilus influenzae

""Whole-genome random sequencing and assembly of Haemophilus influenzae

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
SEQUENCE
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPRO04527; Gltx_bact.
InterPro; IPRO00924; Glu_trNA-synt_lc.
InterPro; IPRO01412; tRNA-synt_l.
Pfam; PF00749; tRNA-synt_lc; 1.
PRINTS; PR00987; TRNASYNTHGLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUN-2002 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995).
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SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYCOPLASMIC.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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1GLN.
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(EC 6.1.1.17) (Glutamate--tRNA ligase)
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TP (BY SIMILARITY)
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RESULT 104

SYE_RHIME

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Matches 5
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InterPro; IPR000924; Glu_tRNA-synt_lc.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00749; tRNA-synt_lc; 1.
PRINTS; PR00987; TRNASYNTHGLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Complete genomic sequence of Pasteurella multocida Pm70
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-I- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) =
diphosphate + L-glutamyl-tRNA(Glu).
-I- SUBUNIT: MONOMER (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                        (Gluks).

GLTX OR R02903 OR SMC03172.

Rhizobium meliloti (Sinorhizobium Bacteria; Proteobacteria; alpha su Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYE_RHIME STANDARD; PRT; 485 AA.
p15189;
01-APR-1990 (Rel. 14, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Clutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
Laberge S., Gagnon Y., Bordeleau L.M., Lap
"Cloning and sequencing of the gltX gene,
synthetase of Rhizobium meliloti A2.";
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Bacteria; Proteobacteria;
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GLTX OR PM1115.
                                                                                                                   MEDLINE-89291743; PubMed-2661539;
                                                                                                                                                         STRAIN=A2;
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PROSITE; PS00178; AA_TRNA_LIGASE_I;
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                  um meliloti).
subdivision;
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o. 1.9e+02;
                                                                        Lapointe
                                          encoding
                                                                                                                                                                                                                                                                                                                                      Rhizobiaceae group;
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Pm70.
                                          glutamyl-tRNA
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Best Local
                                                 PRINTS; PR00987; TRNASYNTHGLU.
TIGRFAMS; TIGR00464; gltx_bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                         StyGene; SG?????; gltX.bact.
InterPro; IPR00452?; GltX_bact.
InterPro; IPR000924; Glu_tRNA-synt_lc.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00749; tRNA-synt_lc; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., 1 Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nh Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.

Aminoacyl-trnA synthetase; Protein biosynthesis; Ligase; ATP-binding.

SITE 15 25 "HIGH" REGION.

SITE 243 247 "KMSKS" REGION.

BINDING 246 246 ATP (BY SIMILARITY).

SEQUENCE 471 AA; 52136 MW; 044E8C102AB5FCB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diphosphate + L-glutamyl-trná(Glu).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 413:852-856(2001).
-!- CATALYTIC ACTIVITY: ATP + L-glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609;
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Pfam; PF00749; tRNA-synt_1c; 1.
PRINTS; PR00987; TRNASYNTHGLU.
                                   Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                        EMBL; AE008809; AAL21313.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of Salmonella enterica
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                             Protein biosynthesis; Ligase;
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b. 1.9e+02;
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Nulvaney
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u S., Layman D.,
Mulvaney E.,
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                                                                                                                                            RESULT 102
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P38770;
01-FEB-1995
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SITE
BINDING
SEQUENCE
SYE_HAEIN STANDARD;
P43818;
01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-94378003; PubMed-8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Johnston M., Andrews S., Brinkman R., Cooper J., Kirsten J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hiller L., Jier M., Johnston L., Langston Y.,
Kucaba T., Hiller L., Macri C., Mardis E., Menezes S., Mouser L.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD; S0001078; YHR036W.
Hypothetical protein; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U00062; AAB68908.1; -. PIR; S46739; S46739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; i
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete nucleotide sequence of Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaudin M.;
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                                                                                                                                                                                                                                                                                                                   5 PHRST
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5; Conserv
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11 53.4 kDa
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POTENTIAL.
; 732209EC74DE3463 CRC64;
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SLT2-PUT2 intergenic region.
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5. 1.9e+02;
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5. 1.9e+02;
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DNA Res.
[4]
                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-57 FROM N.A.

MEDITUR=90355200, PubMed=2201777;

Brun V., Sanfacon H., Breton R., Lapointe J.;

"Closely spaced and divergent promoters for an aminoacyl-tRNA synthetase gene and a tRNA operon in Escherichia coli.

Transcriptional and post-transcriptional regulation of gltx,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kinura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S. Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-86278132; PubMed-3015933;
Breton R., Sanfacon H., Papayannopoulos I., Biemann K., Lapointe
Breton R., Sanfacon H., Papayannopoulos I., Biemann K., Lapointe
"Glutamyl-tRNA synthetase of Escherichia coli. Isolation and prin
"Glutamyl-tRNA synthetase and homology with other aminoacyl-tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Cre
13-AUG-1987 (Rel. 05, Las
16-OCT-2001 (Rel. 40, Las
Glutamyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Construction of a contiguous 874-kb sequence of the Escherichi K12 genome corresponding to 50.0-68.8 min on the linkage map analysis of its sequence features."; DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
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GLTX OR B2400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamagata S., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97349980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-86278132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia
                                                                                                                                                                                                                                               MO1. B101. 214:845-864(1990).
CATALYTIC ACTIVITY: ATP + L-glutamate
diphosphate + L-glutamyl-tRNA(Glu).
SUBUNIT: MONOMER.
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                                                                                                                                                                                                                                                                                                                                      alaW.
                                                                                                                SIMILARITY: BELONGS TO CLASS-I
                                                                                                                                                       SUBCELLULAR LOCATION: Cytoplasmic
MISCELLANEOUS: THIS IS THE SHALLEST AMINOACYL-TRNA
E.COLL; IT DOES NOT BIND GLUTAMATE IN THE ABSENCE C
WHICH IS THEREFORE REQUIRED FOR ACTIVATION OF THE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence nce 277:1453-1474(1997).
                           SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSTPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9205837;
      institutions
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Last annotation update)
ase (EC 6.1.1.17) (Glutamate--tRNA
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      as long
                                                                                                              AMINOACYL-TRNA
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      content
                                                                                                              SYNTHETASE FAMILY.
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Best Local
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InterPro; IPR004527; Gltx_bact.
InterPro; IPR004527; Glt_tRNA-synt_lc.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR001412; tRNA-synt_l.
Pfam; PF00749; tRNA-synt_lc; 1.
PFINTS; PR00987; TRNASYNTHGLU.
TIGREAMS; TIGR0464; gltx_bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
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SEQUENCE
                                                                                                                                                                                          between
the Euro
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
SIMMONS A.E., Mackenzie R.C., Kaplan S.;

"Trp-ing up paradigms: distribution of tryptophan biosyn in Rhodobacter sphaeroides 2.4.1.";

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-glutamate + trNA(Glu) = diphosphate + L-glutamyl-trNA(Glu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYE_RHOSH Q9ZFA3;
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EMBL; M13687; AAA65715.1; -.
EMBL; AE000328; AAAC75457.1; -.
EMBL; D90869; BAA16272.1; -.
EMBL; X55737; CAA39269.1; -.
                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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PIR; ?
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HSSP; P27000; IGLN.
ECOZDBASE; F047-8; 6TH EDITION
ECOGene; EG10407; gltx.
                                                                               or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria;
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30-MAY-2000 (Rel.
16-OCT-2001 (Rel.
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SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE
                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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AF108766;
P27000; 1G
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471 AA;
                                                                               equires a license agreement email to license@isb-sib.c
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ase (EC 6.1.1.17) (Glutamate--tRNA)
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0; Mismatches
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ATP (BY SIMILARITY)
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Matches 5
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gene between Drosophila virilis and Drosophila melanogaster.";
LL Mech. Dev. 49:107-116(1995).
CC -1- FUNCTION: DNA-BINDING REGULATORY PROTEIN IMPLICATED IN EARLY
DEVELOPMENT. INVOLVED IN NEUBRONAL CELL FATE DECISION. MAY ACT AS
CAN OCTAMER-DEPENDENT ACTIVATOR OF TRANSCRIPTION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SUBCELLULAR STAGE: EXPRESSED PRIMARILY DURING THE FIRST HALF OF
CC EMBRYOGENESIS. INITIAL EXPRESSED NI OF CLULLAR BLASTODERM STAGE,
CC THEN IN ECTODERMAL STRIPES DURING GERMBAND EXTENSION. BROAD
EXPRESSION IN THE NEUROECTODERM FOLLOWED BY LIMITATION TO DISCRETE
CC SUBSETS OF CMS CELLS, AND EXPRESSION IN SECIFIC PMS NEURONS AND
CC SUBSETS OF CMS CELLS, AND EXPRESSION IN FACTOR FAMILY.
CC -1- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
                                                                                                                                                                                                                                                 Pfam; PF00157; pou; 1.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000083; POU domain; 1.
SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
SMART; SM00352; POU; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00071; HOMEOBOX_2; 1.
PROSITE; PS00065; POU_1; 1.
PROSITE; PS000035; POU_1; 1.
PROSITE; PS00003; POU_1; 1.
Homeobox; DNA-binding; Transcripti
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                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0020449; Dvir\pdm2.
InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU_domain.
                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00046; homeobox; 1. Pfam; PF00157; pou; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Ensecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95267688; pubMed=7748782; Poole S.J.;
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PDM2 OR PDM-2 OR DIM OR POU-28
                                                                                                                                                                                                                                      Activator;
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Pred. No. 1.9
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POLY-ALA.
POLY-GLN.
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B0D27F895EC2428C CRC64;
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RX MEDLINE=21155231; PubMed=11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Hayashi T., Makino E., Ohnishi M., Kurokawa C., Tanaka M., Tobe T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Yasunaga T.,

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RT Toomplete genome sequence of enterohemorrhagic Escherichia coli

RT Tol57:H7 and genomic comparison with a laboratory strain K-12.";

RDNA Res. 8:11-22(2001).

CICATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) - AMP +

CC diphosphate + L-glutamyl tRNA(Glu).

CI- SUBCULLAR LOCATION: Cytoplasmic.

CI- SUBCLULLAR LOCATION: CYLOBASMIC.

CI- SUBCLULLAR LOCATION: CYLOBASMIC.

CI- SUBCLULLAR LOCATION: CYLOBASMIC.
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Q8XBN2;
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EMBL; AP002561; BAB36701.1; --
INTERPO; IPR004527; G1tX_bact.
InterPro; IPR000924; G1u_trNa-synt_1c.
InterPro; IPR001411; trNa-synt_1.
Pfam; PF00749; trNa-synt_1c; 1.
PRINTS; PR00987; TRNASYNTHGLU.
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MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
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Escherichia coli O157:H7.
Bacteria; Proteobacteria;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
                                                                                                                                        BINDING
                                                                                                                                                                                                                                                     Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                          TIGRFAMs;
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Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:529-533(2001).
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                       33.3%;
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ATP (BY SIMILARITY).
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M., Tobe T.,
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P17712; P17711;
01-AUG-1990 (Rel. 15, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Hexokinase D (EC 2.7.1.1) (Hexokinase type
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SEQUENCE
MEDLINE-91154262; PubMed-1999433;
Hughes S.D., Quadde C., Milburn J.L., Cassidy L., Newgard C.B.;
"Expression of normal and novel glucokinase mrnas in anterior pituitary and islet cells.";
J. Biol. Chem. 266:4521-4530(1991).
-1- FUNCTION: CATALYZES THE INITIAL STEP IN UTILIZATION OF GLUCOSE
-1F BETA-CELL AND LIVER AT PHYSIOLOGICAL GLUCOSE CONCENTRATION.
PANCREATIC GLUCOKINASE PLAYS AN IMPORTANT ROLE IN MODULATING INSULIN SECRETION. HEPATIC GLUCOKINASE HELPS TO FACILITATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol.
[2]
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-15 FROM N.A. (ISOFORM 3).
MEDLINE-89296899; PubMed-2662183;
Magnuson M.A., Andeone T.L., Printz R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayzer D.J., Iynedjian P.B.; "Alternative splicing of glucokinase Biochem. J. 270:261-263(1990).
                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-15 FROM N.A. MEDLINE-90073655; PubMed-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pancreatic beta cell.";
J. Biol. Chem. 264:1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Magnuson M.A., Shelton K.D.;
"An alternate promoter in the
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RESULT 96
PDM2_DROVI
ID PDM2_D
AC Q24705
DT 15-DEC
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Matches
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NP_BIND
BINDING 1
DOMAIN 1.
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SEQUENCE
PDM2_DROVI STANDARD;
Q24705;
15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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                                                                                                                                                                                                                                               PRINTS; PR00475; HEXOKINASE.
ProDom; PD001109; Hexokinase;
PROSITE; PS00378; HEXOKINASES;
                                                                                                                                                                                                                                                                              Pfam; PF00349; hexokinase; 1. Pfam; PF03727; hexokinase2; 1.
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                                                                                                                                                                                              VARSPLIC
                                                                           63
                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UPTAKE AND CONVERSION OF GLUCOSE BY ACTING AS AN INSULIN-SENSITI DETERMINANT OF HEPATIC GLUCOSE USAGE.

CATALYTIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
ENZYME REGULATION: THE USE OF ALTERNATIVE PROMOTERS APPARENTLY
ENABLES THE TYPE IV HEXOKINASE GENE TO BE REGULATED BY INSULIN IN THE LIVER AND GLUCOSE IN THE BETA CELL. THIS MAY CONSTITUTE A IMPORTANT FEEDBACK LOOP FOR MAINTAINING GLUCOSE HOMEOSTASIS.

ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; are produced by alternative splicing.

TISSUE SPECIFICITY: PANCREAS (ISOFORMS 1 AND 2) AND LIVER (ISOFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE HEXOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: IN VERTEBRATES THERE ARE FOUR MAJOR GLUCOSE-PHOSPHORYLATING ISOENZYMES, DESIGNATED HEXOKINASE I, II, II
                                                                          RSTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATING IV (GLUCOKINASE
                                                                                                                                                                                                                                                                                                   $12062; $12062.
; P35557; IGLK.
rPro; IPR001312; Hexokinase
                                                                                                                                                                                                                                                                                                                                    S11465; S11465.
                                                                                                                                                                                                                                                                                                                                              A31810; A31810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M24944;
M24945;
                                                                                                                                                                                                                                                                                                                                                       X53590; CAA37660.
M30770; AAA41231.
                                                                                                                                                                                                                                                                                                                                                                                                                                M24950;
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                                                                                                                   Similarity
5; Conserv
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145
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                                                                                                                    Conservative
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AAA41230 1;
AAA41230 1;
AAA41238 1;
AAA41238 1;
AAA41239 1;
AAA41236 1;
CAA37657 1;
CAA37660 1;
AAA41231 1;
                                                                                                                                                                                                                                       Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA41229.1;
AAA41230.1;
                                                                                                                                                              Ä,
                                                                                                                                                            e; Glycolysis; ATP-binding; Alternative sp

83 ATP (POTENTIAL).

104 ATP (POTENTIAL).

171 GLUCOSE-BINDING (POTENTIAL).

15 MLDDRARWEATKKEK -> MAMDTTRCGAQL

15 ISOFORM 3).

138 MISSING (IN ISOFORM 2).

52116 MW; 65B36673DF9297BE CRC64;
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52116
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104
171
15
                                                                                                                               33.3%;
100.0%;
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.8e+02;
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                                                                                                                                                                                              MAMDITRCGAQLLTL
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tent is in no
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HXK4_
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Best Loc
Matches
                                   HXK4 MOUSE STANDARD; PRT; 465 AA. P52792; P52791; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Hexokinase D (EC 2.7.1.1) (Hexokinase type IV)
                    GCK OR GK
                                                                                                  MOUSE
                                                                                                                                                                                                                         "Neonatal diabetes mellitus due to complete glucokinase deficiency.";
New Engl. J. Med. 344:1588-1592(2001).
-i- FUNCTION: CATALYZES THE INITIAL STEP IN UTILIZATION OF GLUCOSE BY
-i- FUNCTION: CATALYZES THE INITIAL STEP IN UTILIZATION OF GLUCOSE BY
-i- FUNCTION: CATALYZES THE INITIAL STEP IN UTILIZATION OF GLUCOSE BY
-i- FUNCTION: OF GLUCOSE AND SO IT IS EFFECTIVE ONLY
WHEN GLUCOSE IS ABUNDANT. THE ROLE OF GCK IS TO PROVIDE G6P FOR
THE SYNTHESIS OF GLYCOGEN. PANCREATIC GLUCOKINASE PLAYS AN
                                                                                                                                                                                                                                                                                              Njoelstad P.R., Soevik O., Cuesta-Munoz A., Bjoerkhaug L.,
Barbetti F., Undlien D.E., Shiota C., Magnuson M.A., Molven
Matschinsky F.M., Bell G.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ng M.C.Y., Cockburn B.N., Lindner T.H., Yeung V.T.F., Chow C.-C., So W.-Y., Li J.K.Y., Lo Y.M.D., Lee Z.S.K., Cockram C.S., Critchley J.A.J.H., Bell G.I., Chan J.C.N.;

"Molecular genetics of diabetes mellitus in Chinese subjects: identification of mutations in glucokinase and hepatocyte nuclean factor-lalpha genes in patients with early-onset type 2 diabetes mellitus MODY."
  Eukaryota; Metazoa;
          Mus musculus (Mouse)
                             (Glucokinase).
                                                                                                                                                                                                                                                                                                                                                                "Identification of glucokinase mutation in subjects transplantation diabetes mellitus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New
                                                                                                                                                                                                                                                                                                                            MEDLINE=21245203;
                                                                                                                                                                                                                                                                                                                                      VARIANTS MODY2 LYS-210 AND MET-228.
                                                                                                                                                                                                                                                                                                                                                                                      Nam J.H., Lee
Huh K.B.;
                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT MODY2 PRO-164.
MEDLINE=20560768; Pubh
                                                                                                                                                                                                                                                                                                                                                                                                                                                mellitus/MODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20053748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS MODY2 THR-110; ASP-119 AND VAL-385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herold K.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stanley C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glaser B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98084322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT HYPERINSULINISM MET-455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98324778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Familial hyperinsulinism caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mutations in
                                                                                                          94
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                                                                                                                                                                                      Local
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                                                                                                                                                                                                                  IMPORTANT ROLE IN MODULATING INSULIN SECRETION
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                                                                                                                                       RSTPE
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beards F., Ballantyne E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=9435328;
n P., Heyman M., Davis E.,
rnton P.S., Permutt M.A.,
                                                                                                                                                                                                                                                                                                                           PubMed=11372010;
                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11106831;
., Kim Y.H., Cha B.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=10588527;
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  Chordata;
                                                                                                                                                                                     33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-150; T-259; R-299;
                                                                                                                                                                                                                                                                                                                                                        50:169-176(2000)
                                                                                                                                                                            0;
                                                                                                                                                                                      Score 5; I
Pred. No.
Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                             Mismatches
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). 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Cuesta A.,
Matschinsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y-382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appleton M.,
                                                                                                                                                                            0;
                                                                                                                                                                                               Length 465;
                                      (HK IV) (HK4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucokinase
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                                                                                                                                                                                                                                                                                                         Molven
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F.M.,
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                                                                                                                                                                                                                                                                                                                                                                                              S.K.,
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                                                                                                                                                                                                                                                                                                                                                                           post-renal
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                                                                                                                                                                                                                                                                                                                                                                                              Kim
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BINDING
DOMAIN
                                                                                                                                                                                                                                                                                       EMBL;
  CONFLICT
                                                                                                                                PRINTS; PR00475; HEXOKINASE.
ProDom; PD001109; Hexokinase;
PROSITE; PS00378; HEXOKINASES;
                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oka K.
                                      VARSPLIC
                                                                                                                  Fransferase;
                                                                                                                                                                                         Pfam; PF00349; hexokinase; 1. Pfam; PF03727; hexokinase2; 1.
                                                                                                                                                                                                                                 MGD; MGI:95724; Gk.
InterPro; IPR001312; Hexokinase.
                                                                                                                                                                                                                                                                         HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129/Sv; TISSUE-Liver; MEDLINE=96121387; PubMed=8575768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIVER (ISOFORM 2).
MISCELLANEOUS: IN VERTEBRATES THERE ARE FOUR MAJOR GLUCOSE-PHOSPHORYLATING ISOENZYMES, DESIGNATED HEXOKINASE I, II, III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
TISSUE SPECIFICITY: PANCREAS, ANTERIOR PITUITARY (ISOFORM 1)
                                                                                                                                                                                                                                                                     ; L38990; AAB00360.1;
; L41631; AAC42074.1;
; M58755; AAA37703.1;
); P35557; IGLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE HEXOKINASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLUCOKINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A. (ISOFORM 1).
96121388; PubMed-8575769;
-Oka K., Nakamuta M., Chu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        structure of the mouse 29:751-754(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29:740-750(1995).
                                                        ; Kinase;
78 8
104 10
145 17
                                13e; Glycolysis; ATP-binding;
83 ATP (POTENTIAL).
104 ATP (POTENTIAL).
171 GLUCOSE-BINDING (
15 MLDDRAPMENEW:---
                                                                                                                                                       Hexokinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
  133
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MLDDRARMEATKKEK
ISOFORM 2).
F -> L (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISOFORM
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                                                                                              ATP-binding; (POTENTIAL).
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                                      (POTENTIAL)
                                                                                                                Alternative
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Hexokinase D
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Velho
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MEDLINE=94252471; PubMed=8194664.
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MEDILINE=97201951; PubMed=9049484;

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Cohen D., Czernichow P., Velho G.
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"Identification of glucokinase
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Alternative splicing; Developmental protein.

B4 98 POLY-ALA.

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DOMAIN 211 222 POLY-HIS.

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                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=87112952; PubMed=3027382;
Bando H., Kusuda J., Gojobori T., Maruyama T., Kawase
"Organization and nucleotide sequence of a densovirus
host-dependent evolution of the parvoviruses.";
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PIR; A26796; UYPVF1.
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced throu between the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                               Bando H., Choi H., Ito Y., Kawase S.; "Terminal structure of a Densovirus implies a hairpin transfer replication which is similar to the model for AAV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1988 (Rel. 09, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Putative nonstructural protein (ORF1)...
                                                                                                   Nonstructural protein.
SEQUENCE 455 AA; 52488 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91021065; PubMed=2219739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Isolate INA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bombyx densonucleosis virus (BmDNV) (Silkworm densovirus).
Viruses; ssDNA viruses; Parvoviridae; Densovirinae; Iteravirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNS1_BMDNV
P05840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                             J. Virol. 61:553-560(1987).
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 26-455 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10809;
382
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RSTPE 386
                        RSTPE 11
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                                                   Similarity
5; Conserv
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5; Conserv
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POU_2;
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Pred. No. 1.8
0; Mismatches
                                                               Score 5; I
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GHELVDYLKDASLIGPSEDGDQRVTTTSSFHQVILAH
VSADTPPPSMDCKRMESET (IN SHORT ISOFORM)
552A6DC6BB333F5C CRC64;
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                                                                                                       0E5466B06C775A04 CRC64;
                                                    Mismatches
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                                                               DB 1; Le
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b. 1.8e+02;
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                                                                          Length 455
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RESULT 93
HXK4_HUMAN
ID HXK4_H
AC P35557
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P25157;
01-MAY-1992
01-MAY-1992
16-OCT-2001
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NP_BIND
HXK4_HUMAN STA
P35557; Q05810;
01-JUN-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                    EMBL; M94285; AAA82939.1; -.
PIR; A38567; A38567.
HSSP; P04896; 1AZT.
FlyBase; FBgn0000384; cta.
InterPro; IPR001019; Gprotein_alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanine nucleotide-binding protein, alpha subunit homolog (Protein
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                              SMART; SM0027
GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Oregon - R;
MEDLINE=91105860; PubMed=1899050;
Parks S., Wieschaus E.;
                                                                                                                                                                                                                                                                                                                          PRINTS; PR00318; GPROTEINA.
                                                                                                                                                                                                                                                                                                                                           Pfam; PF00503; G-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities
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                                                                                                      103
                                                                                                                                  7 RSTPE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMM THE ALPHA CHAIN THE GUANINE NUCLEOTIDE BINDING SITE. TISSUE SPECIFICITY: DISTRIBUTED UNIFORMLY.

DEVELOPMENTAL STAGE: GASTRULATION.

SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 4 (G(12)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COORDINATING CELL SHAPE CHANGES.
FUNCTION: GUANINE NUCLEOTIDE BINDING PROTEINS (GINVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS SIGNALING SYSTEMS.
SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 64:447-458(1991).
FUNCTION: MAY PLAY A ROLE IN A SIGNAL TRANSDUCTION PATHWAY USED DURING GASTRULATION. REQUIRED SPECIFICALLY FOR THE VENTRAL FURROW AND POSTERIOR MIDGUT INVAGINATIONS, WHERE IT IS NECESSARY FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS\mbox{-PROT} entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                      RSTPE
                                                                                                                                                                                                                       SM00275; G-alpha; 1.
SM00275; G-alpha; 1.
Inding; Transducer; Multigene family; Gastrulation.
ID 139 146 GTP (BY SIMILARITY).
ID 299 303 GTP (BY SIMILARITY).
ID 369 372 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                           PD000281; Gprotein_alpha; 2.
                                                                                                                                                               Similarity 100 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                      107
                              STANDARD;
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   29, Created)
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303
372
52753
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100.0%; Pr
                                                                                                                                                              Score 5; DB 1; Pred. No. 1.8
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RX MEDLING-21016719; PubMed-11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araul R., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araul R., Bomman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araul R., Bomman C.L., Brooks S.Y.,

RA Duhler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Fujii C.Y.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Fujii C.Y.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Liee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Liee A., Luros J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Nguyen M., Rooney T., Rowley D.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

Neturo Johnson-Malver M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Tallalana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 2-439 FROM N.A.
MEDLINE=92390390; PubMed=1518831;
Cerutti H.D., Osman M., Grandoni P., Jagendorf
"A homolog of Escherichia coli Reca protein in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Last annotation update)
DNA repair protein recA, chloroplast precursor.
RECA OR ATIG79050 OR YUD8H12R.18 OR YUP8H12R.33.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                    PROSITE; PS00321; RECA_1; 1.
PROSITE; PS50162; RECA_2; 1.
PROSITE; PS50163; RECA_3; 1.
                                                                                                                                    PRINTS; PR00142; RECA.
ProDom; PD000229; RecA; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electron the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Bioi
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Binet M.N., Osman M., Jagendorf A.T.;
"Genomic nucleotide sequence of a gene from Arabidopsis thaliana
encoding a protein homolog of Escherichia coli Reck.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plants."
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       DNA damage;
                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Chloroplast stroma.
SIMILARITY: BELONGS TO THE RECA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  c. Natl. Acad. Sci. U.S.A. 89:8068-8072(1992) FUNCTION: INVOLVED IN RECOMBINATION ABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFER ACTIVITY.
                                                                                                                                                                                                                                    Pro; IPR003593; AAA_ATPase.
Pro; IPR001553; RecA.
PF00154; recA; 1.
                                                                                                                                                                                                                                                                                                                                                         P26345;
                                                                                                                                                                                                                                                                                                                                                                                          AC002986; AAC17051.1;
M98039; AAA32855.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                L15229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408:816-820(2000).
DNA recombination; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                         AAA32855.1;
1G19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA61781.1; -.
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DNA-binding; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.T.;
plastids of higher
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RESULT 90

PRESULT 90

ID ZP23_BRARE

ID ZP23_BRARE

ID 279745

DT 01-NOV

DT 01-NOV

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DT 01-NOV

DT 15-JUN

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Spaniol P., Bornmann C., Hauptmann G., Gerster T.;
"Class III POU genes of zebrafish are predominantly excentral nervous system.";
Nucleic Acids Res. 24.4874-4881(1996).
-I- FUNCTION: TRANSCRIPTION FACTOR THAT MAY PLAY IMPO.
PATTERNING THE EMBRYONIC BRAIN.
-I- SUBCELLULAR LOCATION: Nuclear.
-I- SUBCELLULAR LOCATION: Nuclear.
-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SH.)
-I- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN TH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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NP_BIND
SEQUENCE
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TRANSIT
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                                                                SMART; SM00389; HOX; 1
SMART; SM00352; POU; 1
                                                                                                                                 PRINTS; PR00028; POUDOMAIN.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000583; POU_domain;
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y07907; CAA69215.1;
EMBL; Y07907; CAA69214.1;
HSSP; P14859; 10CT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- DEVELOPMENTAL STAGE: DETECTED AFTER COMPLETION OF THE GASTRULA PERIOD. MAXIMAL EXPRESSION AFTER 1 TO 2 DAYS OF DEVELOPMENT.
-I- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinopterygii; Neopterygii; Cyprinidae; Danio. NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                               Pfam; PF00046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97169208; PubMed=9016656;
                                                                                                                                                                                                                                                                                                     InterPro;
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SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM.
                                                                                                                                                                                                                                    PF00157;
                                                                                                                                                                                                                                                                                              ZDB-GENE-980526-140; pou23 Pro; IPR001356; Homeobox. Pro; IPR000327; POU_domain.
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   PS00027;
PS50071;
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      HOMEOBOX_1;
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ATP (POTENTIAL).
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ta; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predominantly
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b. 1.7e+02;
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InterPro: IPR003659; Orange.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00351; ORANGE; 1.
PROSITE; PS00038; HLH_1; 1.
PROSITE; PS00888; HLH_2; 1.
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                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                          Differentiation; Developmental protein; Nuclear protein; DNA-binding; Neurogenesis; Repressor; Transcription regulation.
DNA_BIND 41 53 BASIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003838; AAF59113.1; -. FlyBase; FBgn0010109; dpn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brent R., Ish-Horowicz D.; "Groucho is required for Drosophila neurogenesis, segmentation,"
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11 ESRAA 15
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SUBCELLULAR LOCATION: NUCLEAR (Probable).

TISSUE SPECIFICITY: EXPRESSED IN PRIMARY NEURAL PRECURSORS.

TISSUE SPECIFICITY: EXPRESSED IN PRIMARY NEURAL PRECURSORS.

DEVELOPMENTAL STAGE: FIRST DETECTED IN PREBLASTODERM CYCLE 12 I

ALL NUCLEI. DURING MIDDLE TO LATE CYCLE 13, EXPRESSED IN EIGHT STRIPES THAT OVERLAP THOSE OF THE HALRY PROTEIN.

DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG), RATHER THAN THE CARONICAL E-BOX (CANNTG).

DOMAIN: THE CARONICAL E-BOX (CANNTG).

TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA 1

TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAIRY-RELATED PROTEINS. SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH PROTEIN FOR THEIR TRANSCRIPTION. LIKELY TO BE INVOLVED IN THE FUNCTIONAL RATHER THAN THE MORPHOLOGICAL DIFFERENTIATION OF REURONS, LOSS OF DPN FUNCTION RESULTS IN WEAK MOTOR ACTIVITY, LETHARGIC BEHAVIOR, AND DEATH. IMPLICATED IN SEX DETERMINATION AS GROUCHO-DPN COMPLEX ACT DIRECTLY TO REPRESS SXL TRANSCRIPTION. SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A COMPLEX SUBUNIT.
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                                                    . Similarity
5; Conserv
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                                                       Conservative
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POLY-GLN.
WRPW MOTIF.
M -> L (IN REF. 1)
                                                 Score 5; DB 1
Pred. No. 1.7
0; Mismatches
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                                                                                                                                                                   -> L (IN REF. 1)
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Best Local :
RECA_ARATH STAN
Q39199; Q39200;
Q1-NOV-1997 (Rel. 3
Q1-NOV-1997 (Rel. 3
                                                                                                                                                                                                                                                      DOMAIN
CARBOHYD
                                                            ARATH
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Prodom; PD000448; NA_ntran_symport; 2.

PROSITE; PS00610; NA_NEUROTRAN_SYMP_1;

PROSITE; PS00754; NA_NEUROTRAN_SYMP_2;

PROSITE; PS50267; NA_NEUROTRAN_SYMP_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Q9H1V8;
                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 Symport.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00209; SNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000175; Na/ntran_symport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTT4 (Fragment).
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16-OCT-2001 (Rel. 4
Orphan sodium- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
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                                                                                                                                                   8 STPES
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                                                                                                                                                                                                                                                                                                                                                                                                        TER
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                                                                                                                      STPES
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                                                                                                                                                                              Similarity 5; Conserv
                                                                                                                        437
                                                                                                                                                   12
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
um- and chloride-dependent neuro
                                                                                                                                                                                Conservative
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35, Created)
35, Last sequence update)
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100.0%; Pr
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3 6 3
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                                                                                                                                                                                                                                          49011
                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                       11 (POTENTIAL).
12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (PO'
W; 44634308C281C740 CRC64;
                                                                                                                                                                                         Score 5; u
                                                                                                                                                                                                                                                                                                                                                                                                                                Transport; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                               6 (POTENTIAL).
7 (POTENTIAL).
EXTRACELLULAR
8 (POTENTIAL).
9 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                               439
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o. 1.7e+02;
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neurotransmitter transporter
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PRESULT PROCESSULT PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A POU-domain gene of zebrafish, ZFPOU1, specifically exp.
T the developing neural tissues.";
L Biochem. Biophys. Res. Commun. 187:1446-1453(1992).
--- SUBCELLULAR LOCATION: Nuclear.
--- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN THE DEVEL
NEURAL TISSUES.
--- SIMILARITY: BELONGS TO THE POU TRANSCONTINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 5
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00055; FCH; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50133; FCH; 1.
PROSITE; PS50002; SH3; 1.
Endocytosis; SH3 domain; Coiled coil; Phosphorylation.
DOMAIN 10 73 FCH.
                                                              ProDom;
ProDom;
                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
POU domain protein 1 (ZFPOUI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRARE
                       SMART; SM00389; HOX; SMART; SM00352; POU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                    Pfam; PF00046; homeobox; Pfam; PF00157; pou; 1.
                                                                                                                                                                         ZFIN; ZDB-GENE-990415-209; poul InterPro; IPR001356; Homeobox. InterPro; IPR000327; POU_domain
                                                                                                                                                                                                                                                                                       EMBL; D13045; BAA02377.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyprinidae; Dani
NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                  JH0710;
                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Enteropean Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESRAA 132
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P14859; 1ОСТ.
                                                              PRO0028; POUDOMAIN.
PD000010; Homeobox; 1.
PD000583; POU_domain;
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5; Conser
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174
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424 AA;
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                                                                                                                             pou;
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HOMEOBOX_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424
217
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Pred. No. 1.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) (Danio rerio).
; Craniata; Vertebrata; Euteleostomi;
Teleoste1; Ostariophys1; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COILED COIL (POTENTIAL).

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; 00475BC0321485B7 CRC64
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NO. 1.7e+02;
0;
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J.H., Glaser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mchulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Rainer K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Sannders R.D.C., Scheler F., Shith T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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Q26263; Q9V384;
15-DEC-1998 (Rel. 3
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homeobox;
DOMAIN
DOMAIN
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PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bier E., Vaessin H., Younger-Shepherd S., Jan L.Y., Jan "Deadpan, an essential pan-neural gene in Drosophila, en hellx-loop-helix protein similar to the hairy gene produgenes Dev. 6:2137-2151(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=93051333; PubMed=1427077;
Bier E., Vaessin H., Younger-Shep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deadpan protein.
DPN OR CG8704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139
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(TE; PS50071; HOMEOBOX_2; 1.
'box; DNA-binding; Transcription re
84 98 ALA-RICH.
211 227
242 312
330 389
425 AA; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
5; Conserv
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41,
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100.0%;
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Last sequ
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435
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oduct.";
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Length 424

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entities
or send a
                             DOMAIN
CONFLICT
                                                                      DOMAIN
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May play a role in vesicle formation and transport.
-!- SUBUNIT: Homo- and hetero-aggregates with other PACSINs. Binds dynamin 1, synaptojanin, synapsin 1 and the neural Wiskott-Aldrich syndrome protein (N-WASP). Also interacts with MDC9 and MDC15 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                              Endocytosis;
DOMAIN
                                                                                                                                     PROSITE; PS50133; FCH; 1. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                           PRINTS; PR00452; S
ProDom; PD000066;
                                                                                                                                                                                                                                                                                                                                                                              Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The second of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Skin,
Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sumoy L., Pluvinet R., Andreu N., Estivill )
"PACSIN 3 is a novel SH3 domain cytoplasmic
pacsin-syndapin-FAP52 gene family.";
Gene 262:199-205(2001).
                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=21100457; PubMed=11179684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endocytosis."
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                                                                                                                                                                                                                                                                                                                 InterPro; IPR001452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ranigami A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-405 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modregger J., Ritter B., Witter Ball three PACSIN isoforms bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PKC) (Probable).
SIMILARITY: BELONGS TO THE PACSIN SIMILARITY: CONTAINS 1 FCH DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the plasma membrane in cells or myotubes.
TISSUE SPECIFICITY: Expressed in heart and skeletal
lung, kidney, adrenal gland and placenta.
PTM: Phosphorylated by casein kinase 2 (CK2) and pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic. Detected at
                                                                                                                                                                                                                                                                                                                                                                                                                                           BC007914;
BC011889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF149825;
AF242530;
                                                                                                                                                                                                                                                                      PF00611; FCH; PF00018; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                      P29355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF130979;
                                                                                                                                                                                SM00055; FCH; 1.
SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                              HGNC:8572; PACSIN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sci. 113:4511-4521(2000).
                                                                                                                                                                                                                                                                                                                                     IPR001060; Cdc15_Fes_CIP4.
                                               SH3
10
363
167
         424 AA;
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domain; Coiled coil; Phosphorylation.
73 FCH.
424 SH3.
217 COILED COIL (POTENTIAL):
61 A -> V (IN REF. 1).
A; 48486 MW; 6DBD940AE6D1F352 CRC64;
                                                                                                                                                                                                                                               SH3DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bioinformatics and the EMBL outst
titute. There are no restrictions
ns as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B., Paulsson
to endocytic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Χ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujii Y., Ozaki
rashi M., Nishi T.
T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
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RESULT
PAC3_MC
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q99JB8; Q9EQP9;
15-JUN-2002 (Rel. 41, C
15-JUN-2002 (Rel. 41, L
15-JUN-2002 (Rel. 41, L
                                               EMBL;
                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                        entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                    EMBL;
                                                                                                                                                     This
                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                 pacsin-syndapin-FAP52 gene family.";
Gene 262:199-205(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                        g. Cell Sci.
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                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                      rissue=Neuron;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      Sumoy L., Pluvinet R., Andreu N., Estivill 3 "PACSIN 3 is a novel SH3 domain cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-21100457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modregger J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20534871; PubMed=11082044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAC3_MOUSE
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                                                                                       send
                                                                                                                                                                       (PKC) (Probable).
- SIMILARITY: BELON
- SIMILARITY: CONTA
- SIMILARITY: CONTA
                                                                                                                                                                                                           lung.
PTM: Phosphorylated by casein kinase 2 (CK2)
                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Cytoplasmic. Detected at the inner the plasma membrane in cells or myotubes (By similarity) TISSUE SPECIFICITY: Highly expressed in skeletal muscle,
                                                                                                                                                                                                                                                                similarity)
                                      ; AF242531; AAK;
; BC003884; AAH;
; P29355; 1SEM.
                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            egger J., Ritter B., Witter B., three PACSIN isoforms bind to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESRAA 132
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                                                                    AF149824;
                                                                                       s requires a license agreement (See http://www.isb-sib.
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                       : BELONGS TO
: CONTAINS 1
: CONTAINS 1
                                               ; AAG31022.1;
; AAK29208.1;
; AAH03884.1;
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                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11179684;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          casein kinase
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100.0%;
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Last annotation update)
casein kinase II substrate
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                                                                                                                                                                      THE PACSIN |
FCH DOMAIN.
L SH3 DOMAIN.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     Estivill X., Escarceller M.; ytoplasmic adapter protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Paulsson |
endocytic |
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tent is in
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                                                                                                                                          a collaboration - MBL outstation -
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InterPro; IPR001060; InterPro; IPR001452;

MGD; MGI:1891410;

Pacsin3

Cdc15_Fes_CIP4 SH3.

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RESULT GAS7_RE GAS7_RE GAS7_RE GAS7_RE GAS7_RE GAS7_RE GAS7_RN
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Best Local S
Matches
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                                                                                                                                        GAS7_RAT STANDARI

Q55148;

16-OCT-2001 (Rel. 40, C

16-OCT-2001 (Rel. 40, I

15-JUN-2002 (Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
COARBOHYD
CARBOHYD
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DOMAIN
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between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:
MIM; 602836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           +++
NCBI_TaxID=10116;
                                                                                                                        Growth-arrest-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001429; P2X_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>-</del>
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                                                                                                                                                                                                                                                                                                                                  417
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SUBUNIT: HOMO- OR HETEROPOLYMERS (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND PRODUCED BY ALTERNATIVE SPLICING.
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content ifted and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM.
SIMILARITY: BELONGS TO THE P2X RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                PHRST 421
                                                                                                                                                                                                                                                                                                                                                                        PHRST 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGNC: 8536;
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R01307; P2XRECEPTOR. TIGR00863; P2X; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P2X_receptor;
                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47103
                                                                                                                                                                                                                                                                                                                                                                                                                               33.3%;
                                                                                                                      Last sequence update)
Last annotation updat
c protein 7 (GAS-7).
                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).

1 (POTENTIAL).

EXTRACELLULAR, CYSTEINE-RICH (POTENTIAL).

2 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

MISSING (IN ISOFORM B).

GE -> EK (IN REF. 1).

E -> G (IN REF. 2).

YI -> IV (IN REF. 2).

E -> R (IN REF. 2).

E -> R (IN REF. 1).

E -> Q (IN REF. 1).

E -> Q (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GE -> 
                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R -> NV (IN REF. 1).
6B47307AA14C2A6C CRC64;
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Mismatches
                                                                                                                        ation update)
(GAS-7).
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                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Le
o. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                            0;
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PAC3_HUMAN
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Best Local
             two ...
T. Biol.
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Pfam; PF00397; WW; 1.
Pfam; PF00611; FCH; 1.
SMART; SM00055; FCH; 1.
SMART; SM00456; WW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurogenesis;
DOMAIN 25
DOMAIN 14
DOMAIN 25
SEQUENCE 422
               TISSUE-Breast carcinoma;

MEDLIND-20002705; PubMed-10531379;

HOWARD L.N. Nelson K.K., Maciewicz R.A., Blobel C.P.;

"Interaction of the metalloprotease disintegrins MDC9 and MDC15 with

two SH3 domain-containing proteins, endophilin I and SH3PX1.";

two SH3 domain-containing proteins, endophilin I and SH3PX1.";
                                                                                                                                                                                                                 PAC3_HUMAN STANDARD; PRT; 424 AA.

O9UKS6; O9H331; O9NWV9;

15-JUN-2002 (Rel. 41, Created)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Protein kinase C and casein kinase substrate in domain containing protein 6511) (Endophilin I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Rat gas-7: a growth-arrest-specific gene in fibroblasts is preferentially expressed in terminally differentiated Purkinje and associated with the differentiation of cultured PC12 cells. Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY A ROLE IN PROMOTING MATURATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50133; FCH; 1.
PROSITE; PS01159; WW_DOMAIN_1; 1.
PROSITE; PS50020; WW_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ003148; CAA05907.1;
EMBL; AJ131902; CAA10525.1;
HSSP; Q13526; LPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Sprague-Dawley;
Chao C.C.-K., Kuo J.D.,
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MORPHOLOGICAL DIFFERENTIATION OF CEREBELLAR NEURONS.
-1- SUBCELLULAR LOCATION: CYCOPLASMIC (By SIMILARITY).
-1- SIMILARITY: CONTAINS 1 FCH DOMAIN.
-1- SIMILARITY: CONTAINS 1 WW DOMAIN.
 SEQUENCE FROM
                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                           PACSIN3
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"Rat gas-7:
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                                                                                                                                               NCBI_TaxID-9606;
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ilarity 100.0%;
Conservative
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N.A., AND FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 5; DB 1; Pred. No. 1.7
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 422
                                                                                                                                                                                                                                     neurons protein 3 (SH3
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Best Local
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SIAl_CHICK STAND...

SIAL_CHICK STAND...

SIAL_CHICK STAND...

O1-NOV-1997 (Rel. 35, Created)

O1-NOV-1997 (Rel. 35, Last sequence update)

O1-NOV-1997 (Rel. 41, Last annotation update)

15-JUN-2002 (Rel. 41, Last annotation update)

CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,6-sialyltransferase

(EC 2.4.99.1) (Beta-galactoside alpha-2,6-sialyltransferase)

Tinha 2,6-ST) (Sialyltransferase 1) (ST6Gal I).

Vortebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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BINDING
BINDING
BINDING
BINDING
                                                                                                                                                                                                            PROSITE;
                                      PROTEOLYTIC PROCESSING.
-I- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 29.
                                                                                                                                                                                                                                                                                                                                                   Kurosawa N., Kawasaki M.,
Arita M., Tsuji S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                        2,6-beta-D-galactosyl-1,4-N-acetyl-beta-D-glucosamine.
PATHWAY: Glycosylation.
SUBCELULIAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRA
FORM IN TRANS CISTERNAE OF GOLGI, SOLUBLE FORM IN BODY
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTES, BRAIN
AND TO A LESSER EXTENT IN LUNG AND HEART.
PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM B
PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM B
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Nuclear F
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PS50114;
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GATA_ZN_FINGER_2;
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                                                                                                                                                                                                                                                                                                                                                                          Hamamoto T.,
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Pred.
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GATA-TYPE 2.
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"The genomic region encompassing the nephropathic (CTNS): complete sequencing of a 200 kb segment an novel gene within the common cystinosis-causing de Genome Res. 10:165-173(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P2RX5 OR P2X3.

Homo sapiens (Human).

Homo sapiens (Human).

Chordata;

Metazoa; Chordata;

Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q93086; Q93087; O43450; O75540; Q9NZVO;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P2X purinoceptor 5 (ATP receptor) (P2X5) (Purinergic receptor).
P2RX5 OR P2X5.
                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS A AND B).

MEDLINE-20138496; PubMed-10673275;

Touchman J.W., Anikster Y., Dietrich N.L., Maduro V.

Shotelersuk V., Bouffard G.G., Beckstrom-Sternberg
                                                                                                                                                                                                                                                                                                                                                     "Primary structure and express
ATP receptor subunit from bra-
FEBS Lett. 418:195-199(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS A AND B).

TOKLYAMBA Y., Mereu L., Chen X., Rouard M., Bell G.I.;

"Cloning of human P2X purinoceptor new subtype (P2X5).";

Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the E
the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                             Green
                                                                                                                                                                                                                                              Submitted (JUN-1998)
                                                                                                                                                                                                                                                                TISSUE-Brain;
Yu W., Gibbs R.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98074936; PubMed-9414125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                         ouel D., Babinski K., Seguela P.;
expression of a naturally truncated human
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N-LINKED (GLCNAC...)
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)R (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                Maduro V.V., McDowell G., ternberg S.M., Gahl W.A.,
  A LIGAND GATED
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                                           ic cystinosis gene
and discovery of a
deletion.";
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Best Local :
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Erythroid transcription factor (GATA-1) (Eryf1) (GF-1) (NF-E1).
GATA1 OR GF1 OR ERYF1.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001552; Acyl-CoA_dh.

Pfam; PF00441; Acyl-CoA_dh_M; 1.

Pfam; PF02770; Acyl-CoA_dh_M; 1.

Pfam; PF02771; Acyl-CoA_dh_N; 1.

PROSITE; PS00072; ACYL_COA_DH_1; 1.

PROSITE; PS00073; ACYL_COA_DH_2; 1.

PROSITE; PS00073; ACYL_COA_DH_2; 1.

Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.

ACT_SITE 265
BY SIMILARITY.

SEQUENCE 408 AA; 45326 MW; A6351C6DCDCA962D CRC64;
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REVISIONS.
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SEQUENCE FROM N.A.
TISSUE-Bone marrow
                                                                                                                                                                                                                                                                            MEDLINE-90138889; PubMed-2300555;
Zon L.I., Tsai S.-F., Burgess S.,
                                                                                                                                                                                                                                                                                                                                                          TISSUE-Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
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WormPep; C02D5.1; CE24778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                   "The major human erythroid sequence and localization c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 HRSTP 221
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SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE ACYL-COA DEHYDROGENASE FAMILY.
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5; Conserv
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ilarity 100.0%;
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3-methylbutanoyl-CoA + ETF = 3-methylbut-2-
ETF.
                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE
                                                                                                                        id DNA-binding protein (GF-1): primary of the gene to the X chromosome."; S.A. 87:668-672(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 5; DB 1
Pred. No. 1.6
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CELLS:

CELLS:

CHARGE SUBUNIT: THE AMINO-TERMINAL ZINC FINGER INTERACTS WITH FOG1.

CHARGE SUBUNIT: THE AMINO-TERMINAL ZINC FINGER INTERACTS WITH FOG1.

CHARGE SPECIFICITY: ERYTHROCYTE.

CHARGE SPECIFIC: STABLE DIA BINDING. THE FIRST FINGER IS RECEIVE SPECIFIC. STABLE DIA BINDING. THE FIRST FINGER IS NECESSARY ONLY FOR FULL SPECIFICITY AND STABILITY OF BINDING, WHEREAS THE SECOND ONE IS REDOURED FOR BINDING (BY SIMILARITY).

CHARGES IN GATAL ARE THE CAUSE OF X-LINKED DYSERYTHROPOIETIC ANEMIA AND THROMBOCYTOPENIA (XDAT), A DISORDER CHARGETERIZED BY EXYTHROCYTES WITH ABNORMAL SIZE AND SHAPE, AND PERPENSEN SHAPE ABNORMAL SIZE AND SHAPE, AND PERPENSEN SHAPE ABNORMAL THE BONE MARROW CONTAINS ABUNDANT AND ABNORMALLY SMALL MEGAKARYOCYTES.

CHARGITY OF PLATELETS IN PERPENSEN BLOOD. THE BONE MARROW CONTAINS ABUNDANT AND ABNORMALLY SMALL MEGAKARYOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blood 98:2681-2688(2001).

-I- FUNCTION: TRANSCRIPTIONAL ACTIVATOR WHICH PROBABLY SERVES AS A GENERAL SWITCH FACTOR FOR ERYTHROID DEVELOPMENT. IT BINDS TO DNA SITES WITH THE CONSENSUS SEQUENCE (A/T)(ATA(A/G) WITHIN REGULATOR REGIONS OF GLOBIN GENES AND OF OTHER GENES EXPRESSED IN ERYTHROII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT XDAT SER-208.
WEDLINE-21531306; PubMed-11675338;
MEDLINE-21531306; PubMed-11675338;
MEDLINE-21531306; PubMed-11675338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Freson K., Devriendt K., Matthijs G., Van Hoof A., De Vo Minner K., Hoylaerts M.F., Vermylen J., Van Geet C.; "Platelet characteristics in patients with X-linked macrothrombocytopenia because of a novel GATA1 mutation. Blood 98:85-92(2001).
                                                                                                                                             PIR;
                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trainor C.D., Evans T., Felsenfeld G., "Structure and evolution of a human er: Nature 343:92-96(1990).
                                            InterPro;
InterPro;
                                                                                          Genew;
                                                                                                                                                                        EMBL; M30601; AAA35885.1; -. EMBL; X17254; CAA35120.1; -. EMBL; AF196971; AAF06806.1;
                                                                                MIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Familial dyserythropoletic anaemia inherited mutation in GATAl.";
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Maris J.M., Weiss M.J.
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                                                                                                              TRANSFAC;
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"X-linked thrombocytopenia caused
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                                                                              V; HGNC:4170;
305371; -.
                                                                                                                                          A34888; A34888.
S07121; S07121.
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                            PF00320;
                                                                                                                            P17679;
           b; IPR000679; Znf_GATA.
b; IPR001164; hRIP_like.
c00320; GATA; 2.
PR00619; GATAZNFINGER.
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erythroid tra
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01-NOV-1990
01-NOV-1990
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
7-nfromere protein C (CENP-C) (Centromere autoantigen C)
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                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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Mammalia; Eutheria;
Bovidae; Caprinae;
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Transmembrane; Late protein.
TRANSMEM 17 35
TRANSMEM 13 153
DOMAIN 310 337
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                                                                                   177
                                                                                                                         Local Similarity
nes 5; Conserv
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(Rel. 16, Last
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LDc; 2.
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PLD PHOSPHODIESTERASE
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                                                                                                                                    DB 1; Le
D. 1.6e+02;
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Best Local
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
                                                                                                                                                                                                                   STRAIN-Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVD_CAEEL STANDARD; PRT; 408 AA P34275; 91-FEB-1994 (Rel. 28, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces griseolus.";
J. Bacteriol. 172:3335-3345(1990).
-i- FUNCTION: METABOLISM OF A NUMBER OF
-i- INDUCTION: BY HERBICIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
STRAIN=ATCC 11796;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
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HSSP; P23295; 1CMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
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Leto K.J.,
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MEDLINE=90264332; PubMed=2345149;
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                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omer C.A., Lenstra R., Litle P.J., Dean C., Tepperman
Leto K.J., Romesser J.A., O'Keefe D.P.;
"Genes for two herbicide inducible cytochromes P-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYP105B1 OR SUBC.
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TE; PS00086; CY
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5; Conserv
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402 AA;
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onooxygenase; Electron transport;
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(EC 1.3.
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AC P26579;
DT 01-AUG-199
DT 15-JUN-200,
DE MAJOR enve-
GN M011uscum,
OC Viruses; dd
OC M011uscipo;
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RN [1]
RP SEQUENCE F
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RA Blake N.W.
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Matches 5
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01-AUG-1992 (Rel. 23, Created)
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BINDING
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SEQUENCE FROM N.A. MEDLINE=91251209; PubMed=2041084; Blake N.W., Porter C.D., Archard
                                                                                                       MOlluscipoxvirus.
NCBI_TaxID=10280;
                                                                                                                                                       Molluscum contagiosum virus
Viruses; dsDNA viruses, no I
                                                                                                                                                                                                          Major envelope protein P43K.
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Harms N., Duine J.A., van Spanning R.J.M.;
"Mutational analysis of mau genes involved
in Paracoccus denitrificans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95324575;
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InterPro; IPR000345; CytC_heme_k
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SIMILARITY: SOME, TO P.AERUGINOSA CYTOCHROME C PEROXIDASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Blochem. 230:860-871(1995).
FUNCTION: INVOLVED IN METHYLAMINE METABOLISM. ESSENTIAL FOR MATURATION OF THE BETA SUBUNIT OF MADH, PRESUMABLY VIA A STETHE BIOSYNTHESIS OF TRYPTOPHAN TRYPTOPHYLQUINONE (TTQ), THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR OF MADH.
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1 20 POTENTIAL.
21 387 METHYLAMINE
51 51 HEME 1 (COV.)
54 54 HEME 1 (COV.)
55 55 IRON 1 (HEM.)
221 HEME 2 (COV.)
24 224 HEME 2 (COV.)
25 225 IRON 2 (HEM.)
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n (43 kDa protein) (p4
     Archard L.C.;
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Pred. No.
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HEME 1 (COVALENT) (BY SIMILARITY).
HEME 1 (COVALENT) (BY SIMILARITY).
IRON 1 (HEME PROXIMAL) (BY SIMILARITY).
HEME 2 (COVALENT) (BY SIMILARITY).
HEME 2 (COVALENT) (BY SIMILARITY).
HEME 2 (COVALENT) (BY SIMILARITY).
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Poxviridae;
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                                                                                                                                                       Chordopoxvirinae;
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RESULT 76
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PIR: A40340; WMVZM1.

InterPro; IPR001736; PLD.

Pfam; PF00614; PLDc; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P25392;
01-MAY-1992 (Rel. 2
01-MAY-1992 (Rel. 2
15-JUN-2002 (Rel. 4
PIR; B403,
InterPro;
                                                                                                                                                                                                                                                                                          Blake N.W., Porter C.D., Archard L.C.;

"Characterization of a molluscum contagiosum virus homolog vaccinia virus p37K major envelope antigen.";

J. Virol. 65:3583-3589(1991).

-i- FUNCTION: THIS PROTEIN IS THE MAJOR ANTIGEN ON THE ENVEXTRACELLULAR VIRUS.

-i- SIMILARITY: TO VACCINIA VIRUS 37 kDa ENVELOPE PROTEIN.

-i- SIMILARITY: CONTAINS 1 PLD PHOSPHODIESTERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Virol. 65:3583-3589(1991).
-I- FUNCTION: THIS PROTEIN IS THE MAJOR ANTIGEN ON
                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                              EMBL; M63487; AAA46549.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91251209; PubMed=2041084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molluscipoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molluscum contagiosum virus subtype 2 (MCVII).
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Major envelope protein (43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VENV_MCV2
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  B40340; WMVZU2.
CPro; IPR001736;
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annotation update)
kDa protein) (p43K
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PLD PHOSPHODIESTERASE.
; 54697FA9DA796A6F CRC64;
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RESULT 72
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POS_MOS_M
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DT 21-
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21-JUL-1986
15-JUN-2002
                           PRINTS; PR00042; LEUZIPPRFOS.

SMART; SM00338; BRLZ; 1.

SMART; SM0036; BZID_BASIC; 1.

PROSITE; PS00036; BZID_BASIC; 1.

Proto-oncogene; Nuclear protein; Phosphorylation; DNA-binding.

DNA_BIND 139 160 BASIC MOTIF.

DOMAIN 165 193 LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meijlink F., Curran T., Miller A.D., Verma I.M.;

"Removal of a 67-base-pair sequence in the noncoding region of protooncogene fos converts it to a transforming gene.";

Proc. Natl. Acad. Sci. U.S.A. 82:4987-4991(1985)

-1- FUNCTION: NUCLEAR PHOSPHOPROTEIN WHICH FORMS A TIGHT BUT NON-COVALENTLY LINKED COMPLEX WITH THE C-JUNYAP-1 TRANSCRIPTION FACTOR. C-FOS HAS A CRITICAL FUNCTION IN REGULATING THE DEVELOPMENT OF CELLS DESTINED TO FORM AND MAINTAIN THE SKELETON.

IT IS THOUGHT TO HAVE AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION, CELL PROLIFERATION AND DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest:
     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; V00727; CAA24105.1; EMBL; J00370; AAA96699.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-83180421; PubMed-6301687; van Beveren C., van Straaten F., Cu "Analysis of FBJ-MuSV provirus and
                                                                                                                                                                                        InterPro; IPR000837; Leuzip_Fos. InterPro; IPR004827; TF_bZIP. Pfam; PF00170; bZIP; 1.
                                                                                                                                                                                                                                                                            TRANSFAC; T00122; -. MGD; MGI:95574; Fos.
                                                                                                                                                                                                                                                                                                                                 PIR; A01343; TVMSF. HSSP; P01100; 1FOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Analysis of FBJ-MuSV provirus and c-fos (mouse) gene revea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell 32:1241-1255(1983).
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INDUCTION: C-FOS EXPRESSION INCREASES UPON A VARIETY OF INCLUDING GROWTH FACTORS, CYTOKINES, NEUROTRANSMITTERS, POLYPEPTIDE HORMONES, STRESS AND CELL INJURY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE BZIP FAMILY. FOS SUBFAMILY.
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     380 AA;
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(Rel. 01, Last sequence up
(Rel. 41, Last annotation
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     40838 MW;
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; Mismatches 0;
  475966265952B624 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Curran T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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FOS_MSVFB
GREGATO
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                                                                                                                                        MAUG_PARDE
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                                                                                                                                                                RESULT 74
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Best Local S
                                                                                                                                                                                                                                                                                                             Matches
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Best Local (
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                                    01-NOV-1997
01-NOV-1997
15-JUN-2002
                                                                                              MAUG_PARDE
Q51658;
                                                                                                                                                                                                                                                                                                                                                                                                           Oncogene;
DNA_BIND
DOMAIN
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21-JUL-1986
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00042; LEUZIPPRFOS. SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; V01184; CAA24505.1; -. PIR; A01344; TVMVJ. HSSP; P01100; 1FOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bloinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDLINE-83180421; PubMed-6301687;
Van Beveren C., van Straaten F., Curran T., Mueller R., Verma "Analysis of FBJ-MuSV provirus and c-fos (mouse) gene reveals viral and cellular fos gene products have different carboxy
            Methylamine
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00036; BZIP_BASIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; Retroid viruses; NCBI_TaxID=11805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FBJ murine osteosarcoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p55-v-fos transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P01102;
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                                                                                                                                                                                                                            231 STPES
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Pro; IPR004827; TF_bZIP.
PF00170; bZIP; 1.
                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; Phosphorylation; DNA-binding.
139 159 BASIC MOTIF.
165 193 LEUCINE-ZIPPER.
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                                                                                                                                                                                                                                                                                                                                                                                          165
381 AA;
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
                 utilization
                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                       STANDARD;
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41647 MW;
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100.0%; Pr/
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                                                                                                                                                                                                                                                                                                         33.3%; Score 5; DB 100.0%; Pred. No. 1. Live 0; Mismatches
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                 mauG
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              precursor
                                                                                                                       387
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ng as its content
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RESULT 70
PANE_YEAST
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Best Local S
Matches 5
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InterPro; IPR003395; SMC_N.
Pfam; PF02463; SMC_N; 1.
TICRFAMS; TIGR06611; recf; 1.
PROSITE; PS00617; RECF_1; 1.
PROSITE; PS00618; RECF_2; 1.
                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
CONFLICT
PIR;
SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PANE_YEAST STANDARD; PRT; 379 AA. P38787; O1-FEB-1995 (Rel. 31, Created) O1-FEB-1995 (Rel. 31, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 2-dehydropantoate 2-reductase (EC 1.1.1.169) (Ketopantoate
             EMBL; U00061; AAB68390.1; PIR; S46711; S46711.
                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                  <del>-</del>
                                                                                                                                                                                                                                                              Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                  Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dov Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten Kucaba T., Hillier L., Jier M., Johnston L., Langston S., Macticalle P., Louis E.J., Macri C., Mardis E., Menezes S., Monhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaug Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288c / AB972;
MEDLINE-94378003; PubMed-8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not remove
entitles requires a license agreement (So
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                 ÷
                                                                                                                                                                                                                                                                                                         Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharo Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAN5 OR YHR063C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                        Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GPHRS 8
                                                                                                                                                                                                              FUNCTION: Catalyzes the NADPH-dependent reinto pantoic acid (By similarity).

CATALYTIC ACTIVITY: (R)-pantoate + NADP(+)
                                                                                                                                                                   PATHWAY: Pantothenate biosynthesis.
SIMILARITY: BELONGS TO THE KETOPANTOATE REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPHRS
S0001105;
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
169
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40596
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).
RNRLLSEF -> ATGFSRNS (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycotina; Saccl cetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E81F5B937ED05B55
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). 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOS
                                                                                                                                                                                                                                           reduction of ketopantoate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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R.,
                                                                                                                          EMBL outstation
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Matches 5
  Query Match
                                                                                 InterPro; IPR003593; AAA_ATPASE.
InterPro; IPR001238; RecF.
InterPro; IPR003395; SMC_N.
Pfam; PP02463; SMC_N: 1.
SMART; SM00382; AAA; 1.
SMART; SM00382; AAA; 1.
TIGRFAMS; TIGR00611; recf; 1.
PROSITE; PS00617; RECF_1; 1.
PROSITE; PS00617; RECF_2; 1.
PROSITE; PS00618; RECF_2; 1.
DNA damage; DNA replication; DNA-b APP-binding; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasan Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno & Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the nitrogen-fixing symbiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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Pfam; PF02558; ApbA; 1.
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SOS inducibility.
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imura T.,
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RESULT 68
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PTOC. Natl. Acad. Sci. U.S.A. 88:7338-7342(1991).
PTOC. Natl. Acad. Sci. U.S.A. 88:7338-7342(1991).
PTOC. THIS PROTEIN MIGHT BE INVOLVED IN DETERMINATION AND/OR DIFFERENTIATION OF NERVE CELLS IN THE CONTINUOUS REPLACEMENT OF NEURONS IN THE CEPHALIC REGION.
PRESCRIPTION: NUCLEAR (Probable).
PRESCLULAR LOCATION: NUCLEAR AND UNIDENTIFIED PERIPHERAL PARENCHMAL CELLS. SLIGHTLY HIGHER LEVELS IN THE CEPHALIC REGION COMPARED TO OTHER BODY REGIONS.
PRESCRIPTION: SIMILARITY: BELONGS TO THE NK-2 HOMEOBOX FAMILY.
       between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See I
                                                                                                                                                                                                                                                                                                                    01-OCT-1993
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15-JUN-2002
                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restr
                                                                                                                                                              MEDLINE-91334461; PubMed-1714599;
Salo E., García-Fernandez J., Bag
"Planarian homeobox genes: clonin
                                                                                                                                                                                                                                                                        Dugesia tigrina (Planarian).
Eukaryota; Metazoa; Platyhelminthes;
Paludicola; Dugesiidae; Girardia.
                                                                                                                                                                                                                                MEDLINE=93387216; PubMed=8104142; Garcia-Fernandez J., Baguna J., S
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                                                                                                                                                                                                                   "Genomic organization Dth-1 and Dth-2.";
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(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
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P SEQUENCE OF 1-176 FROM N.A.

C STRAIN=SU47 / 1021;

X MEDLINE=98361913; PubMed=9696772;

X MEDLINE=98361913; PubMed=969672;

I Bardin S.D., Voegele R.T., Finan T.M.;

I "Phosphate assimilation in Rhizobium (Sinorhizobium) meliloti:

I identification of a pit-1ike gene.";

J. Bacteriol. 180:4219-4226(1998).

-i- FUNCTION: THE RECF PROTEIN IS INVOLVED IN DNA METABOLISM; IT I

C PROUIRED FOR DNA REPLICATION AND NORMAL SOS INDUCIBILITY. RECE

BINDS PREFERENTIALLY TO SINGLE-STRANDED, LINEAR DNA. IT ALSO SO TO BIND ATP (BY SIMILARITY).

C -i- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

C -i- SUBCELLULAR LOCATION: CYTOPLASMIC (Potential).
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EMBL; X56500; CAA3985
PIR; B41151; B41151.
PIR; S33702; S33702.
                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium mediloti strain 1021.";

Sinorhizobium mediloti strain 1021.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECF_RHIME STANDARD; PRT; 374 AA. p56903; 030497; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) DNA replication and repair protein recf. RECF OR R00188 OR SMC02883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision;
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PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEOBOX; DNA-binding; Developmental protein;
DOMAIN 29 42
DOMAIN 62 94
DNA_BIND 133 192
DOMAIN 134 331
DOMAIN 135 331
DOMAIN 136 331
DOMAIN 137 331
DOMAIN 137 331
DOMAIN 138 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha
Rhizobiaceae; Sinorhizobium.
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s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
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X56500; CAA39855.1;
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.5e+02;
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DOMAIN
                                                                                                                                                                                                             PROSITE;
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                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       Boie Y., Stocco R., Sawyer N., Slipetz D.M., Ungrin M.D.,
Neuschafer Rube F., Puschel G.P., Metters K.M., Abramovitz M.;
"Molecular cloning and characterization of the four rat prostaglandir
E2 prostanoid receptor subtypes.";
Eur. J. Pharmacol. 340:227-241(1997)
-1- FUNCTION: RECEPTOR FOR PROSTAGLANDIN E2 (PGE2). THE ACTIVITY OF
THIS RECEPTOR IS MEDIAATED BY G-S PROTEINS THAT STIMULATES
ADENVIATE CYCLASE. THE SUBSPOUGHT RAISE IN INTRACELLULAR CAMP IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Creat
01-NOV-1997 (Rel. 35, Last
30-MAY-2000 (Rel. 39, Last
Prostaglandin E2 receptor,
receptor, EP2 subtype).
                                  SEQUENCE
                                                                                       TRANSMEM
                                                                                                                                               TRANSMEM
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MEDLINE-98141044; PubMed-9537820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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MEDLINE-98103308;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                     TRANSMEM
                                                                               DOMAIN
                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                 Pfam; PF00001;
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                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                                                                             RESPONSIBLE FOR THE RELAXING EFFECT OF THIS RECEPTOR ON SMOOTH MUSCLE (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                  U48858;
U94708;
                                                                                                                                                                                                              PS00237; G_PROTEIN_RECEP_F1_1; PS50262; G_PROTEIN_RECEP_F1_2;
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35, Last sequence update)
. 39, Last annotation update)
receptor, EP2 subtype (Prostanoid
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100.0%;
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BY SIMILARITY:
N-LINKED (GLCN
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Pred
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Sciurognathi;
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thi; Muridae;
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4e+02;
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prostaglandin E2
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;; Murinae; Rat
                                        (POTENTIAL).
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     RESULT
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PE22_HUMAN
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01-NOV-1995 (Rel. 32, Las
16-OCT-2001 (Rel. 40, Las
Prostaglandin E2 recepton
receptor, EP2 subtype).
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P43116;
                                                                                                                                           PROSITE;
                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                         MIM;
                                                                                                                                                                                                                                                                                                EMBL; U19487; AAA61681.1; -
EMBL; X83868; CAA58749.1; -
EMBL; AR134202; AAD44177.1;
EMBL; AF134201; AAD44177.1;
Genew; HGNC:9594; PTGER2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Owen T.A.; "Cloning, structural characterization, and the dene encoding the human prostaglandin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=94359483; PubMed=8078484; Regan J.W., Bailey T.J., Pepperl D.J., Pierce K.L., Bogardus A.M., Bonello J.E., Fairbairn C.E., Kedzie K.M., Woodward D.F., Gil D.W.; "Cloning of a novel human prostaglandin receptor with characteristics of the pharmacologically defined EP2 subtype.";
                                                                                    G-protein
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the gene encoding the human prostaglandin E2 receptor EP2 sub-
Gene 237:393-402(1999).

-I FUNCTION: RECEPTOR FOR PROSTAGLANDIN E2 (PGE2). THE ACTIV-
THIS RECEPTOR IS MEDIATED BY G-S PROTEINS THAT STIMULATES
ADENYLATE CYCLASE. THE SUBSEQUENT RAISE IN INTRACELLULAR (
RESPONSIBLE FOR THE RELAXING EFFECT OF THIS RECEPTOR ON SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smock S.L., Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-99453300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                   RANSMEM
                                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: PLACENTA AND LUNG.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral me TISSUE SPECIFICITY: PLACENTA AND
PESRA
                                                                                                                                                                                                                                                                      176804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pharmacol. 46:213-220(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PESRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JAN-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109
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1. 32, Last sequence to the common 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=10521663;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update)
annotation update)
EP2 subtype (Prostanoid
                                                                                                                                                                                                                                                                                                                                    JOINED.
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lu B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosomal localization
E2 receptor EP2 subtype.";
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                STRÀIN=ATCC 1569 / PAO1:

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Westbrock-Wadman S., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
UDP-3-0-[3-hydroxymyristoyl] glucosamine N-acyltransferase
(EC 2.3.1.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPXD_PSEAE
Q9HXY6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                             Transferase; Acyltransferase;
                                                PROSITE; PS00101; HEXAPEP_TRANSFERASES;
                                                              Pfam; PF00132; hexapep;
                                                                                                EMBL; AE004784; AAG07034.1; -
                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome. ACT_SITE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE004883; AAG08080.1; -
InterPro; IPR000506; AcH_isom)
                                                                                                                                                                                                                                                                                                                                                                 Nature 406:959-964(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01450; IlvC;
TIGRFAMs; TIGR00465;
                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: UDP-3-O-(3-hydroxytetradecanoy1)glucosamine + (R)-3-hydroxytetradecanoy1-[acy1-carrier protein] = UDP-2,3-bis(3-hydroxytetradecanoy1)glucosamine + [acy1-carrier protein]. PATHWAY: Lipid A biosynthesis; third step.

SIMILARITY: BELONGS TO THE TRANSFERASE HEXAPEPTIDE REPEAT FAMILY.
                                                                                                                                                                                                                                                                    LPXD
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; Complete
CE 353 AA
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                                                                             IPR001451; Hexapep_transf
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               proteome
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WW;
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0; Mismatches
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                             Lipid A biosynthesis; Lipid synthesis;
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4B6C4D329F63EA35 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353
                                                                                                                                               (See http://www.isb-sib.ch/announce/
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1.4e+02;
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RESULT 65
GBAF CAREL
ID AC P9190
DT 15-JU
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P91907; Q9BIG1;
15-JUN-2002 (Rel
                                                                                                                                                                                                  GTP-binding; Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS.
-!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS; ALPHA, BETA AND GAMMA. THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING GAMMA. THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Cuppen E., Jansen G., Plasterk R.H.A.;
"Interaction analysis of the complete G-alpha heterotrimeric G proteins from Caenorhabditis submitted (SEP-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAEEL
                                                                                                                                                                                                                                                                                                                                                       EMBL; AY008137; AAG32090.1;
EMBL; Z83117; CAB05570.2; -
WormPep; M04C7.1; CE12394.
HSSP; P04896; 1AZT.
                                                                                                                                                                                                                                               PRINTS; PR00318; GPROTEINA.
ProDom; PD000281; Gprotein_alpha; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Rhabditidae; Peloder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guanine nucleotide-binding protein alpha-15 subunit. GPA-15 OR M04C7.1.
                                                                                                                                                                                                                                                                                                       Pfam; PF00503; G-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kershaw J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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15-JUN-2002 (Rel. 41,
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                                                                                                  Conservative
                                                                                                                                                                                                  Transducer; Multigene family.
56 AA; 40862 MW; 70F37C61031FA04E CRC64;
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100.0%; Pred. No.
tive 0; Mismatc
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databases.
                                                                                                                                               Length 356;
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PANC_STRCO STANDARD; PRT; 337 AA.

O9X844; O9X8N9;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pantoate-beta-alanine ligase (EC 6.3.2.1) (Pantothenate synthetase)
(Pantoate activating enzyme).
PANC OR SCO3383 OR SCE126.01C OR SCE94.34C.
SEQUENCE FIGURE 12000953;
STRAIN-A3(2) / M145;
STRAIN-A3(2) / M145;
MEDLINE-21996410; PubMed-12000953;
MEDLINE-21996410; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P39242; Q96217;
Ol-FEB-1995 (Rel. 31, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 38.9 kDa protein in nrdC-mobD intergenic region.
Y05G OR NRDC.11 OR TK.-11.
BacterIophage T4.
BacterIophage T4.
BacterIophage T4.
BacterIophage T4.
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BPT4
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                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                      SEQUENCE FROM
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Kutter E., Arisaka
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336 AA; 3
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16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Ketol-acid reductoisomerase (EC 1.1.1.86) (Acetohydroxy-acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pantothenate biosynthesis; Ligase; Complete proteome SEQUENCE 337 AA; 35456 MW; 3C948F7014A2913C CRC6
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EMBL: AL049628: CAB40883.1; -
InterPro: IPR003721: Pantoate_ligase.
Pfam, PF02569; Pantoate_ligase; 1.
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-!- PATHWAY: Pantothenate biosynthesis; last step.
-!- SIMILARITY: BELONGS TO THE PANTOTHENATE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."; coelicolor A3(2)."; Nature 417:141-147(2002).
-i- CATALYTIC ACTIVITY: ATP + (R)-pantoate + beta-alanine - AMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.3%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taylor K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
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ASB1_HUMAN
  Query Match
                                                                                                                                                                                                                                                                                                                           InterPro; IPR002110; ANK
InterPro; IPR001496; SOC:
Pfam; PF00023; ank; 6.
SMART; SM00248; ANK; 2.
SMART; SM00253; SOCS; 1.
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SEQUENCE FROM N.A.
MEDLINE-20564172; PubMed-11111040;
Kile B.T., Viney E.M., Willson T.A.,
Herlihy A.S., Croker B.A., Baca M., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASB1_HUMAN STANDARD; PRT; 335 AA O9Y576; Q9UL54; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update)
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DOMAIN
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REPEAT
                                                                                                                                                                                                                                                          PROSITE; PS50088; ANK_REPEAT; 3.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50225; SOCS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF156777; AAD41894.1; -. EMBL; BC014528; AAH14528.1; -. EMBL; AB032972; BAA86460.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from size-fractionated cDNA libraries from DNA Res. 6:329-336(1999).
-!- SIMILARITY: CONTAINS 6 ANK REPEATS.
-!- SIMILARITY: CONTAINS 1 SOCS BOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and characterization of and SOCS box-containing proteins Gene 258:31-41(2000).
                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohara O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hirosawa M., Nagase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ankyrin repeat and SOCS box containing protein 1 (ASB-1).
ASB1 OR KIAA1146.
Homo sapiens (Human).
                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                               ANK repeat;
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; Q00420; 1AWC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:16011; ASB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20039618; PubMed=10574461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606
                                           Repeat.
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335 AA;
                                           68 A
106 A
139 A
172 A
220 A
220 A
335 A
37014 MW;
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                                                                                         ANK 1.
ANK 2.
ANK 3.
ANK 4.
ANK 5.
ANK 6.
  Score 5;
                                           OCS BOX.
0843C96AD1AF60D9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Brodnicki T
Nicola N.A.,
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Length 335;
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                                                                                   Query Match
Best Local S
Matches 5
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Q9WV74;
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Pfam; PF00023; ank; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-slb.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and characterization of the genes encoding and SOCS box-containing proteins Asb-1, Asb-2, Asb-3 Gene 258:31-41(2000).
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                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50088; ANK_REPEAT; 3. PROSITE; PS50297; ANK_REP_REGION; PROSITE; PS50225; SOCS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00248; ANK; 2. SMART; SM00253; SOCS; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF155352; AAD38808.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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    -!- TISSUE SPECIFICITY: Highest expression

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herlihy A.S., Croker B.A., Baca M., Nicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kile B.T., Viney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20564172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ankyrin repeat and SOCS box containing protein
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144 HRSTP 148
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                                        6 HRSTP 10
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                                                                                     Conservative
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E.M., Willson T.A
                                                                                                                           33.3%;
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                                                                                                           100.0%;
                                                                                                                                                                          MW.
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ANK 2.
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SCCS BOX.
SCCS BOX.
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Pred. No.
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                                                                                     Mismatches
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                                                                                                         DB 1; Le
). 1.4e+02;
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                                                                                                                             Length 336;
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RESULT 58
HX11_MOUSE
ID HX11_MOUSE
AC P43345:
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Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; ...
Genew; 186770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukemia.";
Science 253:79-82(1991).
[5]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Multiple negative elements contribute proto-oncogene.";
Oncogene 17:1787-1795(1998).
-!- FUNCTION: CONTROLS THE GENESIS OF
                                                                                                                                                                                                                                                                                                                                                                         Homeobox; DNA-binding; Nuclear protein; De Proto-oncogene; Chromosomal translocation. DNA_BIND 201 260 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0025; ANTENNAPEDIA.
PRINTS; PRO0026; ENGRAILED.
PRINTS; PRO0024; HOMEOBOX.
PRODOM; PD000010; HOMEOBOX; 1.
SMART; SM00389; HOX; 1.
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Brake R.L., Kees U.R., Watt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-64 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "HUG-1: a novel upsteam gene neighboring in a T-cell leukaemia cell line."; Submitted (AUG-1998) to the EMBL/GenBank,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watt P.M., Ranford
                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFAC;
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InterPro; IPR000747; Engrailed.
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DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(10;14)(Q24;Q11) WHICH INVOLVES HOX11 AND T-CELL RECEPTOR DELTA CHAIN (TCRD) GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA SEQUENCE 5-GGCGGTAAGTGG-3'.
                                                                                                                                                                            HLGPH
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                                                                                                                                     HLGPH
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5; Conser
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330 AA;
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; AAA36719.1; -.
; AAB19293.1; -.
                         STANDARD;
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U.R., Watt P.M.;
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276
34365
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                                                                                                                                                                                                             33.3%; ~~
100.0%; Pr
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contribute
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Pred. No. 1.3
0; Mismatches
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                         PRT;
                                                                                                                                                                                                                                                                                                         -> T (IN REF. 5)
-> R (IN REF. 4)
09A518FB5271F7ED
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                                                                                                                                                                                                                                           1; Le .3e+02;
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Matches 5
                                                                                                                                            PRINTS; PRO0025; ANTENNAPEDIA.
PRINTS; PRO0026; ENGRAILED.
PRINTS; PRO0026; ENGRAILED.
PROMOSION, PRO00010; HOMEOBOX; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX, 1; 1.
PROSITE; PS50071; HOMEOBOX, 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     Mech.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-94206842; PubMed-7908826;
Raju K., Tang S., Dube I.D., Kamel-F
"Characterization and developmental homolog of HOX11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Homeobox protein Hox-11 (T-cell leukemia homeobox 1)
TLX1 OR HOX11 OR TLX-1.
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang
The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94203286; PubMed=7908720; Roberts C.W.M., Shutter J.R., Korsm "Hox11 controls the genesis of the Nature 368:747-749(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                             DNA_BIND
                                                                                        Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95319935; PubMed-7596820. Tang S., Breitman M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                            AND SPLEEN.
HLGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           optimal binding sequence of the Hox11 icted recognition core motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dev. 44:51-64(1993).
                       5; Conservative
                                                                DNA-binding; Nuclear protein; Developmental 203 262 HOMEOBOX. 332 AA; 34644 MW; 79FC71E2E44E6F82 CRC64;
  σ
                                                               34644 MW;
                                 33.3%;
                                   .0%;
                      Score 5; DB 1; Pred. No. 1.4
0; Mismatches
                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Korsmeyer S.J.; f the spleen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reid S., Bryce expression of
                                                                                       Developmental protein
                                   4e+02
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                        0
                                            Length 332;
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Tlx-1, the murine
                        Indels
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MEDLINE=91101290; PubMed=1987375;

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MIAA_RALSO
ID MIAA_R
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DT 15-JUN
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InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS0089; ZF_RING_2; 1.
          MEDLINE-21681879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L. Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Deman Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearu"
                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (IPP
tRNA delta(2)-isopentenylpyrophosphate transferase)
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                                                                                                                                                                                                                                                                                                                                                             Ralstonia solanacearum (Pseudomonas solanacearum). Bacteria; Proteobacteria; beta subdivision; Ralsto
                                                                                                                                                                                                                                                                                                                                                                                                               (IPTase) (IPPT).
MIAA OR RSC2564 OR RS00755.
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            transferase) (Isopentenyl-diphosphate:tRNA isopentenyltransferase)
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Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Entry of the complete DNA sequence of Autographa californica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Virol. 65:805-812(1991).
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SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M62488; AAA46733.1;
L22858; AAA66783.1;
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5; Conserv
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291
321 AA;
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291
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Pred. No
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G -> R (IN REF. 1).
; 4D5ACACB6291A60C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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0. 1.
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                          solanacearum.";
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RESULT 57
HX11_HUMAN
ID HX11_
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DT 01-JI
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DE HOME
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CO HUME
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Best Local
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                                                                                                                                                                                                                                                        "The tcl-3 proto-oncogene altered by chromosomal translocation T-cell leukemia codes for a homeobox protein."; EMBO J. 10:2905-2910(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92020958; PubMed=1681546;
Kennedy M.A., Gonzalez-Sarmiento R.,
Dear N., Boehm T., Rabbitts T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P31314: 075699; Q9HCAO;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Homeobox protein Hox-11 (T-cell leukemia, homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                        "Genomic organization of the putative human homeobox proto-oncogene HOX-11 (TCL-3) and its endogenous expression in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01715; IPPT; 1.
ProDom; PD004674; IPPT; 1.
TIGRFAMs; TIGR00174; miaA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL646070; CAD16271.1; -. InterPro; IPR002627; IPPT. Pfam; PF01715; IPPT; 1.
                             SEQUENCE FROM N.A.
                                                                                                                                                        MEDLINE=92319541; PubMed
Lu M., Zhang N., Ho A.D.
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        MEDLINE=92007734; PubMed=1717256; Lu M., Gong Z., Shen W., Ho A.D.;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLX1 OR HOX11 OR TCL3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oncogene)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HX11_HUMAN
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                                                                          Oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "HOX11, a homeobox-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
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SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSTPE
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5; Conserv
                                                                             7:1325-1330(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sci.
                                                                                                                                                                                     PubMed=1352396
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.3%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell oncogene on
                                                                                                                                                                                                                                                                                                                                                                                                                                             88:8900-8904(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330
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o. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome
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MEDLINE=91289163;

PubMed=1676542;

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RESULT
PFECULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  PFLE_ECOLI
P75794;
Science [2]
                                                                                                      SEQUENCE FROM N.A.
STRAIR-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch
Blattner F.R., Plunkett G. III, Bloch
Riley M., Collado-Vides J., Glasner J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "MAGE-F1, a novel ubiquitously expressed member superfamily identified by SEREX immunoscreening. Submitted (AUG-2000) to the EMBL/GenBank/DDBJ days
                                                                                      Gregor J., Davis N.W.,
                                                                                                                                                                                                                                       NCBI_TaxID=562;
                                                                                                                                                                                                                                                                  Bactería; Proteobactería;
Escherichia.
                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                                                                                                                                              Putative pyruvate YBIY OR B0824.
                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002190; MAGE.
Pfam; PF01454; MAGE; 1.
PROSITE; PS50838; MAGE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF295378; AAG30208.1; EMBL; AF320910; AAG38606.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of new genes of the MAGE famil
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ
-1- TISSUE SPECIFICITY: Ubiquitous.
-1- SIMILARITY: CONTAINS 1 MAGE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nelson B.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
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Melanoma-associated antigen F1 (MAGE-F1 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lucas S., Boon T.;
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                          B., Shao Y.;
e complete genome sequence
ence 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
5; Conserv
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35308 MW;
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Last annotation updat
mate-lyase 3 activatin
                                                                                      Kirkpatrick H.A.,
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; 8FB0092653090580 CRC64;
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                                              of.
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                                                                                                                                                                                                                                                                                 subdivision;
                                              Escherichia
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                                                                                                        D. A
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5. 1.3e+02;
                                                                                                          .A., Perna
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                                            coli K-12.";
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C.K., Mayhew G.F.,
M.A., Rose D.J.,
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RESULT 55
PE38_NPVAC
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Best Local
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EMBL; D90720; BAA35512.1; -.
EMBL; D90721; BAA35512.1; -.
ECOGene; EG13470; yblY.
InterPro; IPR001989; Radical_activat.
Pfam; PF02143; Radical_activat; 1.
proDom; PD004758; Radical_activat; 1.
PROSITE; PS01087; RADICAL_ACTIVATING; 1
                                                                                                                                                                                     01 NOV-1991 (Rel. 20, C
01-NOV-1995 (Rel. 32, I
16-OCT-2001 (Rel. 40, I
Major immediate early E
                                                                                                                                                                                                                                                                                     PE38_NPVAC
P23801;
SEQUENCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
METAL
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *A 718 kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
DNA RES. 3:137-155(1996).

PARENCIS SY GENERATION OF PYRUVATE FORWATE-LYASE 2 UNDER ANAEROBIC CONDITIONS BY GENERATION OF AN ORGANIC FREE RADICAL, USING S-ADENOSYLMETHIONIXE AND REDUCED FLAVODXIN AS COSUBSTRATES TO PRODUCE 5'-DEOXY-ADENOSINE (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + dihydroflavodoxin [formate acetyltransferase]-glycine - 5'-deoxyadenosine + methionine + flavodoxin + [formate acetyltransferase]-glycine-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97061202; PubMed-8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita M., Kanai K., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FF
STRAIN=K12;
                                                               Viruses; dsDNA viruses,
Nucleopolyhedrovirus.
NCBI_TaxID=46015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFACTOR: BINDS 1 4FE-4S CLUSTER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE ORGANIC RADICAL ACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by non-profit institutions as long
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5; Conserv
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ilarity 100.0%;
Conservative
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protein (PE-38).
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Pred. No. 1.3
0; Mismatches
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IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
21A5C573B7578A23 CRC64;
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                                                                                                                    polyhedrosis virus (/
stage; Baculoviridae
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Iron-sulfur;
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1.3e+02;
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MTRE_METJA
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Best Local
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   MTRE_METJA
Q58257;
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Q1-NOV-1997 (
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DNA_BIND
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ProDom; PD000010; Homeobox; 1.
ProDom; PD000583; POU_domain;
SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
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J. Biol. Chem. 268:23390-23398(1993).
-I- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS PREFERENTIALLY TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
REPEAT
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PROSITE; PS00465; POU_2; 1.
PROSITE; PS00027; HOMEOBOX_1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, L23204; -; NOT_ANNOTATED_C
HSSP; P14859; 10CT.
InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU_domain.
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STRAIN-Fischer; TISSUE-Anterior pituitary;
MEDLINE-94043133; PubMed-901208;
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FUNCTION: TRANSCRIPTION FACTOR THAT BINDS PREFERENTIALLY TO A VARIANT OF THE OCTAMER MOTIF ('ATGATAAT').

SUBCELLULAR LOCATION: Nuclear.

TISSUE SPECIFICITY: IN THE EMBRYO, WIDELY EXPRESSED, WITH HIGHES LEVELS IN THE DEVELOFING BRAIN AND SPINAL CORD. IN THE ADULT, MOSTLY FOUND IN THE BRAIN, WHERE IT IS DIFFUSELY EXPRESSED WITH THE EXCEPTION OF AN EMRICHMENT IN LAYER IV OT THE NEOCORREX. ALS FOUND IN KIDNEY, LUNG, HEART, ADRENAL, SKIN, AND PLACENTA. LOW LEVELS IN SPLEEN, MUSCLE, LIVER, ANTERIOR PITUITARY, TESTIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
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                                                                                                                                                                                                                                                                                    78
(Rel. 35, Created)
(Rel. 35, Last sequence update)
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140
234
301 AA;
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                                                                                                          STANDARD;
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56 2
17 1
17 2
26 2
213 P
293 H
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100.0%;
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Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMEOBOX
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2 X 7 AA REPEATS OF N-A-Q-G-Q-V-I
                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44A50F627FEB9F28 CRC64;
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Mismatches
                                                                                                          303
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                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Le .2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 301;
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MGF1_HUMAN
ID MGF1_H
AC Q9HAY2
DT 15-JUN
DT 15-JUN
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                                                                                   RESULT 53
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Matches 5
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dugherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                          TRANSMEM
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jannaschll.
Science 273:1058-1073(1996).
Science 273:1058-1073(1996).
FIRE COMPLEX CATALYZES AN INTERMEDIATE PROPERTY.
METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND METHYL-TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-TETRAHYDROMETHANOPTERIN. THIS IS A ENERGY-CONSERVING, SO
MGF1_HUMAN STANDARD; PRT; 308 AA Q9HAY2; Q9H215; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                        Complete
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Methanocaldococcaceae; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetrahydromethanopterin S-methyltransferase subunit E (EC 2.1.1 (N5-methyltetrahydromethanopterin--coenzyme M methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Last annotation update) Tetrahydromethanopterin S-methyltransferase s
                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanococcus
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                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                   131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY: Methanogenesis.
SUBUNIT: COMPOSED OF 8 DIFFERENT SUBUNITS (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSLOCATING STEP (BY SIMILARITY).

CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopten
mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin
                                                                                                                                                               SHLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (methylthio)ethanesulfonate.
                                                                                                                                   SHLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      U67529; AAB98852.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         MJ0847;
                                                                                                                                                                                             Similarity 100
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR01113; mtrE; 1
                                                                                                                                                                                                                                                                                                                                                                                                         Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jannaschii.
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106
153
177
246
286
31635
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100.0%; F.
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Methanocaldococcus.
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                                                                                                                                                                                              Score 5; DB 1; Pred. No. 1.2
                                                                                                                                                                                                                                                                                          POTENTIAL.
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46BA1BBD80FECCE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Methanogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7,8-tetrahydromethanopterin
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.2e+02;
                                                                                                                                                                                                                            Length 303;
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RESULT PO61_HP ID PO61_PP OF PP OF P
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Best Local S
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y14428; CAA74774.1; -.
EMBL; AE010359; AAM01871.1; -.
EMBL; U57340; AAB02004.1; -.
TIGRFAMS; TIGR01113; mtrE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reductase operons.";
Int. J. Syst. Bacter
-i- FUNCTION: THIS E
SEQUENCE
                                                             Eukaryota;
Mammalia; I
                                                                                                      Homo sapiens (Human)
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"Phylogeny of Methanopyrus kandleri based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Noelling J.,
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                                                                                                                                                                                                                                                                                                                                                                                  130 SHLGP 134
                                                                                                                                                                                                                                                                                                                                                                                                                         1 SHLGP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . J. Syst. Bacteriol. 46:1170-1173(1996).

FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-TETRAHYDROMETHANOPTERIN. THIS IS A ENERGY-CONSERVING, SODIUM-IC TRANSLOCATING STEP (BY SIMILARITY).

CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY:
SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome.
                                                           ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59
84
132
160
230
251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanogenesis,
COMPOSED OF 8 DIFFERENT SUBUNITS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elfner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ξ,
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79
104
152
180
250
271
                                                             Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A., Palmer J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.3%;
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                                                             Craniata; V
Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steigerwald V.J., Pihl T.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Le
5. 1.2e+02;
                                                             Vertebrata;
i; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                         (MPOU
5) (BF
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                                                                                                                                              (BRN-5
                                                                                                                                                                  homeobox protein)
                                                                                 Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kandleri AV19
                                                                                                                                            protein).
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RESULT 51
PO61_RAT
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                               DOMAIN
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDITINE-94192665; PubMed-7908264;

Mey E., Lyons G.E., Schaefer B.W.;

"A human POU domain gene, mPOU, is expressed in developing brain specific adult tissues.";

EUR. J. Biochem. 220:753-762(1994).

11. FUNCTION: TRANSCRIPTION. FACTOR THAT BINDS PREFERENTIALLY TO A VARIANT OF THE OCTAMER MOTIF ('ATGATAAT') (BY SIMILARITY).

12. SUBCELLULAR LOCATION: NUCLEAR.

13. SUBCELLULAR LOCATION: NUCLEAR.

14. TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED EXCLUSIVELY IN THE SUBCELLOPING BRAIN, WHEREAS IN THE ADULT ITS EXPRESSION IS RESTRICTED TO BRAIN, HEART, SKELETAL MUSCLE AND LUNG. IN THE BRAIN, THE HIGHEST EXPRESSION LEVELS ARE FOUND IN SPECIFIC CE
                                                                                                                                                                                                                                                                                                                                                        Homeobox;
                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
POU domain, class 6, transcription factor 1 (Brain-specific homeobox/POU domain protein 5) (BRN-5 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00046; homeobox; 1. Pfam; PF00157; pou; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z21966;
HSSP; P14859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use
                                               POU6F1 OR BRN5
                                                                                                                             P56223;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00389; HOX; 1
SMART; SM00352; POU; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:9224; POU6F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFAC; T04470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
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                                                                                                                                        PO61_RAT
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SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
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                                                                                                                                                                                                                                 STPES
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5; Conserv
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PS00465; POU_2; 1.
PS00027; HOMEOBOX_1; E
PS50071; HOMEOBOX_2; 1
; DNA-binding; Transcri
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301
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32645
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9C552BA84ABAB17A CRC64;
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         Sciurognathi;
          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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RESULT 48
HIA_RHIFR
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30-MAY-2000
30-MAY-2000
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InterPro; IPR002171; Ribosomal L2.
Pfam; PF00181; Ribosomal L2; 1.
TIGREAMS; TIGR01171; rplB_bact; 1.
PROSITE; PS00467; RIBOSOMAL_L2; 1.
                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg

Kolonay J.F., Nelson W.C., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harri Gordon S.V., Eiglmeter K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyo Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted APR-2001) to the EMBL/GenBank/DDBJ databases.
- i- FUNCTION: THIS PROTEIN IS A PRIMARY 23S RRNA-BINDING PROTEIN HAS PEPTIDYLTRANSFERASE ACTIVITY (BY SIMILARITY).
- i- SIMILARITY: BELONGS TO THE L2P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50S ribosomal protein L2.

RPLB OR RV0704 OR MT0731 OR MTCY210.23.

Mycobacterium tuberculosis.

Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
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30-MAY-2000 (Rel. 39, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98295987; PubMed=9634230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis clinical and aboratory strains.";
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                                                                                                                                         RSTPE
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                                                                                                                                                                                            Similarity
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                  STANDARD;
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                  295
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5. 1.2e+02;
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Q49606;
01-NOV-1997 (Rel. 35, Cre
15-JUL-1999 (Rel. 38, Las
15-JUN-2002 (Rel. 41, Las
Tetrahydromethanopterin S
                                                                                                                                                                                                                                                                                                                                                   METKA
                        STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                         Harms U., Thauer R.K.;
"Identification of the active site histidine in MtrA of the energy-conserving methyltransferase Methanobacterium thermoautotrophicum.";
Eur. J. Biochem. 250:783-788(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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Sadowsky M.J., Olson E.R., Foster V.E.,
"Two host-inducible genes of Rhizobium
the inducing compound.";
J. Bacteriol. 170:171-178(1988).
                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98121200; PubMed=9461302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
Rhizobiaceae; Sinorhizobi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1989 (Rel.
01-OCT-1989 (Rel.
30-MAY-2000 (Rel.
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01-OCT-1989
                                                 SEQUENCE FROM N.A
                                                                                                                                                                            Methanopyrus.
NCBI_TaxID=2320;
                                                                                                                                                                                                      Methanopyrus kandleri.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                               subunit
                                                                                                                                                                                                                                                     retranydromethanopterin S-methyltransferase subunit E (EC 2.1.1) (NS-methyltetrahydromethanopterin--coenzyme M methyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                    ESRAA 170
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Sinorhizobium.
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1. 38, Last sequence update,
1. 41, Last annotation update)
nopterin s-methyltransferase sub
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12, Last sequence update)
39, Last annotation update)
cotein A.
cotein fredii).
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0; Mismatches
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[7]
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No. 1.2e+02;
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Slesarev A.I., Mezhevaya K.V., Makarova K.S., Shcherbinina O.V., Shakhova V.V., Belova G.I.,

Polushin, Aravind

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RESULT 45

YOJG_BACSU
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ID YOJG_BACSU
ID P54544
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                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                  EMBL; D84432; BAA12613.1; -. EMBL; Z99116; CAB14320.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390:249-256(1997).
-I- SUBCELLULAR LOCATION: Attached to the membrane by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mizuno M., Masuda S.,
Kobayashi Y.;
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MEDLINE=97124195; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1423;
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation updat)
1 lipoprotein yqjG precursor.
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S., Takemaru K.-I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome containing
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RESULT 47
RL2_MYCTU
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RL2_MYCBO
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15-JUL-1998
15-JUL-1998
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                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98065585; PubMed-9402018; Sander P., Prammananan T., Meter A., Frischkorn K., Bottg "Sander P., Prammananan T., Meter A., Frischkorn K., Bottg "The role of ribosomal RNAs in macrolide resistance."; Mol. Microbiol. 26:469-480(1997).

-i- FUNCTION: THIS PROTEIN IS A PRIMARY 23S RRNA-BINDING HAS PEPTIDYLTRANSFERASE ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Bacteria; Actinobacterineae; Mycobacteriaceae; Mycobacterium.
RL2_MYCTU
                                                                                                                                                                       TIGRFAMS; TIGRO1171; rplB_bact; 1. prosite; ps00467; RIBOSOMAL_L2; 1. Ribosomal protein; rRNA-binding.
                                                                                                                                                                                                            HSSP; P04257; 1RL2.
InterPro; IPR002171; Ribosomal_L2.
Pfam; PF00181; Ribosomal_L2; 1.
                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE L2P FAMILY OF RIBOSOMAL PROTEINS.
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_
                                                                                                                                                                                                                                                 EMBL; Y13228; CAA73675.1; -.
                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      entities requires a license agreement
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5; Conserv
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IPR000437; Prok_lipoprot.
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275 AA;
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30748 MW;
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HYPOTHETICAL LIPOPROTEIN YQJG.
N-ACYL DIGLYCERIDE (POTENTIAL)
, 9BAD79A2BABEA53B CRC64;
  PRT;
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                                                                                                                                                              5F23CBF4C3D4AAAE CRC64;
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RESULT 43
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Best Local
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HSSP; P02259; 1HST.
FlyBase; FBgn0027800; Dvir\Hisl.1.
InterPro; IPR001386; Histone_H1/H5.
InterPro; IPR003216; Linkerhist_N.
Pfam; PF00538; linker_histone; 1.
ProDom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                           SEQUENCE OF 23-253 FROM N.A., AND PARTIAL SEQUENCE. STRAIN-27 / Salesbury laboratory;
MEDLINE-88261435, PubMed-3290678;
Brothers V.M., Kuhn I., Paul L.S., Gabe J.D., Andre Stas S.R., McCaman M.T., Dragon E.A., Files J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Files J.G., Paul L.S., Gabe J.D.; "Identification and characterization antigen of Eimeria tenella.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel.
01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  "Characterization of a surface antigen of Eimeria tenella sporozoites and synthesis from a cloned CDNA in Escherichia coll.";
MO1. Biochem. Parasitol. 28:235-248(1988).
-i- SUBUNIT: THE TA4 ANTIGEN IS COMPOSED OF A 17 kDa AND A 8 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (In) Agabian N., Goodman H., Noguiera N. (eds.);
Molecular strategies of parasitic invasion, UCLA symposia
and cellular biology, pp.713-723, Alan R. Liss, New York (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Alveolata;
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-I- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-I- SUBCELLULAR LOCATION: Nuclear.
-I- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5802;
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                                                                                                                                  CHAIN, LINKED BY A DISULFIDE BOND.

SUBCELLULAR LOCATION: SURFACE OF SPOROZOITES
                                                                                                   DEVELOPMENTAL STAGE:
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antigen precursor (Major
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Bioinformatics and the EMBL outstation -

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RESULT 44
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat:
Hypothetical 31.6 kDa protein F59C6.8 in ch.
F59C6.8.
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15-JUL-1998
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                                                                                                                                       Hypothetical protein. SEQUENCE 274 AA; 31624 MW;
                                                                                                                                                                                                      WormPep; F59C6.8; CE11470.
InterPro; IPR002875; DUF23.
Pfam; PF01697; DUF23; 1.
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modified and this statement is not removed.
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-i- SIMILARITY: BELONGS TO A FAMILY OF C.ELEGANS PROTEINS THAT GROUPS C27A7... C33H5.2, C35A5.5, F13G3.3, F59C6.8, F49C12.5, R07B7.12
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RESULT 41
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RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., RA Oliver S., Osborne J., Quail M.A., Rajandraem M.A., Rogers J., RA Rutter S., Seeger K., Skelton S., Squares R., RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Tromplete genome sequence."; L. Nature 393:537-544(1998).
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Matches 5
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Q9UFM2;
             Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole genome comparison laboratory strains."; Submitted (APR-2001) to 1
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                Putative protein C210RF30.
                                                                        16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative protein C2lorf30 (Fragment).
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InterPro; IPR000524;
Pfam; PF00392; gntR;
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SEQUENCE FROM N.A.
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SIMILARITY: BELONGS TO THE GNTR FAMILY OF TRANSCRIPTIONAL
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AE006952; AAK44737.1; -.
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             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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A Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
A Hattori M., Fujiyama A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
A Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
A Menzel U., Delabar J., Kumpf K., Lebmann R., Patterson D.,
A Menzel U., Delabar J., Kumpf K., Lebmann R., Patterson D.,
A Menzel U., Delabar J., Kumpf K., Lebmann R., Patterson D.,
A Minoshima A., Kudoh J., Schilihabel M., Schudy A., Zimmermann W.,
A Rosenthal A., Kudoh J., Shibuya K., Rawasaki K., Asakawa S.,
A Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
A Minoshima S., Shimizu N., Nordslek G., Hornischer K., Brandt P.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
A Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
A Mehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
A Lehrach H., Reinhardt R., Yaspo M.-L.;
"The DNA sequence of human chromosome 21.";
U. Nature 405.311-319(2000).
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Q24704;
01-NOV-1997 (
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16-OCT-2001 (
Histone H1.1.
                                                                                                                                                                                           Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapo
Insecta; Peterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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   Schienman J.E., Lozu
"Drosophila virilis
                             DISCUSSION OF SEQUENCE.
MEDLINE=99132191; PubMed=9933406;
                                                                         Nagel S., Grossbach U.;
"Histone H1 genes and histone
J. Mol. Evol. 51:286-298(2000)
                                                                                                          STRAIN-Bochum;
MEDLINE-20483906; PubMed-11029073;
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Lozovskaya E.R.,
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0; Mismatches
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                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EE84E0AA0E4BEF4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mewes H.-W.,
   Strausbaugh
kinds and ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e 5;
No.
                                                                                          clusters
                                                                                                                                                                                                                                                                                                                                                250
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                 L.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 247;
                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                         drosophila.";
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RESULT 39
RUM1_SCHPC
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Best Local
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                                          SEQUENCE |
STRAIN=97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2) / M145;

MEDLINB-2196440; PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.

Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                   P40380: 074373;
01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein rum1 (p25-rum1).
                                                                                                                                                                                                                                                                                SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collai between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coelicolor A3(2).";
Nature 417:141-147(2002);
-i- CATALYTIC ACTIVITY: 2-phosphosulfolactate
                                                                                                                                       Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
STRAIN=A3(2) / M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probable 2-phosphosulfolactate phosphatase (EC 3.1.3.-). COMB OR SC07611 OR SC2H2.09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
               Moreno S., Nurse P.;
                               MEDLINE=94166876; PubMed=8121488;
                                                                                          NCBI_TaxID=4896;
                                                                                                          Schizosaccharomyces.
                                                                                                                       Schizosaccharomycetales;
                                                                                                                                                                                                                                                                 RUM1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL450289; CAC16713.1; ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Streptomycineae; NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                            175 ESRAA 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphate.
COFACTOR: Magnesium (By similarity)
SIMILARITY: BELONGS TO THE COMB FAM
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
5; Conserv
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                                                              FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Magnesium;
227 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
progression through the G1 phase of the cell cycle
                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete
                                                                                                                       Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE COMB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 5; Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteome.
475C29AF0A51389D CRC64;
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                                                                                                                                                                                                                                                                230 AA
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Howarth S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL outstation
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RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
The genome sequence of Schizosaccharomyces pombe.";
RA Nature 415:871-880(2002).
C. INTERACTS WITH CDC2 TO INHIBITS ITS ACTION UNTIL THE CELL MASS FOR
C. START IS REACHED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
A. Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
A. Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
A. Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
A. Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
A. Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
A. Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
A. Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
A. Holroyd S., Hornsby T., Howarth S., Hornsby E., Mounders L., Jones M., Leather S., McDean J.,
A. Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
A. Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
A. Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
A. Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
A. Mutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
A. Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
A. Skelton J., Simmonds M., Squares R., Robben J., Grymonprez B.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Wooltins T., Vonctrole F., Briggs M., Schanfer M., Waller M.,
Wooltins T., Volckaert G., Aert R., Robben J., Grymonprez B.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical transcriptional regulator Rv0494
RV0494 OR MTG514 OR MTCY20G9.20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                         Q11159;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                         Bacteria; Actinobacteria;
                                                                                                                                                                                                                     Y494_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X77730; CAA54786.1; -. EMBL; AL023796; CAA19370.1;
                  Actinomycetales;
                                                            Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21848401; PubMed=11859360;
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Nature 367:236-242(1994).
                                                                                                                                                                                                                                                                                                                                    15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S41043; S41043.
                                                                                                                                                                                                                                                                                                                                    STPES
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                      19
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                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                       STANDARD;
                  Corynebacterineae;
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100.0%; Pr
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25288 MW;
                                       Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 5;
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; C5199FE345F7484A CRC64;
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                                                                                                                                                                                                                       PRT;
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                  Mycobacteriaceae; Mycobacterium
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                                                                                                                                                                                                                       242
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97;
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DOMAIN 72 84
CA_BIND 112 123
CA_BIND 148 159
DOMAIN 184 195
SEQUENCE 208 AA; 23687
InterPro; IPRO02048; EF-hand.
InterPro; IPRO02048; EF-hand.
Pfam; PF00036; efhand; 1.
ProDom; PD000012; EF-hand; 1.
PPONSTTE: PS00018; EF_HAND; F/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
01-FEB-1995 (Rel. 31, Last annotation update)
EF-hand protein 5 variant 2 (EFH5) (Calmodulin-ubiquitin protein CUB2.8).
Trypanosoma cruzi.
Eukaryota; Euglanozoa; Kinetoplastida; Trypanosomatidae;
RCBI_TaxID-5693;
                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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"The ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PROSITE;
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                                                                                                       EMBL; L01584; AAA30172.1;
HSSP; P02593; 1CDM.
                                                                                                                                                                                                          entitles requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFH2_TRYCR
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                                                                                                                                                                                                                                                                                                                                                                                                   e calmodulin-ubiquitin associated genes of Trypanosoma c
ir identification and transcription.";
Biochem. Parasitol. 57:127-136(1993).
DOMAIN: THIS PROTEEN HAS FOUR EF-HAND DOMAINS, TWO OF W
BE FUNCTIONAL CALCIUM-BINDING SITES.
SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A48567; A48567.
; P02593; ICDM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J., Swindle J.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o; IPR002048; EF-hand.
PD000012; EF-hand; 1.
PS00018; EF-HAND; FALSE_NEG.
                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                      EFH5 SUBFAMILY.
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5; Conser
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                     license agreement (See http://www.isb-sib
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EF-HAND 2 (POTENTIAL).
EF-HAND 3 (POTENTIAL).
ANCESTRAL CALCIUM SITE 4 ()
W; 30B366D009C127C4 CRC64;
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88;
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                                                                                                                                                                                                                                                                                                          gh a collaboration - EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated
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RESULT 37
GTT1_ANOGA
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Best Local
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DOMAIN 72
CA_BIND 112
CA_BIND 148
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01-NOV-1997
15-JUL-1998
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CA_BIND
DOMAIN
SEQUENCE
                                                                                                                                                                                                      use by non-profit institutions as lone modified and this statement is not remove entities requires a license agreement (Se or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          from Anopheles gambiae.";

J. Biol. Chem. 272:5464-5468(1997).

-I- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
                                                                                                                    InterPro; IPR004046; GST_Cterm.
InterPro; IPR004045; GST_Nterm.
Pfam; PF00043; GST_C; 1.
Pfam; PF02798; GST_N; 1.
                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                    This
                                                                                             Transferase; Multigene family. SEQUENCE 209 AA; 23529 MW;
                                                                                                                                                                      EMBL; Z71480; CAA96104.1; HSSP; P30712; 1LJR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Culicoidea; Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Mandibulata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q94999;
                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathic-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. THETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                      Ranson H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97190266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insecta; Pterygota;
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ESRAA
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8 (Rel. 36, Last
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208
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llarity 100.0%;
Conservative
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84
123
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195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoptera;
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Last annotation update)
rase 1-1 (EC 2.5.1.18) (
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Pred. No. 88;
0; Mismatches
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EF-HAND 2 (POTENTIAL).
EF-HAND 3 (POTENTIAL).
ANCESTRAL CALCIUM SITE 4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a; Mandibulata; Pancrustacea; Hexapoda;
Endopterygota; Diptera; Nematocera;
                                                                                                874577DC752CC403 CRC64;
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                                               Mismatches
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                                                                     Length 209,
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RESULT 38
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Best Local
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LMBV_CHICK STANDAKU; ....,
Q01636;
Q01636;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 41, Last annotation update)
Laminin beta-1 chain variant (Laminin beta-1-2 chain) (Fragment).
Gallus gailus (Chicken).
Gallus gailus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
                                                                                                                              CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of the Bradyrhizobium japonioum degp gene as pa
an operon containing small heat shock protein genes.";
submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSPD.
Bradyrhizobium japonicum.
Bacteria; Proteobacteria; alpha subdivision;
Bacteria; Proteobacteria; Bradyrhizobium.
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PROSITE; PS00586; RIBOSOMAL_L16.1; 1.
PROSITE; PS00701; RIBOSOMAL_L16.2; 1.
Ribosomal protein; rRNA-binding; Complete
SEQUENCE 136 AA; 15517 MW; E971587DDCE
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                  Pfam; PF00011; HSP20; 1. PROSITE; PS01031; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
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30-MAY-2000 (Rel. 39, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRAJA
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                         Heat shock;
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                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
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151 AA; 17272 MW;
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o. 66;
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Best Local S
Matches 5
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          EFH1_TRYCR P41048;
                                                                  SEQUENCE FROM N.A.
MEDLINE=93149197; PubMed=8381204;
Ajioka J., Swindle J.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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-!- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.
                      "The calmodulin-ubiquitin associated their identification and transcription
                                                                                                                                                              Eukaryota; Euglenozoa;
NCBI_TaxID=5693;
                                                                                                                                                                                         Trypanosoma
Eukaryota; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01248; LAMININ_TYPE_EGF; PARTIAL.
Extracellular matrix; Cell adhesion; Glycoprotein; Basement membrane;
Laminin EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L00963; AAA49140.1; -.
InterPro; IPR001886; LamNT.
InterPro; IPR002049; Laminin_EGF
Pfam; PF00055; laminin_Nterm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
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-!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end.
-!- SUBCELLULAR LOCATION:
-!- TISSUE SPECIFICITY: FC
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"A novel laminin Bl chain variant in avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93015947; PubMed=1400373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are to each other by disulfide bonds into a cross-shaped molecule Comprising one long and three short arms with globules at each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PESRA
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31, Last
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variant
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100.0%;
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Last annotation update)
Last 1 (EFH5) (Calmodulin-ubiquitin associated
                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                       Kinetoplastida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOUND
transcription.";
57:127-136(1993)
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Mismatches
                             genes
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                                               Trypanosoma
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Plasmid IncP-alpha RP4.
Bacteria, Proteobacteria;
                                                                                                                                                                                                                                                        TRK4_ECOLI STANDARD; PRT; 133 AA. P17910; 01-NOV-1990 (Rel. 16, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INIT_MET SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                      STRAIN-HB101;
MEDLINE-92190548; PubMed-1665997;
      Ziegelin G.,
                                                                                                                                                                                                                                                                                                                                                                                   ECOLI
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Eukaryota; Fung1; Ascomycota; Pezizomycotina; Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;
                                                                                                                                        Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X76344; CAA53963.1; -
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                                                                    SEQUENCE FROM N.A.,
                                                                                                                  NCBI_TaxID=562;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NADH-ubiquinone oxidoreductase 14.8 kDa subunit
(EC 1.6.99.3) (Complex I-14.8KD) (CI-14.8KD).
NUO-14.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Azevedo J.E., Eckerskorn C., Werner S.;
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SUBCELLULAR LOCATION: Mitochondrial inner membrane;
THE IMPORT OF THIS SUBUNIT IS DEPENDENT ON PROTEINAC
COMPONENTS OF THE MITOCHONDRIAL OUTER MEMBRANE.
SIMILARITY: TO BOVINE COMPLEX I SUBUNIT B14.
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milarity 100.0%;
Conservative 0
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    Σ.
                                                                    SEQUENCE
                                                                                                                                                           gamma
      Strack
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                                                                                                                                                      subdivision;
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    Balzer
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D.,
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Kroeger
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                      RL16_BUCAI
P57584;
          EMBL; AP001119; BAB13210.1; -.
InterPro; IPR000114; Ribosomal
                                                                                                                                     -!- SIMILARITY: BELONGS TO THE
                                                                                                                                                         Nature 407:81-86(2000).
-!- FUNCTION: THIS PROTEIN BINDS
LOCATED AT THE A SITE OF THE
                                                                                                                                                                                                                                                                                                                                            50S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X54459; CAA383
EMBL; M25423; AAA264
PIR; S23003; S23003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                        symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                 Buchnera aphidicola (subsp.
                                                                                                                                                                                                                                                                                                                             RPLP OR BU517
                                                                                                                                                                                                                                                                                 NCBI_TaxID-118099;
                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Conjugative transfer of promiscuous IncP plasmids: plasmid-encoded products with the transfer origin."; Proc. Natl. Acad. Sci. U.S.A. 86:1771-1775(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-58
MEDLINE=89184510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence and organization origin of promiscuous plasmid RP4."; DNA Seq. 1:303-327(1991).
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-OCT-2001 (Rel. 40, 1
-OCT-2001 (Rel. 40, 1
S ribosomal protein 1
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M25423; AAA26422.1;
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                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                           gamma subdivision; Buchnera
                                                                                                                                                                                                                                                                                                                Acyrthosiphon pisum) (Acyrthosiphon pisum
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                                                                                                                                     L16P FAMILY OF RIBOSOMAL PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
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                                                                                                                                                                                                                                                                                                                                                   update:
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                                                                                       restrictions on
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r commercial
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TREAD COCCEPT TRANSPARANCE TO 
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Best Local
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01-AUG-1992 (Rel. 2
15-JUN-2002 (Rel. 4
Hypothetical 11.8 kl
Lily virus X.
Virus ~
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RBFA_CLOPE
Q8XJR9;
                                                                                                                                                            -i- F
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-i- SIMILARITY: TO ORF3 PROTEIN FROM OTHER POTEXVIRUSES AND TO 12
                                                                                                                                                                                                                                                       Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamas
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayash
"Complete genome sequence of Clostridium perfringens,
                                                                                                                                                                                                                                                                                                                                                              STRAIN=13 / Type A;
PubMed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium perfringens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RBFA OR CPE1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribosome-binding factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein;
TRANSMEM 9 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001896; Plant_vir_prot. Pfam; PF01307; Plant_vir_prot; 1. Protbom; PD001561; Plant_vir_prot; 1. Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                flesh-eater.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X15342; CAA33395.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GPHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GPHRS 8
C. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
FUNCTION: Associates with free 30S ribosomal subunits (but not with 30S subunits that are part of 70S ribosomes or polysomes).
Essential for efficient processing of 16S rRNA. May interact with the 5'terminal helix region of 16S RRna (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
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der Vluqt C.I.M., Linthorst H.J.M.
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23,
41,
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92 PC
11767 MW;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridia; Clostridiales; Clostridiaceae;
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B3D699554D57FE5C CRC64;
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                                                                                                                                                                                                                                                       ., Yamashita A.,
, Hayashi H.;
ringens, an anae;
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Best Local :
                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P04138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 13.7 kDa protein in transposable element
Halobacterium halobium.
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _HALHA
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                                                                                                                                                                                                                 EMBL; X01584; CAB37935.1;
PIR; A05114; A05114.
Transposable element; Hypo
SEQUENCE 122 AA; 13792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000238; Rib_bind_factA.
pfam; pF02033; RBFA; 1.
proDom; PD007327; Rib_bind_factA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu W.-L., Doolittle W.F.; "Structure of the archaebacterial transposable element ISH50."; Nucleic Acids Res. 11:4195-4199(1983).
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PROSTIE; PS01319; RBFA; 1.
TRNA processing; Complete proteome.
SEQUENCE 116 AA; 13448 MW; 32D/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP003191; BAB81391.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
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4 TPESR
                                                9 TPESR
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                                                                                                     . Similarity 5; Conserv
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5; Conserv
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                                                                                                        Conservative
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                                                                                             33.3%; 5c.
100.0%; Pr
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100.0%; Pr
                                                                                                                                                                                                                 t; Hypothetical protein.
13792 MW; C70774DA8969FB6E
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                                                                                                                                  Score 5;
Pred. No.
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Pred. No.
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                                                                                                                                  DB 1;
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                                                                                                           0;
                                                                                                                                                           Length 122;
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                                                                                                                                                                                                                    CRC64;
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                                                                                                        0;
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RESULT 30
NB4M_NEUCR
ID NB4M_N
AC P42114

NB4M_NEUCR P42114;

STANDARD;

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RESULT 25
CYC_EUGEN
ID CYC_E
AC P0007
DT 21-JU
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Best Local S
Matches 5
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InterPro; IPRO03088; Cyt_CI.
InterPro; IPRO03088; Cyt_CIAB.
InterPro; IPRO03237; Cyt_CIAB.
Pfam; PF00034; CytCothrome_C; 1.
PRINTS; PR00604; CYTCHRMECIAB.
PRODOm; PD000375; Cyt_CIAB; 1.
PROSITE; PS00190; CYTCCHROME_C; FALSE_NEG.
Mitchondino; Electron transport; Respirato
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
BINDING
METAL
                                                                                                       P05848; P77107; 01-NOV-1988 (Rel. 09, Created) 01-NOV-1997 (Rel. 35, Last sequence up 16-OCT-2001 (Rel. 40, Last annotation Hypothetical protein ybeB. YBEB OR B0637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pettigrew G.W., Leaver J.L., Meyer T.E., Ryle A.P., "Purification, properties and amino acid sequence o cytochrome c from two protozoa, Euglena gracilis an
                    Escherichia.
NCBI_TaxID=562;
                                                         Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                   ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oncopelti.";
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Eukaryota; Euglenozoa;
NCBI_TaxID-3039;
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21-JUL-1986 (Rel. 01, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-76039443; PubMed-170910;
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HSSP; P00004; 1WEJ.
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                                                                                                                                                                                                                                                                                                                                                                                                 11 ESRAA 15
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SUBCELLULAR LOCATION: Mitochondrial matrix.
PTM: Binds one heme group per molecule.
MISCELLAUROUS: COMPARED TO OTHER CYTOCHROME C'S LACKS
TWO CYSTEINES THAT COVALENTLY BIND THE HEME GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hem. J. 147:291-302(1975).

FUNCTION: Electron carrier protein. The oxidized form of the cytochrome c heme group can accept an electron from the heme group of the cytochrome cl subunit of cytochrome reductase. Cytochrome then transfers this electron to the cytochrome oxidase complex, the final protein carrier in the mitochondrial electron-transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUGGR
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    Last sequence update)
    Last annotation updat

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                                                             gamma
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Pred. No. 46;
0; Mismatches
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IRON (HEME AXIAL
IRON (HEME AXIAL
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                                                                subdivision;
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                                                                                                                                                                       update)
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                                                                Enterobacteriaceae;
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Crithidia
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Best Local
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EMBL; AE000168; AAC73738.1; ALT_INIT.
EMBL; U82598; AAB40837.1; -.
EMBL; D90704; BAA35284.1; ALT_INIT.
PIR; A24995; QQECP7.
ECOGene; EG11255; ybeB.
                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a copyred the Swiss institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage med DNA Res. 3:137-155(1996).
-i- SIMILARITY: STRONG, TO H.INFLUENZAE HI0034.
-i- SIMILARITY: TO B.SUBTILIS YQEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H. Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-K12 / MG1655; MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence of the pbpA gene and characteristics deduced amino acid sequence of penicillin-binding protein Escherichia coli K12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-87030266; PubMed-3533535; Asoh S., Matsuzawa H., Ishino F., Ohta T.;
                                                                                                                         Hypothetical SEQUENCE 10
                                                                                                                                                                       InterPro; IPR003456; DUF143.
InterPro; IPR004394; Iojap.
Pfam; PF02410; DUF143; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Blasner J.D., Rode C.K., Mayhew G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-K12;
                                                                                                                       Pfam, PF02410, DUF143; 1.
TIGRFAMS; TIGR00090; Tojap; 1.
Hypothetical protein; Complete
SEQUENCE 105 AA; 11582 MW;
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 58
ESRAA
                               ESRAA
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                                                            5; Conservative
62
                                                       100.0%; ...
                                                                                          33.3%;
                                                                         Score 5;
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7C1315607BD0B610 CRC64;
                                                              Mismatches
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                                                                                          DВ
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                                                                                          Length 105
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2 of
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RESULT 27

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Best Local
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Q03561;
Q1-FEB-1994
Q1-FEB-1994
15-JUN-2002
                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                   Sulston J., Thier., Sulston A., Watson A.,
                                                                                                                                                                                                                                                                                Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A. Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Johnston L., Jones M., Kershaw J., Kirsten A., Callaghan M., Latreille P., Lightning J., Lloyd C., Morttimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I. Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Vaughan 
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CARBOHYD
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MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein B0464.3 in chromosome III.
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                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                             "2.2 Mb of contiguous nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
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CAA79537.1;
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                                                                                                  SEQUENCE
                                                                                                                                                                                          CHAIN
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PROSITE; PS50276; PANCREATIC_HORMONE_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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-i- SUBCELLULAR LOCATION: Secreted.
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WormPep; B0464.3; CE00017.
Hypothetical protein.
SEQUENCE 82 AA; 9427 MW
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-!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
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Daniels R.J.,
Tufarelli C.,
Higgs D.R.;
       between the Swiss Institute of Bioinformat:
the European Bioinformatics Institute. Their
use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
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MEDLINE-99127945; pubMed-9930755;

Williams M.E., Washburn M.S., Hans M., Urrutia A., Brust P.F.,

Prodanovich P., Harpold M.M., Stauderman K.A.;

*Structure and functional characterization of a novel human low-
voltage activated calcium channel.*;

J. Neurochem. 72:791-799(1999).
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J.
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MEDLINE=21096910; PubMed=11157797;
Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21864207; PubMed-11751928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16."; hum. Mol. Genet. 10:339-352(2001).
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AF073931; AAD17668.1;
AB006466; AAK61268.1;
AJ420779; CAD12646.1;
AF223563; AAF60163.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000636; M+channel_nlg.
IPR001696; Na_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001682; Ca/Na_pore.
IPR002077; Ca_channel.
IPR002111; Cat_channel_TrpL.
 1550
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17720
17720
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1301
1622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
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1578
1578
1883
139
 EXTRACELLULAR (POTENTIAL).

S6 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S1 OF REPEAT III (POTENTIAL).

S2 OF REPEAT III (POTENTIAL).

S2 OF REPEAT III (POTENTIAL).

S2 OF REPEAT III (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S4 OF REPEAT III (POTENTIAL).

S5 OF REPEAT III (POTENTIAL).

S5 OF REPEAT III (POTENTIAL).

S5 OF REPEAT III (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S7 OF REPEAT IV (POTENTIAL).

S1 OF REPEAT IV (POTENTIAL).

S2 OF REPEAT IV (POTENTIAL).

S2 OF REPEAT IV (POTENTIAL).

S3 OF REPEAT IV (POTENTIAL).
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S1 OF REPEAT II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT II (POTENTIAL).
S5 OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT II (POTENTIAL).
                  EXTRACELLULAR (POTENTIAL).

$4 OF REPEAT IV (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

$5 OF REPEAT IV (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

$6 OF REPEAT IV (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

POLY-HIS.
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S3 OF REPEAT I (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S4 OF REPEAT I (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S5 OF REPEAT I (POTENTIAL).
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S1 OF REPEAT I (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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S6 OF REPEAT I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT II (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ion transport; Voltage-gated channel;
; Repeat; Multigene family;
ion; Alternative splicing.
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EMBL; L40399; AAC42005.1;

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CHD1_MOUSE
ID CHD1_M
AC P40201
DT 01-FEB
DT 15-JUN
DE Chromo
GN CHD1 O
OS MUS mu
OC EUKARY
OC Mammal
OX NCEIL
RN SEQUEN
RX MEDLIN
RA Delmas
RT SNF2/S
RLI Proc.
CC -!- FU
CC -!- SU
CC -!- TI
CC -!- SI
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CC -!- SI
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                                                                                                                                                                                                                                                                                                                                                                          RESULT
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Best Local Similarity 100.
Matches 6; Conservative
                                                                          SEQUENCE FROM N.A.

MEDLINE-93211972; PubMed=8460153;

MEDLINE-93211972; PubMed=8460153;

Delmas V., Stokes D.G., Perry R.P.;

Delmas V., Stokes D.G., Perry R.P.;

Pamammalian DNA-binding protein that contains a chromodomain and SNF2/SWIZ-like helicase domain.";

Proc. Natl. Acad. Sci. U.S.A. 90:2414-2418(1993).

-i- FUNCTION: SEQUENCE-SELECTIVE DNA-BINDING PROTEIN. COULD PLAY IMPORTANT ROLE IN GENE REGULATION.
                                                                                                                                                                                                                                                                                                                                CHD1_MOUSE
P40201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chromodomain helicase-DNA-binding protein 1 (CHD-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003594; ATPbind_A:
InterPro; IPR002099; DNA_mis_re
Pfam; PF011119; DNA_mis_repair;
Pfam; PF02518; HATPase_c; 1.
SMART; SM00387; HATPase_c; 1.
                                                                                                                                                                                                                                                              CHD1 OR CHD-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                  296 HRSTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                        6 HRSTPE 11
               SUBCELLULAR LOCATION: Nuclear.

TISSUB SPECIFICITY: ABUNDANCE IS HIGHER IN CELLS REPRESENTING EARLY STAGES OF THE B LYMPHOID LINEAGE SUCH AS PRE-B AND B CE THAN IN CELLS REPRESENTING MATURE PLASMACYTES OR OTHER CELL LINEAGES SUCH AS FIBROBLASTS.
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1203
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  TO THE SNF2/RAD54 HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score 6; DB 1; Pred. No. 41; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S -> G (IN SUSPECTED HNPCC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VAR_010790.
N -> S (IN SUSPECTED HNPCC)
                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P -> L (IN REF. 1; AAF23905).
NKFIACL -> TSLLPVW (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR_012947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VAR_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD0519EC110EA43E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S (IN SUSPECTED HNPCC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K (IN SUSPECTED HNPCC).
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                                                                                                                                                                                                                                                                                                                                              1711 AA
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VAR_012951.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
o. 41;
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                                                                                                                                      and
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                                          CELLS,
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RESULT 22
CCAH_HUMAN
QΥ
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                                                                                                                                                                                                                                                                                                                                                                                    Matches
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SITE
                     Cribbs L.L., Lee J.-H., Yang J., Satin J., Zhang Y., Daud & Barclay J., Williamson M.P., Fox M., Rees M., Perez-Reyes E. "Cloning and characterization of alphalH from human heart, of the T-type Ca2+ channel gene family."; Circ. Res. 83:103-109(1998).
                                                                                                                                                                                             CCAH_HUMAN STANDARD; PRT; 2373 AA. 095180; 095802; Q96RZ9; Q9NYY4; Q8WWI6; 15-JUL-1999 (Rel. 38, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Voltage-dependent T-type calcium channel alpha-1H (Low-voltage-activated calcium channel alpha13.2 s
                                                                                                                                                                                                                                                                                                                                     1698 HRSTPE 1703
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00298; CHROMO; 2
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:88393; Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                  MEDLINE=98333998; PubMed=9670923;
                                                                                                TISSUE-Heart;
                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00598; CHROMO_1; 2. PROSITE; PS50013; CHROMO_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
REVISIONS
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                     CACNA1H
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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InterPro; IPR001650;
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                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                            6 HRSTPE 11
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PF00271; helicase_C; 1.
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6; Conserv
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                                                                                                                                    us (Human).
Metazoa; Chordata; C
Metazoa; Primates; (
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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100.0%; Pro
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SER-RICH.
CHROMO 1.
CHROMO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL).
DEAH BOX.
3 X 5 AA REPEATS
                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X 5 AA REPEATS OF H-S-D-H-R.
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 1711;
                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                              subunit (Cav3.1c)
                                                                      Daud A.,
                                                           [F]
                                               a member
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RESULT 20

MIH3_HUMAN STANDARD;

ID MLH3_HUMAN STANDARD;

AC Q9UHC1; Q9UHC0; Q9P292; P49751;

DT 01-CCT-1996 (Rel. 34, Created)

DT 16-CCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

NA mismatch repair protein Mih3 (MutL protein homolog 3).
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                                                                                                                                                                                                  Matches
                                                                                                                                                                                                         Query Match
Best Local
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MOD_RES
CARBOHYD
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00410;
SMART; SM00408;
SMART; SM00219;
                                            Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; 1g; 3. Pfam; PF00069; pkinase;
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING MEDLINE-20082804; Pubmed-10615123; Lipkin S.M., Wang V., Jacoby R., Banerjee-Bai
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tyrosine protein kinase; Receptor; Transmembrane; Glycoprotein; Transferase; Phosphorylation; ATP-binding; Immunoglobulin domai Signal; Proto-oncogene; Chromosomal translocation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000001; Euk_pkinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                  656
                                                                                                                                                                                 1 SHLGPH 6
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173410; -.
                                                                                                                                                                  SHLGPH
                                                                                                                                                                                                 Similarity
6; Conserv
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557
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1106
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TyrKc;
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Primates;
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Ig_like.
RTKinaseIII.
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100.0%;
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   Jacoby R., Banerjee-Basu S.,
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Pred. No.
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BY S
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N-LINKED (GLCNAC. .)
                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                      BETA PLATELET-DERIVED GROWTH FACTOR RECEPTOR.
                                            Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (AUTO-).
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GLCNAC. . .) (
GLCNAC. . .)
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                                            Vertebrata;
i; Hominidae;
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                                                                                                                                                                                                                 Length 1106
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   Baxevanis A.D.,
                                                                                                                                                                                                                                                          (POTENTIAL).
                                                    Euteleostomi;
                                                                                                                                                                                                                                                   (POTENTIAL)
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Ikeda M., Chi H., Lin C., Li G., Holman K., Tsuda T., Mar L., Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rainero I., Pinessi L., Nee L., Chumakov I., Pollen D., Brookes A., Sanseau P., Polinsky R.J., Wasco W., da Silva H.A.R., Haines J.L., Pericak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E., Rommens J.M., St George-Hyslop P.H.;
"Cloning of a gene bearing missense mutations in early-onset familial Alzheimer's disease.";
Nature 375:754-760(1995).
                                                                                                                                                                     between
the Eurc
                                                                                                                                                                                                                                                                  INCREASE IN CANCER SUSCEPTIBILITY. IT IS CHARACTERIZED BY A
FAMILIAL PREDISPOSITION TO EARLY ONSET COLORECTAL CARCINOMA (CRC)
AND EXTRA-COLONIC CANCERS OF THE GASTROINTESTIAL, UNCLOSICAL AND
FEMALE REPRODUCTIVE TRACTS. HNPCC IS REPORTED TO BE THE MOST
COMMON FORM OF INHERITED COLORECTAL CANCER IN THE WESTERN WORLD.
CANCERS IN HNPCC ORIGINATE WITHIN BEBRIGN NEOPLASTIC POLYPS TERMED
ADENOMAS. CLINICALLY, HNPCC IS OFTEN DIVIDED INTO TWO SUBGROUPS.
TYPE I: HEREDITARY PREDISPOSITION TO COLORECTAL CANCER, A YOUNG
AGE OF ONSET, AND CARCINOMA OBSERVED IN THE PROXIMAL COLON. TYPE
II: PATIENTS HAVE AN INCREASED RISK FOR CANCERS IN CERTAIN TISSUES
SUCH AS THE UTERUS, OVARY, BREAST, STOMACH, SMALL INTESTINE, SKIN,
AND LARRYNX IN ADDITION TO THE COLON. DIAGNOSIS OF CLASSICAL HAPCC
IS BASED ON THE ANSTERDAM CRITERIA: 3 OR MORE RELATIVES AFFECTED
BY COLORECTAL CANCER, ONE A FIRST DEGREE RELATIVE OF THE OTHER
TWO; 2 OR MORE GENERATION AFFECTED; 1 OR MORE COLORECTAL CANCERS
PRESENTING BEFORE 50 YEARS OF AGE; EXCLUSION OF HEREDITARY
POLYPOSIS SYNDROMES. THE TERM "SUSPECTED HAPCC" CAN BE USED TO DESCREE FAMILIES WHO DO NOT OR ONLY
PARTIALLY FULFILL THE AMSTERDAM CRITERIA, BUT IN WHOM A GENETIC
STMILABITY. REPLONGS TO THE DAM ATSMACH EPERALD MUTILIFES EAMILY
                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu Y., Berends M.J.W., Sijmons R.H., Mensink R.G.J., Verlind E., Kooi K.A., van der Sluis T., Kempinga C., van der Zee A.G.J., Hollema H., Buys C.H.C.M., Kleibeuker J.H., Hofstra R.M.W.; "A role for MLH3 in hereditary nonpolyposis colorectal cancer."; Nat. Genet. 29:137-138(2001).
-!- FUNCTION: PROBABLY INVOLVED IN THE REPAIR OF MISMATCHES IN DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fukushige S., Kondo I
Submitted (FEB-2000)
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"MLH3: a DNA mismatch repair gene associated with mammalian microsatellite instability.";
Nat. Genet. 24:27-35(2000).
                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1189-1453 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21470348; PubMed=11586295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS HNPCC E-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: UBIQUITOUS.
DISEASE: DEFECTS IN MLH3 MAY BE A CAUSE OF HEREDITARY NON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Nuclear (Potential).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLYPOSIS COLORECTAL CANCER (HNPCC) (LYNCH SYNDROME). HNPCC IS AUTOSOMAL, DOMINANTLY INHERITED DISEASE ASSOCIATED WITH MARKED
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                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-817;
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                                                                                                                              and
                                                                                                                           for
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EMBL; EMBL;

AF195657; AF195658; AB039667;

AAF23904.1; AAF23905.1; BAA92353.1;

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RESULT 19
PGDR_HUMAN
ID PGDR_H
AC P09619
DT 01-MAR
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DE PETA P
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Best Local S
Matches
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SMART; SM00410; IG_like; 2.

SMART; SM00408; IG_2; 1.

SMART; SM00219; TyrKc; 1.

PROSITE; PS001109; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

PROSITE; PS00241; PROTEIN_KINASE_DOM; 1.
                                                                                                        PGDR_HUMAN STANDARD P09619; 01-MAR-1989 (Rel. 10, C 01-MAR-1989 (Rel. 10, L 15-JUN-2002 (Rel. 41, L Beta platelet-derived g (PDGF-R-beta) (CD140b a
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                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Phosphorylation; ATP-binding; Immunoglobulin domain;
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PHOSPHORYLATION (AUTO-) ()
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CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 4.
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BY S
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; Mismatches
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EMBL; J03278; AAA60049.1;
EMBL; M21616; AAA36427.1;
EMBL; U33172; AAC51675.1;
PIR; A28206; PFHUGB.
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use
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"Cloning and expression of a cDNA coding
platelet-derived growth factor receptor:
receptor class.";
                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Integration of proviral DNA into HTIV-1-infected T-cells results in with transforming activity."; Oncogene 15:1051-1057(1997).
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MEDLLNE-89096941; PubMed=2850496;

Claesson-Welsh L., Eriksson A., Moren A., Severinsson L., Ek B.,

Oestman A., Betsholtz C., Heldin C.-H.;

"CDNA cloning and expression of a human platelet-derived growth
factor (PDGF) receptor specific for B-chain-containing PDGF

molecules.";
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Gronwald R.G.K., Grant F.J., Hald
Hagen F.S., Ross R., Bowen-Pope D
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MEDLINE-89376563; PubMed-2550144;
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"Tandem linkage of human CSF-1 receptor (c-fms) and PDGF receptor genes.":
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European Bioinformatics Institute. T
by non-profit institutions as long
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SUBUNITS: DIMER OF EITHER ALPHA-ALPHA, BETA-BETA OR ALPHA-BETA
SUBUNITS: DIMER OF EITHER ALPHA-ALPHA, BETA-BETA OR ALPHA-BETA
SUBCELLULAR LOCATION: Type I membrane protein.
DISBASE: INVOLVED IN A FORM OF CHROWIC MYELOMONOCYTIC LEUKEMIA
(CMML) CHARACTERIZED BY ABNORMAL CLONAL MYELOID PROLIFERATION I
(CMML) CHARACTERIZED BY AUGUSTE MYELOGENOUS LEUKEMIA (AML). IT IS
BY PROGRESSION TO ACUTE MYELOGENOUS LEUKEMIA (AML). IT IS
CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(5;12)(Q33;P13)
BETWEEN THE ETS-LIKE PROTEIN TEL AND PGDE RECEPTOR B (PDGFRB).
SEMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSI
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CATALYTIC ACTIVITY: ATP + a
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Murray M.J.;
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062683;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tight junction protein 20-3 (Zonula occlude
occludens 3 protein) (Tight junction protei
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                InterPro: IPR000619; Guanylate_kin.
InterPro: IPR001478; PDZ.
InterPro: IPR001478; SH3.
Pfam; PF00595; PDZ; 3.
Pfam; PF00625; Guanylate_kin; 1.
                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haskins J., Gu L., Wittchen E.S., Hibbard J., Stevenson B.R.;
"20-3, a novel member of the MAGUK protein family found at the tight
junction, interacts with Z0-1 and occludin.";
J. Cell Biol. 141:199-208(1998).

I SUBUNIT: INTERACTS WITH OCCLUDIN, CLAUDINS AND Z0-1.
ISIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
ISIMILARITY: CONTAINS 1 SH3 DOMAIN.
ISIMILARITY: CONTAINS 1 SH3 DOMAIN.
ISIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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RESULT
PGDR_MO
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tight junction;
DOMAIN 11
DOMAIN 187
DOMAIN 369
DOMAIN 464
DOMAIN 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Beta platelet-derived growth factor receptor
(PDGF-R-beta)
                                                                                       between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
                                                                                                                                                                                                                                                  Yarden Y., Escobedo J.A., Kuang W.-J., Yang-Feng T.L., Daniel T.O Tremble P.M., Chen E.Y., Ando M.E., Harkins R.N., Francke U., Fried V.A., Ullrich A., Williams L.T.;

"Structure of the receptor for platelet-derived growth factor hel define a family of closely related growth factor receptors.";

Nature 323:226-232(1986).

-!- FUNCTION: THIS RECEPTOR BINDS PLATELET-DERIVED GROWTH FACTOR HAS A TYMOSINE-PROTEIN KINASE ACTIVITY. THIS RECEPTOR BINDS SPECIFICALLY TO PDGF-B.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                          EMBL; X04367; CAA27882.1; PIR; A25742; PFMSRB.
                                                                                                                                                 This
                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: T
                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fibroblast;
MEDLINE=87014762; PubMed=3020426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGDR_MOUSE
P05622;
                                                                                                                                                                    -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS
                                                                                                                                                                                                                             tyrosine phosphate.
                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00856; GUANYLATE_KINASE_1; PROSITE; PS50052; GUANYLATE_KINASE_2; PROSITE; PS50106; PDZ; 3.

PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDGFRB OR PDGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         689 PESRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 PESRAA
                                                                                                                                                                                                                      SUBUNITS
                                                                                                                                                                                  PROTEIN KINASES
                    ; P11362; 1FGI.
MGI:97531; Pdgfrb.
                                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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SM00326;
                                                                             an
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6; Conser
                                                                           equires a license agreement (S email to license@isb-sib.ch).
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; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SH3 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Rodentia;
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264
435
538
750
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100.0%;
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Pred. No
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PDZ 1.
PDZ 2.
PDZ 3.
SH3.
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; 8091D6132DB9F15D CRC64;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Mismatches
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27;
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                                                                                                                                                                                         protein.
RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                BETA-BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                      http://www.isb-sib
                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor (EC
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; Murinae; Mus.
                                                                                                                                                                                                                                ALPHA-BETA
                                                                                                   and
                                                                                                                                     EMBL
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                                                                                                                                             a collaboration
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                                                                                                                                     outstation
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InterPro; InterPro; MGD;

Euk_pkinase Ig_MHC.

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RESULT 15
CN8A_MAC
ACC 088502
DT 15-JUL
DT 15-
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Best Local s
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Createu)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUR-2002 (Rel. 41, Last annotation update)
High-affinity cAMP-specific and IBMX-insensitive
hosenhodiesterase 8A (EC 3.1.4.17) (MMPDE8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphodiesterase.";
Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98338029; PubMed=9671792;
Soderling S.H., Bayuga S.J., Beavo J.A.;
"Cloning and characterization of a CAMP-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CN8A_MOUSE O88502;
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PIR; A35311; RRVGCT.
InterPro, IPR002564; PV_RdRp.
Pfam; PF01615; PV_RdRp; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bloinformatics and the I
the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090
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PATHWAY: Cyclic nucleotide metabolism.

TISSUE SPECIFICITY: HIGHEST LEVELS IN TESTIS > EYE > LIVER > SKELETAL MUSCLE > HEART > 7-DAY EMBRYO > KIDNEY > OVARY > BRAIN. IN THE TESTIS, EXPRESSED SPECIFICALLY IN THE SEMINIFEROUS EPITHELIUM IN A SPATIAL AND TEMPORAL MANNER.

DEVELOPMENTAL STAGE: LEVELS OF EXPRESSION DEFERES SOMETIME BETWEEN EMBRYO DAY 7 AND DAY 11. IN THE TESTIS, EXPRESSION RESTRICTED TO MIDDLE AND LATE PACHYTENE SPERMATOCYTES.

DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN COMPAINING TWO PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN. SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Natl. Acad. Sci. U.S.A. 95:8991-8996(1998).

FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE FUNCTION PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS PHOSPHODIESTERASE, WHICH HAS A HIGH AFFINITY FOR CAMP, MAY BE INVOLVED IN MAINTAINING BASAL LEVELS OF THE CYCLIC NUCLEOTIDE AND/OR IN THE CAMP REGULATION OF GERM CELL DEVELOPMENT.

CATALYTIC ACTIVITY: Adenosine 5'-cyclic phosphate + H(2)O = adenosine 5'-phosphate.

COPACTOR: REQUIRES DIVALENT CATIONS. MAGNESIUM OR MANGANESE COPACTOR: REQUIRES DIVALENT CATIONS.
                                                                                                                                                                                                                                                                                                                                                                                             ENZYME REGULATION: INHIBITED BY DE SELECTIVE PDE INHIBITOR ROLIPRAM INHIBITOR, IBMX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPESRA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REQUIRED FOR MAXIMUM ACTIVITY, IN VITRO (BY SIMILARITY)
YME REGULATION: INHIBITED BY DIPYRIDIMOLE. INSENSITIVE T
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92141 MW;
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Pred. No. 24;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A polymerase.
PROTEIN P33.
; ACD829D016762E4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; i
Sciurognathi; Muridae;
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; Murinae; Mus
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RESULT 16
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                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                    Ross L.J.N., Sanderson M., Scott S.D., Binns M.M., Doel T.
"Nucleotide sequence and characterization of the Marek's c
virus homologue of glycoprotein B of herpes simplex virus,
J. Gen. Virol. 70:1789-1804(1989).
                                                                                                                                                       MEDLINE-89293086; PubMed-2544666;
                                                                                                                                                                                                        Warek's disease herpesvirus (strain RB-IB) (MDHV). Viruses; dSDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Marek's disease-like viruses. NCBI_TaxID=33707;
                                                                                                                                                                                                                                                                                  01-NOV-1990
16-OCT-2001
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P18538;
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Pfam; PF00989; PAS; 1.
PRINTS; PR00387; PDIESTERASE1.
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SMART; SM00091; PAS; 1.
TIGRFAMS; TIGR00229; sensor;
PROSITE; PS00126; PDEASE_I;
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InterPro; IPR000014; PAS_domain.
InterPro; IPR002073; PDEase.
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                                                                                                        SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
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EASE_I; 1.
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M OR MANGANESE 1 (E
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RESULT 13
RRPO_CRV
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Best Local S
Matches 6
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EMBL; U01732;
EMBL; U01743;
TIGR; MG072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequencing.";

J. Bacteriol. 175:7918-7930(1993).

J. Bacteriol. INVOLVED IN PROTEIN EXPORT. INTERACTS WITH THE SECY/SECE SUBUNITS. SECA HAS A CENTRAL ROLE IN COUPLING THE HYDROLYSIS OF ATP TO THE TRANSFER OF PRE-SECRETORY PERIPLASMIC AND OUTER MEMBRANE PROTEINS ACROSS THE MEMBRANE (BY SIMILARITY).

HENDER OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS COUPLING THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                               Complete NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; Pubmed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hut
"A survey of the Mycoplasma genitalium
                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                       PROSITE; PS01312; SProtein transport;
                                                                                                                                                                                                                                                                                                                   TIGRFAMs;
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Pfam; PF01043;
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STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; PubMed-7569993;
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6; Conservative
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transport; ATP-binding; Membrane; Translocation;
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AAD10553.1;
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S -> T (IN REF. 2).
KORDKFLLA -> TREVEIS (IN REF. 2)
MI -> WS (IN REF. 2).
T. -> H (IN REF. 2).
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Pred. No. 24;
0; Mismatches
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RESULT 14
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p15962;
01-APR-1990 (Rel. 14, 0
01-APR-1990 (Rel. 14, i
15-JUN-2002 (Rel. 41, i
Probable RNA-directed i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grieco F., Burgyan J., Russo M.;
"The nucleotide sequence of cymbidium ringspot virus RNA.";
Nucleic Acids Res. 17:6383-6383(1989).
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate
                                    SEQUENCE FROM N.A.

MEDLINE-90281577; PubMed-2353450;

MEDLINE-90281577; PubMed-2353450;

Hearne P.Q. Knorr D.A., Hillman B.I., Morris

"The complete genome structure and synthesis
clones of tomato bushy stunt virus.";

Virology 177.141-151(1990).

-!- CATALYTIC ACTIVITY: N nucleoside triphosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-AUG-1990 (Rel. 15,
15-JUN-2002 (Rel. 41,
Probable RNA-directed
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MISCELLANDOUS: READTHROUGH OF THE TERMINATOR CODON UGA OCCURS BETWEEN THE CODONS FOR 296-LYS AND 297-GLY.

SIMILARITY: TO OTHER TOMBUSVIRUSES RNA POLYMERASE.
MISCELLANEOUS: READTHROUGH OF 1
BETWEEN THE CODONS FOR 296-LYS
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(Rel. 14, Last sequence (Rel. 41, Last anno
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Last annotation
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RNA polymerase (EC 2.7.7.48)
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                                                                                            073925;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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-I- FUNCTION: ACTS AS A TRANSCRIPTIONAL REPRESSOR FOR ZINC FINGER
-TRANSCRIPTION FACTORS EGR1 AND EGR2. ISOFORM 2 LACKS REPRESSION
ABILITY (BY SIMILARITY).

-I- SUBUNIT: HOMOMULTIMERS MAY ASSOCIATE WITH EGR1 BOUND TO DNA (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Svaren J. Apel E.D., Simburger K.S., Jenkins N.A., Gilbert D.J., Copeland N.A., Milbrandt J.; "The Nab2 and Stat6 genes share a common transcription aregion."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
Squalus acanthias (Spiny dogfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
                                                       KCNQ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:7627; NAB2 MIM; 602381; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                           Voltage-gated
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Submitted (SEP-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation;
                                                                                                                                                                                                                                                                                                                             188
                                                                                                                                                                                                                                                                                                                                                      7 RSTPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: THE NAB CONSERVED DOMAIN 1 (NCD1) INTERACTS WITH EGRI INHIBITORY DOMAIN AND MEDIATES MULTIMERIZATION.
DOMAIN: THE NAB CONSERVED DOMAIN 2 (NCD2) IS NECESSARY FOR TRANSCRIPTIONAL REPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: WIDELY EXPRESSED AT EXPRESSED IN MELANOMA CELL LINES. INDUCTION: BY SERUM AND PMA STIMULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
SUBCELLULAR LOCATION:
NUCLEUS (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE NAB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEUS (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                             RSTPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF268380; AAF72545.1; -. X70991; CAA50318.1; -. AJ011081; CAA09472.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U48361; AAC50589.1;
                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320
323
426
257
525
                                                                                                                                                                                                                                                                                                                             193
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                                                                             potassium channel
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489
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56594 .
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356
384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repressor; Alternative splicing. NCD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEAR. ISOFORM 2 IS NOT LOCALIZED TO THE
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LTI -> ASP (IN ISOFORM 2).

MISSING (IN ISOFORM 2).

MISSING (IN ISOFORM 3).

PR -> Q (IN REF. 3 AND 4).

PR -> Q (IN REF. 3 CRC64;
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Pred. No
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                                                                           KQT-like
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A_MYCGE

SECA_MYCGE

947318; Q49438;

101-FEB-1996 (Rel. 33, Last sequence update)

T 01-FEB-1996 (Rel. 33, Last sequence update)

T 16-OCT-2001 (Rel. 40, Last annotation update)

Proprotein translocase secA subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RA WALDEGE S. Fakker B., Belch M., Barth P., Hopf A., Schulte U.,
RA Busch A.E., Aller S.G., Forrest J.N. Jr., Greger R., Lang F.;
Busch A.E., Aller S.G., Forrest J.N. Jr., Greger R., Lang F.;
RY Shack A.E., Aller S.G., Forrest J.N. Jr., Greger R., Lang F.;
RY Shack A.E., Aller S.G., Forrest J.N. Jr., Greger R., Lang F.;
RY Pflugers Arch. 437:298-304(1999).
RY Channel from rectal gland of Squalus acanthlas.";
RP Pflugers Arch. 437:298-304(1999).
RY Pflugers Arch. 437:298-304(1999).
RY Pflugers Arch. 437:298-304(1999).
RY Pflugers Arch. 437:298-304(1999).
RY Pflugers ARCHARLY IMPORTANT IN CARDIAC REPOLARIZATION. ASSOCIATES
CC WITH KCNE1 (MINK) TO FORM THE I(KS) CARDIAC POTASSIUM CURRENT. IS
CC ALSO A POTENTIAL CANDIDATE RESPONSIBLE FOR THE BASOLATERAL
CC POTASSIUM CONDUCTANCE OF SECRETORY EPITHELIA.
CC -I- SUBGULTI: HETEROMULTIMER WITH KCNE1 (MINK).
CC -I- SUBGLELLIAR LOCATION: INTEGRAL Membrane protein.
CC -I- SUBGLELLIAR LOCATION: INTEGRAL Membrane protein.
CC -I- TISSUE SPECIFICITY: EXPRESSED ONLY IN RECTAL GLAND AND HEART.
CC -I- TISSUE SPECIFICITY: EXPRESSED ONLY IN RECTAL GLAND AND HEART.
CC -I- TISSUE SPECIFICITY: EXPRESSED ONLY THE VOLTAGE-SENSOR AND IS
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches
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_d0520; K.
_onic channel; T-
_unitigene fam'
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TRANSMET
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SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Rectal gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus
                                                                                                                                                                                                               58
                                                                                                                                                                                                                                              10 PESRAA 15
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                                                                                                                                                                                                                                                                                Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000636; M+channel_nlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001622; K+channel_pore
IPR003946; KCNQ1_channel.
                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                Conservative
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149
190
219
255
293
321
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                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POSITION (BY SIMILARITY).
BELONGS TO THE POTASSIUM CHANNEL FAMILY. KQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trans;
                                                                                                                                                                                                                                                                                                                                                 74686
                                                                                                                                                                                                                                                                                             40.0%;
100.0%;
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SEGMENT S3.
SEGMENT S4.
SEGMENT S4.
SEGMENT S5.
SEGMENT S6.
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Pred. No
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                                                                                                                                                                                                                                                                                red. No. 20 Mismatches
                                                                                                                                                                                                                                                                                        DB
. 20;
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Mycoplasma genitalium. Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

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The mammalian HSF4 gene generates both an activator and a repressor RT of heat shock genes by alternative splicing.";

RL J. Biol. Chem. 274:27845-27856(1999).

CC I. FUNCTION. DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK CC PROMOTER ELEMENTS (HSE). THE HSF4A ISOFORM REPRESSES TRANSCRIPTION CC PROMOTER HSF4B ISOFORM ACTIVATES TRANSCRIPTION.

CC PROMOTER ELEMENTS (HSE). THE HSF4A ISOFORM REPRESSES TRANSCRIPTION CC PROMOTER HSF4B ISOFORM ACTIVATES TRANSCRIPTION.

CC PROMOTER ELEMENTS (HSE). THE HSF4A ISOFORM REPRESSES TRANSCRIPTION CC I. SUBGUNIT: HOMOTRIMER. EXHIBITS CONSTITUTIVE DNA BINDING AND FORMS CC I. SUBGULTUAR LOCATION: Nuclear.

CC I. SUBCELLULAR LOCATION: Nuclear.

CC ARE PRODUCED BY ALTERNATIVE SPLICING.

CC ARE PRODUCED BY ALTERNATIVE SPLICING.

CC I. SIMILARITY: BELONGS TO THE HSF FAMILY.

CC I. SIMILARITY: BELONGS TO THE HSF FAMILY.

CC I. SIMILARITY: BELONGS TO THE HSF FAMILY.
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Transmem 4
Transmem 9
Transmem 12
Transmem 16
Transmem 16
Transmem 21
Transmem 21
Transmem 21
Transmem 21
Transmem 24
Transmem 39
Carbohyd 24
Carbohyd 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSF4 HUMAN STANDARD; PRT; 493 AA.

Q9ULV5; Q9ULV6; Q99472;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Heat shock factor protein 4 (HSF 4) (Heat shock transcription factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                               Nakai A., Tanabe M., Kawazoe Y., Inazawa J., Morimoto R.I., Nagata K. "HSF4, a new member of the human heat shock factor family which lacks properties of a transcriptional activator.";
Mol. Cell. Biol. 17:469-481(1997).
                                                                                                                                                                                                                                                                                 Tanabe M., Sasai N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                MEDLINE-99419073;
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97127404; PubMed=8972228;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM HSF4A).
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Pfam; PF01080; Presenilin; 1.
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6; Conser
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Thrane; Glycoprotein.
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127
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N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

; 71CCEE3F6BB9COAF CRC64;
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                              Liu X.-D., Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
        There are no restrictions ong as its content is in
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and
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                                          SEQUENCE OF 50-525 FROM N.A. (ISOFORM MEDLINE-96243039; PubMed-8649813; Kirsch K.H., Korradi Y., Johnson J.P.; "Mader: a novel nuclear protein over e oncogene 12:963-971(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAB2_HUMAN STANDARD; PRT; 525
Q15742; Q14797; Q76006;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation up
NGFI-A binding protein 2 (EGR-1 binding
                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1). Gerilnger M., Johnson J.P.; "Genomic organization of the Mader/NAB2 submitted (MAY-2000) to the EMBL/GenBank
                                                                                                                                                                                                                                                                                              "NAB2, a corepressor of NGFI-A (Egr-1) and Krox20, proliferative and differentiative stimuli."; mol. Cell. Biol. 16:3545-3553(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription regulation; Nuclear protein; DNA-binding; Activate Repressor; Heat shock; Multigene family; Alternative splicing. DNA_BIND 18 122 BY SIMILARITY.

DOMAIN 130 204 HYDROPHOBIC REPEAT HR-A/B.

DOMAIN 365 390 HYDROPHOBIC REPEAT HR-C.

VARSPLIC 246 320 LPETNLGLSPHRARGPIISDIPEDSPSPEGTRL
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96251303; PubMed-8668170;
Svaren J., Sevetson B.R., Apel E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAB2 OR MADER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGFI-A binding protein 2 (EGR-1 binding protein 2) (Melanom associated delayed early response protein) (MADER protein)
                                                                                                                                                                                                                                                                                                                                                                           Milbrandt J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000232; HSF_DNA_bi;
InterPro; IPR002341; HSF_ETS.
Pfam; PF00447; HSF_DNA-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFAC; T04923; -. Genew; HGNC:5227; HSF4. MIM; 602438; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00056; HSFDOMAIN.
ProDom; PD001788; HSF_DNA_b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D87673; BAA13433.1; HSSP; P22813; 1HKT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB029348; BAA84582.1; -. EMBL; AB029347; BAA84581.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00434; HSF_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STPESR
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 6; Conserv
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is (Human).

Metazoa; Chordata; C

Metazoa; Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493
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(ISOFORM
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                                                                                                                                     (ISOFORM 1).
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYDROPHOBIC REPEAT HR-A/B.
HYDROPHOBIC REPEAT HR-C.
LPETMLGLSPHARAGPINDLPEDSPERGTRLSPSSDGRR
EKGLALLKEEPASPGGDGEAGLALAPNECDFCYT -> STY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLSQRQIWALALTGPGAPSSLTSQKTLHPLRGPGFLPPVMA
G (IN ISOFORM HSF4A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IN ISOFORM HSF4/
F16389F79EE2BFDE
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                                                                  expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525
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                                                                                                                                                                                                        gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae;
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                                                                  in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                  human
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                                                                  melanomas
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Best Local s
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPS3_DROPS
P28680;
01-DEC-1992
                                                                       InterPro; IPR001760; Opsin.

Pfam; Pr00001; 7tm_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS0262; G_ROTEIN_RECEP_F1_2;

PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Variable rates of evolution among Drosophila opsin genes.";
Genetics 132:193-204(1992).

1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECUI
MEDIATE VISUAL THEY CONSIST OF AN APOPROTEIN, OPSIN, COV
LINKED TO CIS-RETINAL.

1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
SEQUENCE
                                                                                                                                                                                FlyBase; FBgn0012709; Dpse\Rh3.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001760; Opsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Apple Hill;
MEDLINE=93012921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila pseudoobscura (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992 (Rel.
01-NOV-1995 (Rel.
01-OCT-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRRAMS; TIGRO0611; recf; 1.
PROSITE; PS00611; RECF_1; 1.
PROSITE; PS00618; RECF_2; 1.
DNA damage; DNA replication; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carulli J.P., Hartl D.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Opsin Rh3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DROPS
                                                 Photoreceptor; Retinal protein; Transmembrane; Phosphorylation;
                                                                                                                                                                                                                                                                          HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: OPSIN RH3 IS SENSITIVE TO UV LIGHT. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE PHOSPHORYLATED.
MISCELLANEOUS: EACH DROSOPHILA EYE IS COMPOSI
OMMATIDIA. EACH OWNATIDIUM CONTAINS 8 PHOTORR
THE R1 TO R6 CELLS ARE OUTER CELLS, WHILE R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM:
                                                                                                                                                                                                                                                                                           ; x65879; CAA46710.1;
S24607; S24607.
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                                                                                                                                                                                                                                                                        P02699; 1F88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELLULAR LOCATION: Integral membrane protein.

SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 AA;
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G-protein coupled receptor; Vision.

1 56 EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=1398053;

    Jast sequence update)
    Jast annotation update)
    photoreceptor cells opsin).

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42280 MW; 08FFD4025D037373 CRC64;
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%; Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPOSED OF 800 FACETS OR PHOTORECEPTOR CELLS (R1-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOS response; DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND R8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARE INNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COVALENTLY
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"Cloning of Xenopus presentiin-alpha and -bety conests.";

differential expression in ogenesis and embryogenesis.";

Biochem. Biophys. Res. Commun. 231:392-396(1997).

-1- FUNCTION: MAY PLAY A ROLE IN REGATIVE REGULATION OF APOPTOTIC CASCADES DURING COGENESIS AND EMBRYOGENESIS, AND IN

DEVELOPMENTALLY MATURED TISSUES SUCH AS BRAIN TISSUE.

-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN OVARIES AND TO A LESSER EXTENT IN TESTIS, INTESTINE, KIDNEY, BRAIN, EYE AND LUNG. WEAK FYDRRESSTON IN LIVER AND HEART. PRESENT IN TRACE AMOUNTS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, C
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Presenilin alpha.
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                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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O12976;
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DOMAIN
                      EMBL; D84427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97223465; PubMed=9070286;
Tsujimura A., Yasojima K., Hashimoto-Gotoh T.;
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                                                         cities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  SKELETAL MUSCLE.
DEVELOPMENTAL STAGE: ABUNDANT IN EARLY STAGES
EXPRESSION IS RAPIDLY REDUCED BETWEEN MEIOTIC
FERTILIZATION STAGES.
SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
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                      BAA19570.1;
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6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL).
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BETWEEN MEIOTIC
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InterPro; IPRO01412; tRNA-synt_I.
InterPro; IPR002304; tRNA-synt_met.
Pfam; PF00133; tRNA-synt_1; 1.
PRINTS; PR01041; TRNASYNTHMET.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
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MEDLINE=97105885; Pubmed=8948633;
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Aminoacyl-tRNA synthetase; Protein biosynthesis;
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(See http://www.isb-sib.ch/announce/
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RESULT
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RA Alvarenga R., Alves L.M.C., Arryda J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Carrer H.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Kuramae E.E., Laigret F., Lambais M.R., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Marcins E.A.L., Marcins S.A., Lopes C.R., Machado J.A.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marsuma A.Y.,
RA Manck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Mono D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Manck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Mono D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mono D.B., Roberto P.G., Nones L.R., Oliveira M.A.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Silveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Gouza A.P., R.M., Meidanis J., Setubal J.C.;
RT Tregenome seequence of the plant pathogen Yella fastidiosa.
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                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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                                                             EMBL; AE003855; AAF82816.1;
                                                                                                                 entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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STRAIN=Wistar; TIS:
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CONFLICT
SEQUENCE
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the Eurc
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15-JUL-1999 (Rel. 38, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takahashi H., Murayama M., Takashima A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Wistar; TISSUE=Brain;
MEDLINE=96255262; PubMed=8710164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurosci. Lett.
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                                                                                 1 SHLGPHRSTPESRAA 15
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PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE PRESENILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: MAY PLAY A RÔLE IN INTRACELLULAR SIGNALING AND GENE EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE. MAY FUNCTION IN THE CYTOPLASHIC PARTITIONING OF PROTEINS. SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A C-TERMINAL (CTF) ENDOPROTEOLYTICAL FRAGMENT (BY SIMILARITY). SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
                                                                      SHLGPHRSTPESRAA 361
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D82363; BAA11564.1;
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15; Conser
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BIOCHEM. BIOPHYS. Res. COMMUNI. 228:430-439(1996).

-! FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GEIEXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE.

MAY FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS.

-! SUBUNIT: PREDOMINANTLY HETERODIMER OF A.-TERMINAL (NTF) ANI C-TERMINAL (CTF) ENDOPROTEDLYTICAL FRAGMENT (BY SIMILARITY) ANI C-TERMINAL (CTF) ENDOPROTEDLYTICAL FRAGMENT (BY SIMILARITY).

-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND ENDOPLASMIC RETICULUM (BY SIMILARITY).

-! ALTERNATIVE PRODUCTS: 2 ISOFORMS; I-467 (SHOWN HERE) AND I-463; ARE PRODUCED BY ALTERNATIVE SPLICING.

-! TISSUE SPECIFICITY: FOUND PREDOMINANTLY IN NEURONS OF THE DIFFERENT CORTICAL LAYERS AND HIPPOCAMPUS BUT ALSO IN SUBCOLUMENTS.
                                                                                                                      SITE
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16-OCT-2001 (Rel. 40,
Presenilin 1 (PS-1).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; A22.001;
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  MISSING (IN ISOFORM I-463)
D986FF2CA7F2975C CRC64;
                                                 ALTERNATIVE PROTEOLYTIC CLEAVAGE SIMILARITY).
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SUBCORTICAL
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                           "Molecular cloning and tissue distribution of presentiin-1 in
senenscence accelerated mice (SAM P8) mice.";

Submitted (MAY-1999) to the EMEL/GenBank/DDBJ databases.

C -!- FUNCTION: MAY PLAY A ROLE IN INTRACELLULAR SIGNALING AND GENE
EXPRESSION OR IN LINKING CHROMATIN TO THE NUCLEAR MEMBRANE.

C MAY FUNCTION IN THE CYTOPLASMIC PARTITIONING OF PROTEINS.

C -!- SUBUNIT: PREDOMINANTLY HETERODIMER OF A N-TERMINAL (NTF) AND A

C -TERMINAL (CTF) ENDOPROTEOLYTICAL FRACMENT (BY SIMILARITY).

C -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI AND
ENDOPLASMIC RETICULUM (BY SIMILARITY).

C -!- SIMILARITY: BELONGS TO THE PRESENLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSNI_MOUSE STANDARD; PRT; 467
P49769; 09JLP9;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation up
Presenilin 1 (PS-1) (S182 protein).
PSENI OR PSNLI OR AD3H.
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                             MEDLINE-97442406; PubMed-9295283; Mitsuda N., Roses A.D., Vitek M.P.; "Transcriptional regulation of the mouse J. Biol. Chem. 272:23489-23497(1997).
                                                                                                                                                                                                                                                                                                                                                                                          Rommens J.M., St George-Hyslop P.H.; "Cloning of a gene bearing missense Alzheimer's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crook R.,
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MEDLINE=97369208; PubMed=9225696;
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Alzheimer's disea
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Ogihara T.;
  between
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                                                                                                                                                                                                                       Kumar V.B., Vyas K.C.,
                                                                                                                                                                                                                                      STRAIN-SAM P8;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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ett. 208:195-198(1996).
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               entry
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ase families.";
 ixy is copyright. It is produced t
Institute of Bioinformatics and
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Rodentia;
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Pred. No.
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                                                                                                                                                                                                                       Franko M., Flood
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Matches 15
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P97887; P97529;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Presenilin 1 (PS-1) (S182 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
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STRAIN-Wistar; TISSUE-Brain;
MEDLLNE-9719371; PubMed-9047347;
Taniguchi T., Hashimoto T., Taniguchi R., Shimada K., Kav
Yasuda M., Nakai M., Terashima A., Koizumi T., Maeda K.,
"Cloning of the cDNA encoding rat presentlin-1.";
Gene 186:73-75(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                  RAT
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EMBL; AF007560; AAB72049.1;
EMBL; AF149111; AAF73153.1;
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                      PSEN1 OR PSNL1
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S; PR01072;
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ALTERNATIVE PROTEOLYTIC CLEAVAGE SITE (ESIMILARITY).
S -> T (IN STRAIN SAM P8).
D -> E (IN STRAIN SAM P8).
E -> CM (IN STRAIN SAM P8).
ER -> RRD (IN STRAIN SAM P8).
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PRESENILIN 1 CTF SUBUNIT (
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B haemophilus
5 pasteurella
9 rhizobium m
9 drosophila
8 klebsiella
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9 arabidopsis
5 brachydanio
0 bombyx dens
7 drosophila
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8 rattus norv
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3 rhizobium m
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hypothetical protein YHR063c - yeast (Saccharomyces N;Alternate names: hypothetical protein H8025.16 C;Species: Saccharomyces cerevisiae C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #C;Accession: $46711 R;Latreille, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chitinase (EC 3.2.1.14) 35 - Streptomyces thermoviolaceus (;Speciaes: Streptomyces thermoviolaceus C;Date: 30 - Jun - 2001 #sequence_revision 30 - Jun - 2001 #text_change C;Accession: JC7555 R;Tsujibo, H.; Okamoto, T.; Hatano, N.; Miyamoto, K.; Watanabe, Biosci. Biotechnol. Biochem. 64, 2445-2453, 2000 A;Title: Family 19 chitinases from Streptomyces thermoviolaceus A;Reference number: JC7535; MUID:21036907; PMID:11193414 A;Accession: JC7535
submitted to the EMBL Data Library, May 1994 A; Description: The sequence of S. cerevisiae A; Reference number: S46696
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JC7535
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A;Experimental source: strain OPC-520
C;Comment: This enzyme, a member of t
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogucl DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A/1000; MUID:98344137; PMID:9679194
A;Accession: H/1081
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C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000
C;Accession: H71081
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamot
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A; Residues: 1-377 <TSU>
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lysaccharide-binding domain that is important in the efficient hydrolysis of insoluble o
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M.; Ohfuku, Y.; Funahashi, T.;
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Pred. No.
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                      cosmid 8025
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Search completed: March 10, 2003, 14:30:46
Job time: 59 secs

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A;Introns: 47/3; 131/3; 167/3
C;Superfamily: fos transforming protein;
C;Keywords: DNA binding; leucine zipper
F;132-172/Domain: fos/jun DNA-binding dom
F;165-193/Region: leucine zipper motif
                                                                                                                                                                                                        C; Genetics:
A; Gene: c-f
                                                                                                                                                                                                                                                                                                    R;Van Beveren, C.; van Straaten, F.; Curran, T.; Mueller, R.; Verma, I.M. Cell 32, 1241-1255, 1983
A;Title: Analysis of FBJ-MuSV provirus and c-fos (mouse) gene reveals that viral and A;Reference number: A03986; MUID:83180421; PMID:6301687
                                                                                                                                                                                                                                                                                                                                                                                  transforming protein fos - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 24-Sep-1999
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A; Residues: 1-380 < VAN>
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C; Keywords: tran
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A;Residues: 1-379 <LAT>
A;Cross-references: EMBL:U00061; NID:g487943; PIDN:AAB68390.1; PID:g487959; MIPS:YHRC
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C; Genetics:
A; Gene: YPO3352
C; Superfamily: #
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submitted to the EMBL Data Library, November A;Reference number: Z20398
A;Accession: T27643
A;Status: preliminary; translated from GB/EMB
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C;Speciles; Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0407
R;Parkhill, J; Wren, B.W.: Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, I., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
Nature 413, 848-852, 2001

A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A; Reference number: ABO502; PMID:11677608
                                                                                                           probable bacteriophage protein STY1893 [imported] - Salmonella enterica subsp. C:Species: Salmonella enterica subsp. enterica serovar Typhi A:Note: this species has also been called Salmonella typhi C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C:Accession: AD0719 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.
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A; Molecule type: DNA
A; Residues: 1-371 < KUR>
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AD0719
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A; Map position: 3
A; Introns: 36/1; 71/1
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A; Cross-references:
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A; Residues: 1-371 <WIL>
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ilarity 100.0%;
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100.0%; Pred. No.
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Succinate dehydrogenase (EC 1.3.99.1) flavoprotein - human (f C.Species: Homo sapiens (man) C;Date: 20-May-1994 #sequence_revision 10-Nov-1995 #text_chan C;Accession: $21302 R.Malcovati, M.; Marchetti, L.; Zanelli, E.; Tenchini, M.L.; submitted to the EMBL Data Library, July 1990 A;Description: Cloning of the flavoprotein subunit of human s A;Reference number: $21302 A;Molecule type: mRNA A;Residues: 1-377 cMAL> A;Residues: 1-377 cMAL
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A; Introns: 55/2; 102/3; 156
C; Superfamily: GTP-binding
                                                                                                                                                                                             A;Cross-references: EMBL:X53943; NID:g36642; PIDN:CAA37886.1; PID:g36643 C;Superfamily: fumarate reductase flavoprotein; 3-oxosteroid 1-dehydrogenase homology C;Keywords: flavoprotein; mitochondrion; oxidoreductase C;Keywords: flavoprotein; mitochondrion; oxidoreductase E;149-239/Domain: 3-oxosteroid 1-dehydrogenase homology <OXD>
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A;Molecule type: DNA
A;Residues: 1-375 <WIL>
A;Cross-references: EMBL:Z83117; pIDN:CAB05570.1; GSPDB:GN00019; CESP:M04C7.1
A;Experimental source: clone M04C7
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-374 <PAR>
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A; Map position: 1
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;Gene: STY1893
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.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes: Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens. A;Reference number: AD3252; PMID:11756688
A;Rocession: AD3557
A;Status: preliminary
A;Molecule type: Name of the facultative intracellular pathogen Brucella melitens. A)
                  A; Molecule type: mRNA
A; Residues: 1-365 < NOT>
A; Residues: 1-365 < NOT>
A; Residues: 1-365 < NOT>
A; Cross references: GB: M27130; NID:g192530; PIDN: AAA37407.1; PID:g309161
A; Cross references: GB: M27130; NID:g192530; PIDN: AAA37407.1; PID:g309161
R; Wolffe, E.J.; Gause, W.C.; Pelfrey, C.M.; Holland, S.M.; Steinberg, A.D.; August, J.T.
J. Biol. Chem. 265, 341-347, 1990
A; Title: The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antige A; Reference number: A34907; MUID:90094420; PMID:2403559
A; Accession: A34907
                                                                                                                                                                                                                                                     R; Nottenburg, C.; Rees, G.; St. John, T.

Proc. Natl. Acad. Sci. U.S.A. 86, 8521-8525, 1989
A; Title: Isolation of mouse CD44 cDNA: structural features
A; Reference number: A34424; MUID:90046829; PMID:2682651
A; Accession: A34424
                                                                                                                                                                                                                                                                                                                                                                             CD44 membrane glycoprotein precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 15-Jun-1900 #sequence_revision 15-Jun C;Accession: A34424; A34907
A;Status: preliminary
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A;Residues: 1-364 <KUR>
A;Residues: 1-364 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53623.1; PID:g17984538; GSPDB:GN00191
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A;Accession: B41151
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A; Residues: 1-363 <GA2>
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C;Accession: G83180
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, ; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 191
G83180
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A; Residues: 8-195, 'G', 197-365 <WOL>
A; Cross-references: GB.305163; NID:9200334; PIDN:AAA39923.1; PID:g200335
C; Superfamily: human cell adhesion protein CD44
C; Keywords: cell adhesion; glycoprotein; membrane protein
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                                                                                                                                                                                                                                                                            A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: G83180 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable FMN oxidoreductase PA3723 [imported] - Pseudomonas aeruginosa (strain PAO1)
C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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A;Note: part of this sequence was confirmed by protein sec
C;Superfamily: severin; gelsolin repeat homology
F;47-366/Domain: gelsolin repeat homology <GEL>
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Eur. J. Biochem. 225, 773-779, 1994
A;Title: The complete sequence of a 40-kDa actin-modulating protein A;Reference number: S51363; MUID:95045533; PMID:7957213
A;Accession: S51363
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C;Species: Lumbricus terrestris (common earthworm)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change
C;Accession: S51363; S49320
                                                                                                                                                 A;Gene: PA3723
C;Superfamily: NADPH dehydrogenase chain OYE2
                                                                                                                                                                                      C; Genetics:
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A; Residues: 1-368 <STO>
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S51363
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A; Residues: 1-366 <GIE>
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prostaglandin E2 receptor - human C;Species: Homo sapiens (man) C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999 C;Accession: 138920 R;Regan, J.W.; Bailey, T.J.; Pepperl, D.J.; Pierce, K.L.; Bogardus, A.M.; Donello, Mol. Pharmacol. 46, 213-220, 1994 A;Title: Cloning of a novel human prostaglandin receptor with characteristics of th A;Reference number: 138920; MUID:94359483; PMID:8078484 A;Accession: 138920
                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-358 <RESS
A;Cross-references: EMBL:U19487; NID:g639719; PIDN:AAA61681.1;
C;Superfamily: prostaglandin E receptor EP1
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A; Map position: linear chromosome
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A;Molecule type: DNA
A;Residues: 1-356 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein AGR_L_636 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 C;Accession: C98171
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C98171
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C:Superfamily: Mycobacterium tuberculosis hypothetical protein
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A;Accession: H70882
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Residues: 1-356 <COL>
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kelz, B.;
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submitted to the EMBL Data
submitted to umber: S51312
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C; Date: 07-May-1995 #sequence
C; Accession: S51312
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A;Molecule type: mRNA
A;Residues: 1-358 <OAK>
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S51312
                                                                                                  A; Reference number: A; Accession: S33702
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A; Residues: 1-361 <STO>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-363 <GAR>
A;Cross-references: EMBL:X69202; NID:g312390; PIDN:CAA49140.1; PID:g312391
A;Cross-referenandez, J.; Baguna, J.; Salo, E.
R;Garcia-Fernandez, J.; Baguna, J.; Salo, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 7338-7342, 1991
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
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0; Mismatches
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unknown protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 C;Accession: D96761
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; Species: Caenorhabditis elegans
C; Species: Ci-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C; Accession: T24015
R; Harris, B.
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A;Introns: 4/1; 55/3; 92/1; 148/3; 224/2; 278/3; 336/3
C;Superfamily: Caenorhabditis elegans hypothetical protein R07B7.8
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A;Experimental source: clone R07B7
C;Genetics:
A;Gene: CESP:R07B7.9
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A; Molecule type: DNA
A; Residues: 1-348 <STO>
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A; Residues: 1-349 <WIL>
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                       #text_change 31-Mar-2001
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C;Accession: F83190
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
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                                                                                                                                    A; Gene: lpxD; PA3646 C; Superfamily: UDP-3-0-[3-hydroxymyristoyl] glucosamine N-acyltransferase C; Keywords: acyltransferase
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A;Residues: 1-353 <STO>
A;Cross-references: GB:AE004784; GB:AE004091; NID:g9949799; PIDN:AAG07034.1; GSPDB:GN
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 02-Feb-2001
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                                                                                                                                                                                                                               A; Experimental source: strain PAO1
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A; Residues: 1-351 <STO>
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A; Title: Deciphering A; Authors: Sqares,

.; Sulston, J.E.; Taylor, K.;
the biology of Mycobacterium

Whitehead, tuberculosis

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Barrell,

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Holroyd,

hypothetical protein Rv2777c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequencerium tuberculosis C;Date: 17-Jul-1998 #sequencerium tuberculosis (strain H37RV) C;Accession: H70882

#text_change 20-Jun-2000

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ster, E.W.

A; Title: The Genome of the Natural Genetic Engineer A; Pitle: A
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A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Accession: B85757

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-342 <STO>
A; Cross-references: GB:AE005174; NID:g12515491; PIDN:AAG56518.1; GSPDB:(A; Genetics: A; Genetics: A; Genetics: A; Genetics: Strain O157:H7, substrain EDL933

C; Genetics: A; Gene: 22506
oxidoreductase Atu3965 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: A13043 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Verage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; M.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-lett, E.W.
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AB3116
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A; Note: T28A8.40
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C;Superfamily:
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A;Authors: Yoo, H.; Tao, Y.; Biddle, ster, E.W.
A;Title: The Genome of the Natural (A;Reference number: AB2577; PMID:111
A;Accession: AB3116
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-342 <KUR>
A;Cross-references: GB:AE008689; PII
A;Experimental source: strain C58 (I C;Genetics: A;Gene: Atu4550
A;Map position: linear chromosome
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C:C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999
C;Accession: C75139
R:Anonymous, Genoscope
R:Anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence:
                                                                                                                                                                                   submitted to the Protein A; Reference number: 22440 A; Accession: T47411
                                                                                                                                                                                                                                                       hypothetical protein T28A8.40 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change C;Accession: T47411
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A;Residues: 1-346 <KAW>
A;Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49828.1; PID:g545
                                                                                   A; Experimental source: C; Genetics:
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                                                                                                                                                                                                                                       Lemcke, K.;
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R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.; C.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzie Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallc Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; pMID:11130712
                   A; Reference number: A82950; A; Accession: E83059
                                      A; Title: Complete genome sequence of Pseudomonas aeruginosa A; Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                             ketol-acid reductoisomerase PA4694 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: E83059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Genome: plasmid
A; Note: expressed during exponential gro
C; Superfamily: fission yeast pyridoxine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Farahani, R.; Imbeault, J.C.; St Jean, A.; Chan, C.C.Y.; Allard, G.; Charlebois, submitted to the EMBL Data Library, March 1997
A;Description: Hereditary instability of the megaplasmid pHV3, and filamentation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Haloferax volcanii
C;Date: 21-Jan-2000 #sequence_revision
C;Accession: T44988
R;Farahani, R; Imbeault, J.C.; St Jean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 169
T44988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE005172; NID:g6634766; C;Genetics: A;Map position: 1
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A;Molecule type: DNA
A;Residues: 1-336 <FAR>
A;Cross-references: EMBL:U95374; PIDN:AAB71807.1
  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: megaplasmid
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A; Residues: 1-335 <STO>
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Pred. No.
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Pred. No. 3.1e+02;
                                                                                                                       Coulter, S.N.; Folger, F
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), 3.1e+02;
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K.R.; Kas, A.;
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldr A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194
A;Accession: C98242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 171
A83835
NADH oxidase BH1481 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: A83835
R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83835
                                                                                                                  A; Gene: AGR_L_1
A; Map position:
                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-338 < KI
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C;Superfamily: NADPH dehydrogenase chain OYE2
                                                                                                                                                                           A; Residues: 1-338 < KUR>
A; Cross-references: GB: AE007870;
                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein AGR_L_1780 [imported] - Agrobacterium tumefaciens (strain C58, (C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 C;Accession: C98242
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A; Residues: 1-338 <STO>
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C; Superfamily:
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A; Cross-references: GB:
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3 LGPHR 7
                                                                                                                  AGR_L_1780 sition: linear chromosome
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100.0%; F.
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                                      Score 5; DB 2; Le
; Pred. No. 3.1e+02;
0; Mismatches 0;
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.1e+02;
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IJ

155 LGPHR

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probable membrane protein STY2661 [imported] - Salmonella enterica subsp. enterica Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: AG0809 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; C th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; S; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stev A;Title: Complete genome sequence of a multiple drug resistant Salmonella enteri A;Reference number: AB0502; PMID:11677608 A;Accession: AG0809 A;Status: preliminary A;Status: preliminary A;Cross-references: GB:AL513382; PIDN:CAD07657.1; PID:g16503644; GSPDB:GN00176 C;Genetics: STY2661
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A;Gene: Tlx-1
A;Introns: 192/1; 259/2
A;Introns: 192/1; 259/2
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
E;204-260/Domain: homeobox homology <HOX>
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A;Title: Characterization and developmental expression of A;Reference number: I57032; MUID:94206842; PMID:7908826

A;Accession: I57032

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-332 <RES>
A;Cross-references: GB:S70632; NID:9546379; PIDN:AAB3054
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A:Residues: 1-332 <ADE>
A:Residues: 1-332 <ADE>
A:Cross-references: GB:AE000719; NID:g2983517; PIDN:AAC07097.1;
A:Experimental source: strain VF5
C:Genetics:
A:Gene: hypE
A:Gene: hypE
C:Superfamily: hydrogenase expression/formation protein hypE
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Pred. No. 3.1
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b. 3.1e+02;
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B 2; Length 332;
3.1e+02;
es 0; Indels
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conserved hypothetical protein PA2430 [imported] - Pseudomonas aeruginosa (;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-IC;Accession: A83342 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, ; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
F26G16.5 protein - Arabidopsis thaliana (;Species: Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001 C;Accession: B86429 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White
                                                                                                        RESULT 168
B86429
                                                                                                                                                                                                                                                                                                                                                    A; Gene: PA2430 C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DAA
A;Residus: 1-334 CSTO>
A;Cross-references: GB:AE004670; GB:AE004091; NID:g9948470; PIDN:AAG05818.1; GSPDB:GN
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C;Superfamily: COI intron
C;Keywords: mitochondrion
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                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain C; Genetics:
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C;Genetics:
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A; Residues: 1-334 <WAR>
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o. 3.1e+02;
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S.; White,

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homeotic protein Hox 11 - human
N;Alternate names: tcl-3 proto-oncogene
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 24-Sep-1999
C;Accession: A40855; S17311; A41224
                                                                                 R:Hatano, M.; Roberts, C.W.M.; Minden, M.; Science 253, 79-82, 1991
A;Title: Deregulation of a homeobox gene, 1
A;Reference number: A40855; MUID:91289163;
A;Accession: A40855
A;Cross-references: GB:S38742; NID:g232582; PIDN:AAB19293.1; R;Lu, M.; Gong, Z.; Shen, W.; Ho, A.D.
                                         A; Molecule type: mRNA
A; Residues: 1-330 <HAT>
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483; PMID:11016950
A; Accession: A84291
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A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: F96522
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A;Molecule type: DNA
A;Residues: 1-326 <STO>
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C;Accession: A84291
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                                                                                                                                                                                                                                                                                                                     RESULT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-328 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005173; NID:g5733881; PIDN:AAD49769.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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5; Conser
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5; Conserv
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                                                                                                                                                                  C.W.M.; Minden, M.; Crist, W.M.; Korsmeyer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.3%;
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Pred. No.
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Pred.
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                                                                                                       HOX11, by the PMID:1676542
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. 3e+02
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3e+02;
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                                                                                                                        t(10;14) in T cell leukemia.
                 PID:g232583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maddocks,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Khaykin, E.,
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.G.; Jabl
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A;Reference number: A70300; MA;Accession: A70388
                                                                                                                                                        hydrogenase expression/formation protein - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 162
S44743
                                                                                                           C;Accession: A70388
R;Deckert, G.; Warren, P.V.; Gaasterland, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C02D5.1 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 16-Sep-1994 #sequence_revision 12-May-1995 #text_change 19-May-2000
C;Accession: S44743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:119607; OMIM:186770 A;Map position: 10q24-10q24 C;Superfamily: unassigned homeobox proteins; C;Keywords: DNA binding; homeobox; leukemia; F;202-258/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-275, 'L', 277-330 <LUM>
A;Rennedy, M.A.; Gonzalez-Sarmiento, R.; Kees, U.R.; Lampert, F.; Dear, N.; Boeh
Proc. Natl. Acad. Sci. U.S.A. 88, 8900-8904, 1991
A;Title: HOX11, a homeobox-containing T-cell oncogene on human chromosome 10q24.
A;Reference number: A41224; MUID:92020958; PMID:1681546
A;Recession: A41224; MUID:92020958; PMID:1681546
A;Recession: A41224; MUID:92020958; PMID:1681546
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                                                                          Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                RESULT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references:
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A; Residues: 1-332 <DUZ>
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A; Accession: S44743
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A; Residues: 1-189, 'VALSPTVTRRI', 190-275, 'L', 277-330
A; Cross-references: GB: M75952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: The tcl-3 proto-oncogene altered by chromosomal translocation in T-cell A;Reference number: S17311; MUID:92007734; PMID:1717256
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dehydrogenase
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100.0%; Pr
0;
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100.0%; Pr
                              e of the hyperthermophilic bacterium Aquifex aeolicus MUID:98196666; PMID:9537320
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Pred. No.
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                                                                                                                 ₩.G.;
                                                                                                               Lenox, A.L.; Graham,
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown

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hypothetical protein - Autographa californica nuclear polyhedrosis virus C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV A:Note: dsDNA virus
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-Jan-2000 C:Accession: C72869
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J. Virol. 65, 805-812, 1991
A;Title: Identification of the very early transcribed baculovirus gene PE-38.
A;Reference number: A43681; MUID:91101290; PMID:1987375
A;Accession: A43681
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A43681
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phospholipase A [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AB0330
A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66783.1; PID:g559222
C;Genetics:
A;Gene: Ac-PE38
C;Superfamily: Orgyia pseudotsugata nuclear polyhedrosis virus PE-38 protein
                                                                                                                   A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-321 <AYR>
                                                                                                                                                                                       R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D. virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Accession: C72869
A;Accession: C72869
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A; Residues: 1-321 <KRA>
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C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: A43681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-320 <KUR>
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Best Local
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5; Conserv
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 5; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 5; DB 2
Pred. No. 3e+
0; Mismatches
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o. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID: 915980684; GSPDB: GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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ugan, G.;
Barrell,
                                                                                   hypothetical protein F11A17.17 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: F96522
                                                                 R; Theologis,
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F96522 RESULT 159

Chin, C.W.; insen, N.F.;

A.; Ecker, J.R.; Palm, Chung, M.K.; Conn, L.; Hughes, B.; Huizar, L.

C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

```
hypothetical protein 45 - equine herpesvirus 2
C;Species; equine herpesvirus 2
C;Date: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C;Accession: S55640
                              ρ
                                                                                                                                                                                                     A;Cross-references: EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.40 A;Experimental source: cultivar Columbia; BAC clone T24C20
                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-323 <CHO>
                                                                                                                                                                                                                                                                           A; Reference number: Z17586
A; Accession: T13005
                                                                                                                                                                                                                                                                                                             R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; submitted to the Protein Sequence Database, July 1999
                                                                                                                                                                                                                                                                                                                                             hypothetical protein T24C20.40 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 11-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 22-Oct-1999 C;Accession: T13005
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A; Residues: 1-321 <TEL>
A; Residues: 1-321 <TEL>
A; Cross-references: GB:U20824; NID:g695172; PIDN:AAC13833.1; PID:g695218
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Mol. Biol. 249, 520-528, 1995
A;Tille: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55640
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В
                                                                                                                                      A; Introns:
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                                                                                                                                                                    A; Gene: ATSP:T24C20.40
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; J. Mol. Biol. 249, 520-528, 1995
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Best Local S
Matches 5
                                                                                  Query Match
Best Local (
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Best Local
                                                                    Matches
250 STPES
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                                STPES 12
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5; Conserv
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5; Conserv
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5; Conserv
254
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                                                                                                                                      29/3;
                                                                  Conservative
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                                                                                                                                      55/3; 73/3; 111/1; 133/3; 159/1; 179/3
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                                                                  33.3%; Score 5; DB
100.0%; Pred. No. 3e
tive 0; Mismatches
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100.0%; Pred. No.
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Pred. No.
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                                                                                                    DB 2;
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                                                                                                    Length 323
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                                                                     Indels
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                                                                                                                                              A;Gene: CESP:Y18D10A.9
A;Introns: 51/1; 98/2; 140/1; 169/3; 203/3; 257/2
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-314 <WIL>
A; Cross-references: EMBL; ALO34393;
                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, December 1998 A;Reference number: 220226 A;Accession: T26531
                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Y18D1OA.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
C;Accession: T26531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Trans 5; Conserve
뭐
                                                                                                                                                                                                                                A; Experimental source: clone Y18D10A
                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated
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A;Experimental source: isolate T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A;Reference number: Z22020; MUID:99281911; PMID:10355780
A;Accession: T41889
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Date: 03-Dec-1999
C; Accession: T41889
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C;Date: (03-Dec-1999 #sequence_revision 03-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-309 <KAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PE38 orf153 - Bombyx mori nuclear polyhedrosis virus (isolate C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
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                                                                            Matches
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Best Local
263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
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                                                                        Local Similarity
nes 5; Conserv
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                                    8 STPES 12
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STPES
                                                                          Conservative
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                                                                          0;
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                                                                                            Score 5; I
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Pred. No.
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                                                                                                                                                                                                                                                  PIDN:CAA22322.1;
                                                                          Mismatches
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                                                                                              DB 2; Le
o. 2.9e+02;
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5. 2.9e+02;
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                                                                                                          Length 314;
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RESULT 152

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274

ESRAA

278

RESULT 154

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A;Experimental Source: Strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: F820/2
R;anonymous, The Xyle
Nature 406, 151-157,
                                                                                                                                                                                   C; Genetics:
A: Gene: XF1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-317 <SIM>
A;Cross-references: GB:AE003980; GB:AE003849; NID:g9106531; PIDN:AAF84309.1; GSPDB:GN
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R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; A; Accession: F87260
                                                                                                                                                          A; Gene: XF1500
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
                                                                                                                                                                                                                                                                         M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.;
A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CC0095
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A; Residues: 1-316 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                   Matches
                                                                             Query Match
Best Local
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11 ESRAA 15
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                                                                               Similarity
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5; Conserv
                                                                                                                                                            nodulation protein nodP
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  small subunit XF1500 [imported] - Xylella fastidiosa (strain 9a5c)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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100.0%; Pr
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100.0%;
                                                                       Score 5; 1; Pred. No.
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                                                      Mismatches
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40. 2.9e+02;
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                                                                             . DB
                                                B 2; Length 317;
2.9e+02;
es 0; Indels
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RESULT 146

$75481
$75481
$75481

polysialic acid transport protein kpsM - 52...

N;Alternate names: protein $1r2107

C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: $75481
C;Accession: $75481
C;Kiesko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miya o, K.; Okumura, S.; Simpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, }

nva Res. 3, 109-136, 1996

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G64405
                                                          tetrahydromethanopterin S-methyltransferase (EC 2.1.1.86) chain E [similarity] - Methanopterin S-methyltransperin S-methylt
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C;Genetics:
A;Gene: VNG1779C
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.;
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: F84329
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A;Note: the nucleotide sequence w
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A; Residues: 1-302 <51
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A; Title: Complete genome sequence A; Reference number: A64300; MUID: 9
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A; Residues: 1-302 <KAN>
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ilarity 100.0%;
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100.0%; Pr
0;
   quence of the methanogenic archaeon,
MUID:96337999; PMID:8688087
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b; Pred. No. 2.8
0; Mismatches
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o. 2.8e+02;
tches 0; Inde
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                                   jannaschi
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).G.; Jabl
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H64819
                                                                                                                                                                       A;Cross-references: GB:AE000184; GB:U00096; NID:g1787036; A;Experimental source: strain K-12, substrain MG1655 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                      R;Blattner, F.R.; Plunkett III, G.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence
A;Reference number: A64720; MUID:974
A;Accession: H64819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                formate acetyltransferase activating enzyme C;Species: Escherichia coli C;Date: 10-Sep-1999 #sequence_revision 10-Se C;Accession: H64819
                           A; Description: activation of A; Pathway: anaerobic glucose
                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-308 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 맗
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A; Pathway:
A; Note: iro
                                                                                                             C; Function:
                                                                                                                                                A; Gene: ybiY
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anaerobic g on dependent

pyruvate formate-lyase under
metabolism

anaerobic

conditions

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gen

MUID:97426617; PMID:92785

PMID:9278503

Bloch, C.A.;

Perna,

N.T.;

Burland,

V.; Riley,

X

10-Sep-1999

#text_change 01-Mar-2002

(EC 1.97.1.4) 3 -

Escherichia coli

(strai

not

shown;

translation not shown

PIDN: AAC73911.1;

PID:g17870

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A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; A; Title: Deciphering the biology of Mycobacterium tuberculosis fi A; Reference number: A70500; MUID:98295987; PMID:9634230 A; Accession: B70835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: G64405
A;Status: preliminary; nucleic acid
A;Molecule type: DNA
A;Residues: 1-303 <BUL>
A;Cross-references: GB:U67529; GB:L7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: FOR773706-774617
C; Superfamily: Methanobacterium
C; Keywords: methyltransferase
                                                                                                                                                                                                                                                                                                                                           C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998
C;Accession: B70835
                                                                                                                                                                                                                                                                             R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S., Nature 393, 537-544, 1998
                                                                                                                A;Gene:
                                                                                                                                                A;Cross-references: GB
A;Experimental source:
                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-306 <COL>
                                                                                                                                                                                                        A; Status: preliminary; nucleic
                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Rv0276 - Mycobacterium tuberculosis
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Matches
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120 STPES
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                                                                                                                    Rv0276
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5; Conserv
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124
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ce: strain H37Rv
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28
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8.8e+02
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Holroyd,
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transcription factor Brn-5 - rat
N;Alternate names: homeobox protein mPOU; TCR beta enhancer binding protein TCFbetal
C:Species: Rattus norvegicus (Norway rat)
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 24-Oct-1997
C;Accession: A4880
R;Andersen, B; Schonemann, M.D.; Pearse II, R.V.; Jenne, K.; Sugarman, J.; Rosenfeld, M.
J. Biol. Chem. 268, 23390-23398, 1993
A;Title: Brn-5 is a divergent POU domain factor highly expressed in layer IV of the neoc
A;Reference number: A48880; MUID:94043133; PMID:7901208
A;Accession: A48880
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-301 <AND>
A;Cross-references: GB:L23204; NID:9349723
A;Experimental source: anterior pituitary
A;Note: sequence extracted from NCBI backbone (NCBIN:138920, NCBIP:138921)
C;Superfamily: transcription factor Brn-5; homeobox homology; POU domain homology
F;146-213/Domain: POU domain homology <HOX>
F;235-291/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: GDB:POU6F1; BRN5; MPOU; TCFB1
A;Gene: GDB:POU6F1; BRN5; MPOU; TCFB1
A;Gross references: GDB:361078
A;Gross references: GDB:361078
A;Gross references: GDB:361078
C;Superition: Czpter-12qter
C;Superitamily: transcription factor Brn-5; homeobox homology; POU domain homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;146-213/Domain: homeobox homology <POU>
F;235-291/Domain: homeobox homology <HOX>
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C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 22-Jun-1999
C;Accession: A54687; S42575; S40151
R;Messier, H.; Brickner, H.; Gaikwad, J.; Fotedar, A.
Mol. Cell. Biol. 13, 5450-5460, 1993
A;Title: A novel POU domain protein which binds to the T-cell receptor beta enhancer.
A;Reference number: A54687; MUID:93360980; PMID:8102789
A;Accession: A54687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:L14482
R;Wey, E.; Lyons, G.E.; Schaefer, B.W.
Eur. J. Biochem. 220, 753-762, 1994
A;Title: A human POU domain gene, mPOU, is expressed in A;Reference number: $42575; MUID:94192665; PMID:7908264
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A; Molecule type: mRNA
A; Residues: 1-301 <WEY>
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A; Residues: 1-301 <MES>
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nes 5; Conserv
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b. 2.8e+02;
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                                 RESULT 145
F84329
     hypothetical protein Vng1779c [imported] - Halobacterium sp. NRC-1
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hypothetical protein T19F6.80 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 04-Mar-2000 C;Accession: T13457 R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancr submitted to the Protein Sequence Database, July 1999 A;Reference number: Z17587 A;Accession: T13457 A;Accession: T13457 A;Accession: T13457 A;Accession: T1302 <BEV>A,Cross-references: EMBL:AL109619; GSPDB:GN00062; ATSP:T19F6.80 A;Experimental source: cultivar Columbia; BAC clone T19F6
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T13457
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                                                                                                                                    A;Map position: 4
A;Introns: 129/3; 244/1
C;Superfamily: Arabidopsis thaliana hypothetical
                                                                                                                                                                                                             A; Experimental source: C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 01-Mar-2002
C;Accession: B84282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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C;Superfamily:
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A; Residues: 1-301 <STO>
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C;Species: Halobacterium sp. NRC-1
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                                                                  Mismatches
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o. 2.8e+02;
                                                                                  DB 2; Le
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                                                                                                                                        protein T19F6
                                                                    0
                                                                                                     Length 302
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                                                                    Indels
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ugh, D.W.; Maddocks, D.G.;
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G.; Ja
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R;Hayashi, T.; Makino, I
gasawara, N.; Yasunaga,
DNA Res. 8, 11-22, 2001
                                                                                     hypothetical protein ECs0902 [imported] - Escherichia coli (strain 0157:H7, c;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: F90741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable exported protein YPO0800 [imported] - Yersinia pestis (C:Species: Yersinia pestis C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change C:Accession: AF0098
                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-297 <STA>
A;Cross-references: EMBL:U88974; NID:g2444080; PID:g2444107; PIDN:AAC79543
A;Experimental source: host Streptococcus thermophilus strain CNRZ1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Sequence analysis and characterization of phi 01205, a A; Reference number: 217654; MUID:98048466; PMID:9387220 A; Accession: T13317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein 28 - Streptococcus phage phi-01205
C;Species: Streptococcus phage phi-01205
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change
C;Accession: T13317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Genome sequence of Yersinia pestis, the causative A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AF0098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, II, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001
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F90741
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A; Residues: 1-295 < KUR>
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nes 5; Conser
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Complete genome
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5; Conserv
                                                  Makino, K.; Ohnishi, M.;
Masunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                                                33.3%;
ilarity 100.0%
Conservative
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                 sequence
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Pred. No. 2.8
0; Mismatches
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                 of
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Pred. No.
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; Mismatches
               enterohemorrhagic
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                                                  Kurokawa, K.; Ishii, K.;
Shiba, T.; Hattori, M.;
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hes 0;
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2.8e+02;
0;
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2.8e+02;
es 0; Indels
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                                                ; Yokoyama,
; Shinagawa,
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             coli
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               O157:H7
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Jugan, G.;
Barrell,
                                                                      Han,
               and
                                                                      C
                                                                                                                                              R
           A; Gene: ybiy
C; Superfamily:
C; Keywords: oxi
                                                                                                   A; Residues: 1-299 <PARS

A; Moule, S.; O'Gaora, P.

Mature 413, 848-852, 2001

A; Authors: Parry, C.; Quail, M.; Rutherford, K.;

A; Title: Complete genome sequence of a multiple d

A; Reference number: AB0502; PMID:11677608

A; Accession: AH0602

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-299 <PARS
                                                                                                                                                                                                                                                                                         probable formate acetyltransferase activating enzyme (EC 1.97.1.4) [imported] C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 03-Jun-2002 C;Accession: AH0602
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.;
                                                                  A;Cross-references: GB:AL513382;
C;Genetics:
                                                                                                                                                                                                                                                k; Parkhill, J.; Dougan, G.; James,
th, T.; Connerton, P.; Cronin, A.;
, S.; Moule, S.; O'Gaora, P.
Nature /12 010.55
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probable pyruvate idoreductase

formate-lyase

N

activating

enzyme;

ferredoxin

2[4Fe-

PIDN:CAD05290.1;

PID:g16502054; GSPDB:GN00176

Davis,

Thomson, N.R.; , P.; Davies, R.

.; Pickard, R.M.; Dowd,

L.,

Wain, J.; Church; White, N.; Farr

Salmo

Simmonds, M.; drug resistant

Skelton, J.; Stevens, Salmonella enterica s

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A; Gene: ECs0902
C; Superfamily:
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A;Accession: F90741
A;Accession: Full and a status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule ty
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Best Local
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5
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PESRA
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5; Conserv
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85592
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-299 <STO>
A;Cross-references: GB:AE005174; NID:g12513827; PIDN:AAG55197.1; GSPDB:GN00145;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein ybiY [imported] - Escherichia C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 C;Accession: A85592
                                                                                                                                                 A; Gene: ybir C; Superfamily:
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                                                                                                                                                                                        C; Genetics:
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A85592
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                                     10 PESRA 14
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PESRA
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5; Conserv
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b. 2.8e+02;
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                                                                                                              Length 299
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A;Residues: 1-291 <COL>
A;Cross-references: GB:Z92774; GB:AL123456; NID:g3261729; PIDN:CAB07143.1; PID:g1877300
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                            G;Species: Mycobacterium tuberculosis
G;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
G;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
G;Accession: G70605
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: G70605
                                                                                                                                                                                                         Rajandream, M.A.; Rogers, Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                     probable hydrolase - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                     G70605
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A;Introns: 45/3
C;Superfamily: unassigned collagens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, March A;Description: The sequence of C. elegans A;Reference number: 218401
A;Accession: T15779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C35B8.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t;C;Accession: T15779
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T15779
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Nature 402, 761-768, 199
N;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84807
A;Accession: B84807
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <STO>
                                                                    A; Molecule type: DNA
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A; Map position: 2
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Pred. No. 2.7e+02;
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5. 2.7e+02;
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C;Genetics:
A;Gene: Rv3569c
C;Superfamily: t
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A; Gene: T9J22.30;
A; Gene: T9J22.30;
                                                                                                                     C;Species: Rhizobium fredii
C;Date: 03-Mar-1993 *sequence_revision 03-Mar-1993 *text_change 04-Mar-2000
C;Date: 03-Mar-1993 *sequence_revision 03-Mar-1993 *text_change 04-Mar-2000
C;Accession: A43663
R;Sadowsky, M.J.; Olson, E.R.; Foster, V.E.; Kosslak, R.M.; Verma, D.P.S.
J. Bacteriol. 170, 171-178, 1988
A;Title: Two host-inducible genes of Rhizobium fredii and characterization of the A;Reference number: A43663; MUID:88006864; PMID:2447061
A;Accession: A43663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AC002505; NID:g2739359; PID:g2739387
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; submitted to the EMBL Data Library, April 1998
A;Description: Arabidopsis thallana chromosome II BAC T9J22 genomic sequence.
A;Reference number: 214161
A;Reference number: 214051
A;Reference number: 214051
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A;Cross-references: GB:M1
C;Superfamily: Rhizobium
                                                 A; Molecule type: DNA
A; Residues: 1-295 <S.
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host-inducible protein A - Rhizobium fredii
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                                                                                                  A; Status: preliminary
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A; Residues: 1-292 <STO>
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A; Residues: 1-292 < ROU>
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les 5; Conserv
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                                                 1-295 <SAD>
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                       GB:M19019; NID:g152247; PIDN:AAA26294.1; PID:g152248
fredii host-inducible
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100.0%; Pred. No.
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100.0%; Pred. No.
tive 0; Mismatc
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Query Match

33.3%;

Score 5;

DВ 2;

Length 295;

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probable ribosomal protein L2 rplB - Mycobacterium tuberculosis (strain H37RY) C;Species: Mycobacterium tuberculosis (c;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: C70642 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gord; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroy Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete ge A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: C70642 A;Accession: C70642 A;Accession: C70642 A;Accession: C70642 A;Cross-references: GB:Z84395; GB:AL123456; NID:g3261698; PIDN:CAB06467.1; PID:g180 A;Experimental source: strain H37Rv C;Genetics: A;Gene: rplB
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hypothetical protein PA1522 [Imported] - Pseudomonas aeruginosa (strain PAO1)
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: E83456
R; Stover; C:K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li; LOTY, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: B69025
A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-278 < MTH>
A:Residues: 1-278 < MTH>
A:Cross-references: GB:AE000887; GB:AE000666; NID:92622289; PIDN:AAB85675.1; PID:9262229
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1186
C:Superfamily: conserved hypothetical protein MJ1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83456
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <STO>
A;Cross·references: GB:AE004580; GB:AE004091; NID:g9947468; PIDN:AAG04911.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA1522
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                                                      ; GB:AL123456; NID:g3261698; PIDN:CAB06467.1; PID:g1806172
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No. 2.6e+02;
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probable RNA-binding protein (imported) - Arabidopsis thaliana
C;Speciles: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84807
                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-284 <LUC>
A;Cross-references: EMBL:AF057033; NID:g3320432; PID:g3320434; PIDN:AAC34398.1
A;Experimental source: specific_host Streptococcus thermophilus
                                                                                                                                                                                                                                                                                                                                                            Virology 246, 63-73, 1998
A;Title: The structural gene module in Streptococcus thermophilus bacteriophage phi S A;Reference number: 217696; MUID:98321150; PMID:9656994
A;Accession: T13621
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein gp284 - Streptococcus phage phi-Sfil1
C;Species: Streptococcus phage phi-Sfil1
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: CESP:R03E9.1
A;Map position: X
A;Introns: 52/1; 145,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U40947; PIDN:AAC48067.1; GSPDB:GN00028; CESP:R03E9.1
A;Experimental source: strain Bristol N2; clone R03E9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-281 <WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T28857
                                                                         RESULT 131
B84807
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T13621
R;Lucchini, S.; Desiere, F.; Bruessow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: T28857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: The sequence A; Reference number: Z20533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid R03E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily:
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T13621
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Best Local :
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Best Local
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                                                                                                                                                  238 PESRA
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nes 5; Conserv
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5; Conserv
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s; Pred. No. 2.7
0; Mismatches
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Pred. No.
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o. 2.6e+02;
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                                                                                                                                                                                                                                                        Length 284;
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hypothetical protein F59C6.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T22993 R;Wilkinson, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AG2215
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shinpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Suna Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain C; Genetics: A; Gene: all3278
                                                                                                                                                                                                                                                                                                                                                                                                        A; Decide type: DNA
A; Molecule type: DNA
A; Residues: 1-272 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB74977.1; PID:g17132373; GSPDB:GN00179
A; Cross-references: GB:BA000019; PIDN:BAB74977.1; PID:g17132373; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene:
A; Map po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein AGR_C_2792 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: H97543
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A; Accession: H97543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE007869; PIDN:AAK87305.1; PID:g15156600; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-271 <KUR>
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Science 294, 2323-2328, 2001
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                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome
                                                                                                                                                                                                                                                                                                                            33.3%;
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; Pred. No. 2.6
0; Mismatches
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Pred.
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                                               15-Oct-1999 #text_change 15-Oct-1999
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Markelz, B.
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conserved hypothetical protein MTH1186 - Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C;Accession: B69025 R;Smith, D.R.; Deloughery, C.; Lee, H.; Dubois, J.; Aldr R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldr Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Qiu, D.; Spadafora, R.; Deloughery, J.; Rice, P.; Noelling, J.; Reeve, J.
                                                                                                                                                               RESULT 126
B69025
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C;Accession: G69963

C;Accession: G69963

C;Accession: G69963

C; Bron, S; Brouillet, S; Bruschi, C.V; Caldwell, B; Capuano, V; Carter, N.M.; R; Bron, S; Brouillet, S; Bruschi, C.V; Caldwell, B; Capuano, V; Carter, N.M.; R; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y; Fuma, S; Galizzi, A.; Galicch, J; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S; Hosono, S; Hullo, I Koetter, P; Koningstein, G; Krogh, S; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinc A;Authors: Lauber, J.; Lazarevic, V; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S; Mau, Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B; Park, S.H.; Parro, V; Pohl, T.M.; Portetr Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scan, A; Authors: Schletch, S.; Schrocher, F.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; S; akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiy, Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A; H.; Complete genome sequence of the Gram-postiive bacterium Bacillus subtil: A;Reference number: A65580; MUID:98044033; PMID:9384377

A;Schrocher, A; Muldischer, A; Muldisch
                                                                                                                                                                                                                                                  C; Superfamily: s
F; 43-257/Domain:
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                                                                                                                                                                                                                                                                                                         A; Gene: yqjG
                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                             A; Experimental
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-275 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP:F59C6.8
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A; Residues: 1-274 <WIL>
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Best Local
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160 RSTPE 164
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                                   7 RSTPE 11
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main: stage III sporulation proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SpoIIIJ-like homolog yqjG - Bacillus subtilis
                                                                                                                       Similarity
5; Conserv
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source: strain
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                                                                                                                              Conservative
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Pred. No.
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No. 2.6e+02;
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in homology
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L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, ire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

(strain

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RESULT 119
AD0898
PTS-transport family phosphoryl transfer protein STY3438 [imported] - Salmonella enterid C;Species: Salmonella enterida subsp. enterica serovar Typhi C;Species: Salmonella enterida subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: AD0898
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
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A; Gene: Atul514
A; Map position:
                                                                                                                                                                                                                                                                        Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Reference number: AB0502; PMID:11677608
A;Recession: AD0988
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-268 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07778.1; PID:g16504327; GSPDB:GN00176
C;Genetics:
C;Genetics:
A;Gene: STY3438
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A;Cross-references: GB:AE007869; PIDN:AAK88438.1;
C;Genetics:
A;Gene: AGR_C_4930
A;Map position: circular chromosome
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; PMID:11743194

A;Accession: E97685
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <KUR>
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D. 2.5e+02;
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A;Experimental source: strain 1021, megaplasmid pSymB
R;Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-H
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher,
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change
C;Accession: C96010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 121
C96010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross references GB: AE001827;
A; Experimental source: strain R1
C; Genetics: <WHIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: G75411; C75638
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, , M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable transposase - Deinococcus radiodurans (strain R1)
C; Species: Deinococcus radiodurans
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_c
                                                                                               C; Genetics:
A; Gene: SMb21517
                                                                                                                                                                      A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-271 <KUR>
A; Cross-references: GB:AL591985; PIDN:CAC49747.1; PID:g15141234; GSPDB:GN00167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb psymB megaplasmid from the N2-fixing e A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 1
C; Genetics: <WH2B>
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A; Residues: 1-270 <WHI>
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A95842; A; Accession: C96010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein SMb21517 [imported] - Sinorhizobium meliloti (strain 1
C; Species: Sinorhizobium meliloti
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C; Superfamily:
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A; Note: plasmid CP1
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A; Residues: 1-270 <WH2>
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                                                                                                                                               A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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     Best Local Similarity
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5; Conserv
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100.0%; Pr
.... 0;
     33.3%;
100.0%;
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Score 5; I
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Pred. No.
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     DB 2; Length . 2.6e+02;
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2.5e+02;
0;
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T.; Zalewski,
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N.A.; Fisher, R.
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hypothetical protein mtgA [imported] - Agrobac C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence_revision 11-Jan-C; Accession: AG2910 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner, F.; Karp, P.; Romero, P.; Zhang, S.
                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: serotype 2, 281M1/1 A; Note: sequence inconsistent with nucleotide translation A; Note: sequence extracted from NCBI backbone (NCBIN:137884,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Camp, H.S.; Silva, R.F.; Coussens, P.M.
Virology 196, 484-495, 1993
A;Title: Defective Marek's disease virus DNA contains a A;Reference number: A48725; MUID:93383373; PMID:8396799
A;Accession: B48725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: CESP:T22E5.6
A;Introns: 53/3; 99/1; 149/1; 177/3
C;Superfamily: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A;Description: The sequence of C. el A;Reference number: Z18606 A;Accession: T16924
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C;Accession: B48725
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C;Accession: T16924
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                                                                                                                                                        RESULT 115
                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: nucleic acid
A;Residues: 1-252 <CAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U43282; NID:g1125825; PID:g1125830; PIDN:AAA83617.1; CESP:T22E
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A; Residues: 1-249 <MIN>
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Best Local
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b; Pred. No. 2.4
0; Mismatches
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elegans cosmid T22E5
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                                                                                 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                     Agrobacterium tumefaciens
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5. 2.4e+02;
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                             D.; Chen, L.; Wood, G.E.; Chen, Y.; D.; Kutyavin, T.; Levy, R.; Li, M.; I
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2s 0;
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                           Levy,
                                                                                                                     (strain C58,
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                                                                                                                     Dupont)
                             ; Woo,
A; October: DNA
A; Molecule type: DNA
A; Residues: 1-266 < KUR>
A; Cross-references: GB: AEO08688; PIDN: AAL42519.1;
A; Cross-references: Strain C58 (Dupont)
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                                                                               A;Status: preliminary
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Conserved hypothetical protein Atu1514 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: A12762 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001 Science 294
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A87345
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; PMID:11743193 A; Accession: AIZ762
                                                                                                                  ster, E.W.
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C;Accession: A87345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-265 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription regulator, TetR family [imported] - Caulobacter crescentus
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A; Residues: 1-263 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule
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5; Conserv
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oo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan,
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100.0%; Pred. No. 2.
Live 0; Mismatches
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                                                                            Engineer
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2.5e+02;
es 0; Indels
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                                                                                                                                                    M.; Gordon-Kai
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PID:g17739939;

GSPDB:GN00186

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hypothetical protein AGR_C_4681 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: B97669
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T17311
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                                                  R;Goodner, B.; Hinkle, G.; Go
A.; Liu, F.; Wollam, C.; All
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of t
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A; Accession: T17311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein DKFZp434C128.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: H69030
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                A; Reference number: A97359; A; Accession: B97669
                                                                                                                                                                                                   RESULT 110
B97669
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source:
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A; Residues: 1-247 <OTT>
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C;Keywords: iron; r
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R; Smith, D.R.; Douce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
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preliminary
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Conservative (
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                                                                                      G.; Gattung, S.;
C.; Allinger, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        adult
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                                                the Plant Pathogen and Biotechnology Agent Agrobacterium
                                   PMID:11743194
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                                                                                    Miller, N.; 1
Doughty, D.;
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5. 2.4e+02;
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tember 1999
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                                                                                    Blanchard, N
; Scott, C.;
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                                                                                    M.; Qurollo, Lappas, C.;
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Markelz,
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R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
R; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Kr
Connor, R.; Davles, R.; Devlin, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Whitehead, S.; Barrell, B.G.
Nature 393, 537-544, 1998
                                                                                                                                                                A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; A; Title: Deciphering the biology of Mycobacterium tuberculosis fr A; Reference number: A70500; MUID:98295987; PMID:9634230 A; Accession: A70745
A; Gene: Rv0494
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                    probable transcription regulator Rv0494 - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer
A;Reference number: AB2577; PMID:11743193
A;Accession: AG2893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: AG2893
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; C erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Ku ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.;
                                                              A;Cross-references: GB:Z77162;
A;Experimental source: strain F
                                                                                                      A; Molecule type: DNA
A; Residues: 1-249 <COL>
                                                                                                                                             A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                        A70745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Thes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: circular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE008688; IA;Experimental source: strain C58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-247 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Date: 11-Jan-2002 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein Atu2584 [imported] - Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens
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AG2893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE007869; PIDN:AAK88307.1; PID:g15157779; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-247 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: AGR_C_4681
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Best Local S
Matches 5
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  regulatory protein uxuR
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100.0%;
                                                              GB:AL123456;
H37Rv
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s; Pred. No. 2.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN: AAL43565.1; PID: g17741079;
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0; Mismatches
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                                                                                NID: g3261606;
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2.4e+02;
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2.4e+02;
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                                                                                                                                               translation not shown
                                                                                  PIDN:CAB00955.1; PID:g14492
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Score

5; DB

2:

Length

249;

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sporulated oocyst antigen TA4 precursor - Eimeria tenella (fragment) C. Species: Eimeria tenella (C. Species: Eimeria tenella (C. Species: O-oct-1994 #sequence_revision 15-Oct-1994 #text change 07-... C: Accession: A54501
                                                                                                                                    A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bioloc A;Reference number: A75000; MUID:905916; PMID:9851916
A;Reference number: A75000; MUID:905913; PMID:9851916
A;Note: see websites genome wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleA;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                             protein F53C3.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change
C;Accession: B88115
                                                                                                                                                                                                                                                                                                                                                                           в88115
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C;Superfamily: short-chain ATP-binding cassette
F;10-206/Domain: ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 08-Sep-2000
C;Accession: C72576
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A;Title: Characterization of a surface antigen of Eimeria tenella sporozoites and synthe A;Reference number: A54501; MUID:88261435; PMID:3290678
A;Accession: A54501
A;Cross-references: GB:chr_II;
C;Genetics:
                                           A; Molecule type: DNA
A; Residues: 1-244 <STO>
                                                                                         A; Accession: B88115
A; Status: preliminary
                                                                                                                                                                                                                                  R; anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy: A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: C72576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable glutamine transport ATP-binding protein APE1891 - Aeropyrum pernix (strain
C;Species: Aeropyrum pernix
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C72576
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C;Keywords: disulfide bond
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A; Residues: 1-230 < BRO>
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Matches 5; Conserv
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100.0%;
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                   PIDN:AC67455.1; PID:g3786482; GSPDB:GN00020; CESP:F53C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 2.2
0; Mismatches
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homology <ABC>
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A;Map position: X
A;Introns: 88/2; 103/3; 128/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F43B10:1
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T33469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Raccession: AG2071
R; Kaneko, T.; Wakamura, Y.; Wolk, C.P.; Kuritz, T.;
Nakaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, N
                                                                                                                                                                                                                                                                                                R; Fulton, R.; Hawkins, J.; Rohlfing, T. submitted to the EMBL Data Library, October 1998 A; Description: The sequence of C. elegans cosmid A; Reference number: Z21351 A; Accession: T33469
                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F43B10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;MoLecule type: DNA
A;Residues: 1-244 <KUR>
A;Residues: 1-244 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73824.1;
A;Experimental source: strain PCC 7120
                                                                                                                                                                                A; Gene: CESP:F43B10.1
                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                   A; Experimental source:
                                                                                                                                                                                                                                  A; Cross-references:
                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-247 <FUL>
                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T33469
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A; Gene: alr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: Nostoc sp. strain PCC 7120 is a synonym of C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001
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AG2071
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                                                                                                                                                                                                                                                                                A; Status: preliminary; translated
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                                                                 Matches
                                                                                  Query Match
Best Local
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162 SHLGP 166
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205-213, 2001
                                                               Similarity 5; Conserv
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                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                               EMBL:AF098500; PIDN:AAC67400.1; GSPDB:GN00028; CESP:F43B10.1 se: strain Bristol N2; clone F43B10
                                                               100.0%; P
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                                                          DB 2; L., No. 2.4e+02; 0;
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2
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2.3e+02;
0;
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#text_change 30-Jun-2002
                                                                                              Length 247
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probable pentose-5-phosphate-3-epimerase protein (EC 5.1.3.-) [imported] - Sinorhizobium C;Species: Sinorhizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: D95865
R;Finan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endd A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95865
A;Status: preliminary
A;Cross-references: GB:AL591985; PIDN:CAC48588.1; PID:g15140060; GSPDB:GN00167
A;Cross-references: GB:AL591985; PIDN:CAC48588.1; PID:g15140060; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Science 293, 668-672, 2001
A;Autbors: Kahn, D.; Kahn, M.; Kalman, S.; Keafing, D.H.; Kiss, E.; Komp, C.; Lelaure, A; Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Barloy-Bar
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Contents: annotation

C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable hypoersensitive response protein [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C; Accession: D85018 R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Col Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A; Reference number: A85001; MUID:20083488; PMID:10617198
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D95865
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A;Accession: A87094
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-224 <STO>
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A; Residues: 1-227 <STO>
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nes 5; Conserv
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0; Mismatches
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rumlp - fission yeast (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #te;
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #te;
C; Accession: T40233
R; Moreno, S: Wood, V: Rajandream, M.A.; Barrell, B.G
submitted to the EMBL Data Library, June 1998
A; Reference number: Z21915
A; Accession: T40233
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-230 < MOR>
A; Cross-references: EMBL:AL023796; PIDN:CAA19370.1; GS:
A; Experimental source: strain 972h-; cosmid c32F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Moreno, S.; Nurse, P.
Nature 367, 236-242, 1994
A;Title: Regulation of progression through the
A;Reference number: S41043; MUID:94166876; PMI
A;Recession: S41043
A;Rolecule type: DNA
A;Residues: 1-230 <MOR>
A;Cross-references: EMBL:X77730; NID:g456668;
A;Cross-references: EMBL:X77730; NID:g456668;
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C;Keywords: isomerase
                                                                                                                      A:Experimental source: strain C;Genetics:
A;Gene: SPDB:SPBC32F12.09
A;Map position: 2
C;Superfamily: Schizosaccharon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: ppe; SMb20195
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position:
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: rum1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: S41043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Schizosaccharomyces pombe
C; Date: 31-Mar-1992 #sequence_revision
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Best Local S
Matches 5
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Best Local S
Matches 5
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Best Local :
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5; Conserv
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Similarity 100.0%;
5; Conservative
                                                           Similarity
5; Conser
                                                                                                                         Schizosaccharomyces ruml protein
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Schizosaccharomyces ruml
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0; Mismatches
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Pred. No. 2.2e+02
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Pred. No.
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PMID:8121488
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                                                                                          Length 230
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hypothetical protein F48B9.5 - Caenorhabditis elegans
(;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000
C;Accession: T16393
R;Miller, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Bulones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.; submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, C.Y. A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa, A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei, M.F.; Marino, C.Y.; Savasa, A; M.F.; Marino, C.Y.; Savasa, A; M.F.; Marino, C.Y.; Savasa, A; M.F.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; M. Silva, M.R.; Verjovski-Almeida, S.; Vettore, A.L.; M. S
                                                                                                                                                                                                                                                                                                                                                  A; Introns: 23/3;
C; Superfamily: p
F; 97-215/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP:F48B9.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U40955; NID:g1072262; PID:g1072263; PIDN:AAA81747.1; CESP:F48B9C;Genetics:
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A; Residues: 1-214 <SIM>
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Pred. No.
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2.1e+02;
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ATP-dependent Clp proteinase proteolytic subunit [imported] - Mycobacterium C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 27-Nov-2001 C;Accession: A87094
                                                                                                                                                              R;Cole, S.T.; Eiglmeier, K.; Parkhill, R.; Davies, R.M.; Devlin, K.; Duthoy,
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C;Species: Pseudomonas aeruginusa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-D
C;Date: 100 #sequence_revision 15-Sep-2000 #text_change 31-D
C;Accession: H83475
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, .; Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                               R;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, J. Gen. Virol. 79, 1197-1203, 1998
A;Title: The DNA sequence of equine herpesvirus-4.
A;Reference number: Z22173; MUID:98264497; PMID:9603:
A;Accession: T42605
                                                                                                                                                                                                                                                                                                                                                                                        envelope protein - equine herpesvirus 4 (strain NS80567)
c;Species: equine herpesvirus 4
A;Variety: strain NS80567
c;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42605
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A;Experimental source:
C;Genetics:
                                                                                                                                                A;Gene: 62
C;Superfamily:
                                                                                                                                                                                                       A;Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AAC59581.1; A;Experimental source: strain NS80567
                                                                                                                                                                                                                        A; Residues: 1-219 <TEL>
A; Cross-references: EMBJ
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A; Residues: 1-218 <STO>
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Gene: 62
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ce: strain PAO1
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100.0%;
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                                                                                           .1e+02;
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Duthoy, S.;

J.; James, K.D.; S.; Feltwell, T.;

Thomson, Fraser, A

N.R.; Wheeler, A.; Hamlin, N.;

Holro

K.;

Simon, S.; Simmon leprosy bacillus

Simmonds,

Skelton,

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probable heme transport protein CCB206 - rape mitochondrion

N;Alternate names: HelB-homolog
C;Species: mitochondrion Brassica napus (rape)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 18-Aug-2000
C;Accession: T09503
R;Itanl, K.; Handa, H.
Curr. Genet. 34, 318-325, 1998
A;Title: Rapeseed mitochondrial ccb206, a gene involved in cytochrome c biogenes 206 locus.
A;Reference number: Z16701; MUID:99015983; PMID:9799366
A;Accession: T09503
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-206 <HAN>
A;Residues: 1-206 <HAN>
A;Gene: ccb206
A;Genome: mitochondrion
C;Function:
A;Description: involved in cytochrome c biogenesis
C;Superfamily: cytochrome c biogenesis protein CycW
C;Keywords: mitochondrion; RNA editing
hypothetical protein A133R - Chlorella virus PBCV-1
C. Species: Chlorella virus PBCV-1
C. Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C. Accession: T17623
R. Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A. Reference number: Z18806
A. A. Accession: T17623
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: DNA
                                                                                                                                                                              RESULT 91
T17623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein YPO4106 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AF0498
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Mature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-206 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC93555.1; PID:g15981995; GSPDB:GN00175 C;Genetics:
A;Gene: YPO4106
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A; Molecule type: DNA
A; Residues: 1-206 < KUR>
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o. 2e+02;
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5. 2e+02;
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ougan, G.;
Barrell,
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C;Superfamily:
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A; Status: preliminary
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A;Molecule type: nucleic acid
A;Residues: 1-208 <AJI>
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A48567
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A; Residues: 1-214 < KUR>
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A;Experimental source: specific host Chlorella strain NC64A C;Genetics:
A;Note: A133R
                                                                                                                                                                                                                                                                                                                                                                           A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AB2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L01583; NID:g162020; PIDN:AAA30171.1; A;Note: sequence extracted from NCBI backbone (NCBIN:123773; C;Superfamily: EF-hand protein EFH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A48567
R;Ajioka, J.; Swindle, J.
Mol. Biochem. Parasitol. 57, 127-136, 1993
Mol. Biochem. Parasitol. 57, 127-136, 1993
A;Title: The calmodulin-ubiquitin associated genes of Trypanosoma
A;Reference number: A48567; MUID:93149197; PMID:8381204
A;Accession: A48567
                                                                                                                                          A;Cross-references: GB:BA000019; PIDN:BAB74508.1; PID:g17131902; GSPDB:GN00179 A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sas
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Trypanosoma cruzi
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein alr2809 [imported] - Nostoc sp. (strain PCC 7120)
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100.0%; Pr
0;
                                                                                 hypothetical protein sll1186
                   33.3%;
100.0%;
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b; Score 5; DB 2
b; Pred. No. 2.1
0; Mismatches
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5. 2e+02;
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M.; Yamada, M.;
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NCBIP:123775)
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues; 1-201 < KUR>
A;Cross:references: GB:AE008688; PIDN:AAL41471.1; PID:g17738796; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Generics:
A;Gene: Atu0452
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Atu0452 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AI2631 R;Accession: AI2631 R;Wood, D.W;Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCleil Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                  ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Reference number: AB2577; PMID:11743193
A;Accession: AIZ631
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Best Local Similarity
Watches 5; Conserv
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J. Biol. Chem. 267, 20555-20557, 1992
A;Title: A novel laminin B1 chain variant in avian eye.
A;Reference number: A45067; MUID:93015947; PMID:1400373
A;Accession: A45067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:L00963; NID:g212883; PIDN:AAA49140.1; PID:g212884
A;Experimental source: eye
A;Note: sequence extracted from NCBI backbone (NCBIP:115996)
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide bon F;82-87/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                      A; Authors: Yoo, H.; Tao, ster, E.W.
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C;Species: Gallus gallus (chicken)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 10-Dec-1999
C;Accession: A45067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: nucleic acid
A; Residues: 1-198 <01R>
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                                            33.3%; Score 5; 100.0%; Pred. No.
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Pred. No. 1.9e+02;
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). 2e+02;
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RESULT
T09503
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                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:D84426; PIDN:BAA12352.1
A;Experimental source: cultivar Sekai-ichi; leaves
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T07771
R;Shikanai, T:; Nakata, S.; Harada, K.; Watanabe, K.
R;Shikanai, T:; Nakata, S.; Harada, K.; Watanabe, K.
Plant Cell Physiol. 37, 692-696, 1996
A;Title: Analysis of the heterologous transcripts of the highly edited orf206 in A;Reference number: Z16123; MUID:96416432; PMID:8819315
A;Reference number: Z16123; MUID:96416432; PMID:8819315
A;Accession: T07771
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T07771
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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C;Species: mitochondrion Lycopersicon esculentum (tomato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Jun-2000
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A; Residues: 1-206 <S
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A; Residues: 1-201 <STO>
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tive 0; Mismatches
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                                                                                                                                                                                                   DB 2;
o. 2e+02;
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.

ansen, N.F.; Hughes, B.; Hulzar, L.

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                 conserved hypothetical protein XF2007 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 03-Jun-2002 C;Accession: A85G13
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
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A;Molecule type: DNA
A;Residues: 1-189 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB35238.1; PID:g13361280;
A;Cross-references: strain O157:H7, substrain RIMD 0509952
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90855
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c;Species: Escherichia coli
c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
c;Accession: G90855
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa A; Reference number: A82515; MUID:20365717; PMID:10910347
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A;Molecule type: DNA
A;Residues: 1-189 <STO>
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Kasunaga, T.; Kuhara, S.;
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Shiba, T.; Hattori, M.;
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                                               A; Status: preliminary
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A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
awa, H.; Takamiya, M.; Masuda, DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequer A;Reference number: A72450; MUJA;Accession: B72471
                                                                                                                                                                     hypothetical protein APE2411 - Aeropyrum pernix (strain C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text C;Accession: B72471
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C;Species: Streptomyces coelicolor
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T28682
T. Doct-10: C D. Doct-10: C D. Doct-10: D C D. Date-dream M A
                                                                                                              R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanc
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A; Residues: 1-191 <SIM>
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A; Status: preliminary
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                                  sequence of an aerobic hyper-thermophilic Crenarchaeon,
50; MUID:99310339; PMID:10382966
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T.; Kudoh, Y.; Yamaz
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type: DNA: 1-197 <KP

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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-176 <OLI>A;Cross-references: EMBL:ALO49628; PIDN:CAB40883.1; GSPDB:GN00070; A;Experimental source: strain A3(2)
                                                                                                                                                               probable pantoate-amino acid ligase - Streptomyces coelicolor (fragment) C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Nov-2000 C;Accession: T36394 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajand R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajand Submitted to the EMBL Data Library, April 1999
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A; Accession: T36394
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C; Keywords:
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A;Title: Human placental sphingomyelinase. Purification
A;Reference number: S14747; MUID:91273814; PMID:2054099
A;Accession: S14747
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R; Kurth, J.; Stoffel, W.
Biol. Chem. Hoppe-Seyler
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C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
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Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75274
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A; Residues: 1-16; 17-32; 33-43; 44-57; 58-74; 75-84; 85-99; 100-107; 108-127; 128-138; 139-153; 154
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A; Experimental source: strain R1
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A; Residues: 1-173 <WHI>
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C.; M
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R;Madsen, C.; Graves, T.; Cotton, M.; Modde, submitted to the EMBL Data Library, July 199 A;Description: The sequence of A. thaliana F
                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F8M12.19 - Arabidopsis thallana (;Species: Arabidopsis thallana (mouse-ear cress) C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Mar-1999 C;Accession: T01887
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI1820
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A; Introns: 64/3;
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A; Accession: T01887
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A; Gene: alı
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A; Gene: SCC
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A; Residues: 1-183 < KUR>
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100.0%; Pr
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100.0%; Pred. No. 1.1
Live 0; Mismatches
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L.8e+02;
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#text_change 30-Jun-2002
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                                                                                                     Length 185
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Tabata
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glucokinase - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: I49694
C.Accession: I49694
R.Hughes, S.D.; Quaade, C.; Milburn, J.L.; Cassidy, L.; Newgard, C.B.
J. Biol. Chem. 266, 4521-4530, 1991
A.;Title: Expression of normal and novel glucokinase mRNAs in anterior pituitary and isle A;Reference number: I49694; MUID:91154262; PMID:1999433
A.;Accession: I49694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thom R.; Davles, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fras eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Authors: Rutter, S.; Seeger, K.; Simon S.; Simonds, M.;
A;Aritle: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: D87241
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D87241
VPS29-like phosphoesterase-related protein ML2654 [similarity] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-Aug-2001
C:Accession: D87241
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                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: somatic embryo C;Superfamily: transcription factor BTF3 C;Keywords: transcription factor
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A; Residues: 1-165 <BOR>
A; Cross-references: EMBL: Y09106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data A; Reference number: Z18621 A; Accession: T16984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription factor homolog BTF3 - curled-leaved tobacco C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change C;Accession: T16984
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A; Molecule type: DNA
A; Residues: 1-165 <STO>
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b; Pred. No. 1.6
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Best Local :
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submitted to the EMBL Data Library, July 1996
A;Description: The sequence of S. cerevisiae (
A;Reference number: S68471
A;Accession: S68480
A;Molecule type: DNA
A;Residues: 1-168 <VAU>
                                                                                                                                                                                                                                                                                                                                            N;Alternate names: hypothetical prot
C;Species: Saccharomyces cerevisiae
C;Date: 20-Jul-1996 #sequence_revis:
C;Accession: S68480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Hughes, S.D.; Quaade, C.; Milburn, J.L.; Cassidy, L.; Ne
J. Biol. Chem. 266, 4521-4530, 1991
A;Title: Expression of normal and novel glucokinase mRNAs
A;Reference number: I49694; MUID:91154262; PMID:1999433
A;Accession: I84740
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02
C;Accession: I84740
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C;Superfamily: hexokinase; hexokinase homology
F;25-166/Domain: hexokinase homology (fragment) <HXK>
                                                                                                                                                                                                        A; Cross-references: EMBL: U51921;
                                                                                                                                                                                                                                                                                                                                                                                                    succinate dehydrogenase homolog YLR164w - yeast N;Alternate names: hypothetical protein L9632.1
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nitrogen regulatory protein p-II [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 17-May-2002 C;Accession: A97573 R;Goodner, B.; Hinkle, G.; Gattung, S.: Miller N · Blanchard N · Communication of the comm
A;Title: Genome Sequence of the Plant Pathogen and A;Reference number: A97359; PMID:11743194 A;Accession: A95757 A;Status: preliminary
                                                                                                                                  R;Goodner, B.; Hinkle, G.; Gattung, S.;
A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: fetal kidney; clone DKFZp566F0546 C; Genetics: A; Note: DKFZp566F0546.1
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A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An: A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AD2345
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A; Residues: 1-150 <OTT>
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A; Accession: T08734
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R;Ottenwaelder, B.; Obermaier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: AL050075
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A;Molecule type: DNA
A;Residues: 1-145 <KUR>
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Pred. No.
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Database, May 1999
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Doughty, D.; Scott,
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; Scott, C.; Lappas, C.;
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30-Jun-2002
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Markelz, B.;
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; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, Jung, K.H.; Alam, M.; Freitas, T. 12176-12181, 2000 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; A; Title: Genome sequence of Halobacterium species NRC-1. A; Reference number: A84160; MUID:20504483; PMID:11016950 A; Accession: E84172
                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Vng0121h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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Best Local Similarity
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A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced
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DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: A71062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
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A71062
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A; Residues: 1-163 <STO>
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                                                                                                                                 A;Cross-references: GB:AE004437; NID:g10579769; PIDN:AAG18745.1;
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A; Residues: 1-160 < KAW>
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M.; Ohfuku, Y.; Funahashi, T.;
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Tanaka, T.; Kudoh, Y.;
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; Kushida, I
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RESULT 62
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A;Tille: Nucleotide sequence and organization of genes flanking A;Reference number: $22992; MUID:92190548; PMID:1665997
A;Accession: $23003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical cytosolic protein BMEI1918 [imported] - Brucella melitensis (st C;Species: Brucella melitensis C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C;Accession: AH3491
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghar Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Bruce A;Reference number: AD3252; PMID:11756688
A;Accession: AH3491
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-124 <AZES
A;Cross-references: EMBL:X76344; NID:g475914; PIDN:CAA53963.1; PID:g475915
C;Superfamily: human NADH dehydrogenase (ubiquinone) CI-B14 chain
C;Keywords: NAD; oxidoreductase
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C:Species: Escherichia coli
C:Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-134 <ZIE>
                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S23003
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A; Residues: 1-127 < KUR>
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O'Callaghan, F
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submitted to GenBank, June 2000

A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajina, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Swan A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva, A.C.R.; da Silva, A.M.; Silva, A.C.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., A.Reference number: A59328
                                                                                                                                                                                                                                                                                                            A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera A;Reference number: A84930; MUID:20445173; PMID:10993077 A;A;Accession: B84990
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A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-136 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50S ribosomal protein L16 [imported] - Buchnera sp. C;Species: Buchnera sp. C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
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A; Residues: 1-135 <S:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 [similarity] - Xylella C; Species: Xylella fastidiosa
                                                                                                      C; Superfamily:
                                                                                                                                                                                   A; Experimental source:
                                                                                                                                                                                                               A; Cross-references: GB:AP000398; GSPDB:GN00144
                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                          R;Shigenobu, S.; Watana
Nature 407, 81-86, 2000
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C; Superfamily:
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                                                                                                      Escherichia coli ribosomal protein
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11 ESRAA 15

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-102 cpg7
C; Superfamily: cytochrome c; cytochrome c homology
C; Keywords: acetylated amino end; chromoprotein; electron transfer; heme
F; 4-97, Domain: cytochrome c homology <CYC>
F; 1,4-97, Domain: cytochrome c homology <CYC>
F; 1,7 Modified site: acetylated amino end (Gly) #status experimental
F; 11,7 Binding site: heme (Cys) (covalent) #status experimental
F; 18,79/Binding site: heme iron (His, Met) (axial ligands) #status prediffers the company of the covalent of the cova
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-87 < KUR>
A; Cross-references: GB: AE008917; PIDN: AAL52655.1;
A; Cross-references: GB: AE018917; PIDN: AAL52655.1;
                                                     A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0318
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-105 <KUR>
A;Cross references: GB:AL590842; PIDN:CAC92849.1; PID:g15980593; GSPDB:GN00 C;Genetics:
A;Gene: YP02606
C;Superfamily: Escherichia coli ybeB protein
                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein YPO2606 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0318
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, I.M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
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cytochrome c [validated] - Euglena gracilis
C;Species: Euglena gracilis
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change
C;Accession: A00068
R;Pettigrew, G.W.; Leaver, J.L.; Meyer, T.E.; Ryle, A.P.
Biochem. J. 147, 291-302, 1975
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  Query Match
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S43840
                    R;Azevedo, J.E.; Eckerskorn, C.; Werner, S.
Blochem. J. 299, 297-302, 1994
A;Title: In organello assembly of respiratory-chain complex I: primary structure
A;Reference number: S43840; MUID:94220045; PMID:8166654
                                                                                                                                     C;Species: Neurospora crassa
C;Date: 13-Jan-1995 #sequence_revision 13-Mar-1997
C;Accession: S43840
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A; Residues: 1-122 < XUW>
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A; Residues: 1-118 <VRI>
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C;Species: Halobacterium salinarum C;Date: 05-Jun-1987 #sequence_revision C;Accession: A05114
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A;Action of the methylotrop
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C;Accession: S70089
R;Vrijbloed, J.W.; Jelinkova, M.; Hessels, G.I.; Dijkhuizen, Mol. Microbiol. 18, 21-31, 1995
Mol. Microbiol. 18, 21-36 the minimal replicon of plasmid p
                                                                                                                                                                                                                       Nucleic Acids Res. 11, 4195-4199, 1983
A; Reference number: A93475; MUID:83246542;
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Nucleic Acids Res. 11, 4195-4199,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Amycolatopsis methanolica
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
                                                                                          A; Mobile element: insertion sequence ISH50
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                                                                                                                             -references: GB:X01584; NID:g43515; PIDN:CAB37935.1; PID:e1390961; PID:g446743 the source is designated as Halobacterium halobium
                                                                                                                                                                                                                                                                                                                                       protein E-122 - Halobacterium salinarum insertion sequence ISH50
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Conservative
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100.0%; Pr
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Pred. No.
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(EC 1.6.5.3) - Neurospora crassa

#text_change 03-Jun-2002

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RESULT 200
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ID 079373
AC 079373
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OS Brassi
OG Mitoch
OC Eukary
OC Sperma
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Search completed: March 10, Job time: 94 secs
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Best Local Similarity 100.
Matches 5; Conservative
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Shikanai T., Nakata S., Harada K., Watanabe K.;
Shikanai T., Nakata S., Harada K., Watanabe K.;
"Analysis of the heterologous transcripts of the highly edited orf206
in tomato mitochondria.";
Plant Cell Physiol. 0:0-0(1996).
EMBL; D84426; BHA12352.1;
InterPro: IPR003544; Cytc_biog_CcmB.
Pfam; PF03379; CcmB; 1.
PRINTS: PR01414; CCMBBIOGNSIS.
Mitochondrion.
SEQUENCE 206 AA; 23069 MW; 381F42431443295D CRC64;
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01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. ISUZU-NATANE; TISSUE-LEAF; Itani K., Handa H.; Itani K., Handa H.; "Rapeseed mitochondrial ccb206, a gene involved in cytochrome c biogenesis is cotranscribed with the nad3 and rps12 genes: organization, transcription, and RNA editing of the nad3/rps12/ccb206 locus.";
                                                                                                                                                                                                        Mitochondrion.
SEQUENCE 206 AA;
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EMBL; D13697; BAA32558.1; -.
InterPro; IPR005544; Cytc_biog_CcmB.
Pfam; PF03379; CcmB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica napus (Rape).
Mitochondrion.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eparmatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Brassicales; Brassicaceae; Brassica.
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46 SHLGP 50
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                2003, 14:29:57
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08, Last sequence update)
21, Last annotation update)
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RESULT 108
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines of peptide therapy. The polypeptides have various cytokine-like activities e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity/insurance growth factor activity, immunomodulatory activity and activity/insurance growth factor activity, the diagnosis and/or
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colypeptide (II) sequences. (II) is useful as hybridisation probes, colymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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upplement; medical imaging; diagnostic; genetic
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                      (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding a priners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in trading disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chrome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                  polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
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CC Specification, but was obtained in electronic format directly from WIPO
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food supplement; medical imaging; diagnostic; genetic disorder.
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     CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC diagnostics, forensics, gene mapping, identification of mutations
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                           diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
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Pred. No.
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167 AA

Query Match Best Local Similarity

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed cat for wino intromblable of in electronic format directly from WIPO at fraction, but was obtained in electronic format directly from WIPO at fraction.
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Best Local 9
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23-AUG-2000; 2000US-0649167
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food supplement; medical imaging; diagnostic; genetic disorder.
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ftp.wipo.int/pub/published_pct_sequences
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CC Note: The sequence data for this patent did not appear in the printed CC at fip.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID No 36597; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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N-PSDB; AAS70425.
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23-AUG-2000;
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upplement; medical imaging; diagnostic; genetic disorder.
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2000US-0649167
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                                          40.0%; Score 6;
100.0%; Pred. No.
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5. 60;
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ABG28263
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                                                                                                                                                                                                    CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, cligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II), (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II), (I) and (II) are useful in redical CC disgonstics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations compositions, for enettic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed content wince in the number of the formal of the polypear of the invention.
                                                                Matches
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                 Sequence
                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 58622; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #28254.
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3 LGPHRS
                                                                                    Local
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                                                            Similarity 6; Conserv
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                                                            Conservative
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medical imaging; diagnostic; genetic disorder.
                                                     40.0%; 5c.
100.0%; Pr
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LGPHRS

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                                                                                                                                                                                                   polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                             Matches
                                                                            Query Match
Best Local
                                                                                                                           Sequence
                                                                                                                                                                        Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity
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23-AUG-2000, 2000US-0649167.
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 181
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                              3 LGPHRS 8
                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
LGPHRS 186
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                                                            Similarity 6; Conserv
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                                                                                                                             205
                                                             Conservative
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medical imaging; diagnostic; genetic disorder.
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RESULT 120
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AAB65725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   programmed cell death (PCD; apoptosis). The coding sequences and proteins of the present invention are useful for modulating a PCD or cell death pathway and various developmental pathways in a forestry plant, by stably incorporating one of the present coding sequences into the genome of the forestry plant, where the coding sequence provides a PCD pathway that is not present in a native form of the forestry plant.
Prediction; secondary structure; alignment; evolutionary conservation; homology; periodicity; co-variation analysis; antigenic site; site directed mutagenesis; interaction.
                                                                                     Mouse
                                                                                                                               21-DEC-1999
                                                                                                                                                                         AAY43977
                                                                                                                                                                                                                   AAY43977 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22; Pages 67-68; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel defender against cell death polynucleotide useful for modulating programmed cell death pathway and specific development pathways in forestry plant -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flinn B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell death modulator; programmed cell death; PCD; apoptosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           forestry plant.
                                                                                                                                                                                                                                                                                                                          184 PESRAA 189
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DB; AAF44751.
                                                                                     protein kinase
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RESULT 121
ABG08486
ID ABG084
XX ABG084
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AC NOVe1
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KW Food s
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Best Local
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     N-PSDB; AAS72673.
                              WPI; 2001-639362/73
                                                                                   Drmanac RT,
                                                                                                                                                                                                                      31-MAR-200
                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG08486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG08486 standard; Protein; 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BENN/) BENNER S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1992;
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                                                                                                                                        (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #8477.
                                                                                                                                                                                             23-AUG-2000)
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                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                      2000US-0540217
                                                                                                                                                                                             2000US-0649167
                                                                                                                                  NC.
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100.0%;
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Pred. No.
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RESULT 122
AAW24231
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and to produce other types of data and products dependent on DNA and amino acid sequences. AB600010-AB630377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique
                                                                                                                                                                                                                                                                                                                     MADER protein; growtl cancerous condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 38845; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                    07 - AU
                                                                                                                                                                                                                                      WO9₹28193-A1
                                                                                                                                                                                                                                                                                                     MADER antigen.
                                                                                                                                                                                                                                                                                                                     Melanoma associated delayed early response gene; MADER gene; MADER protein; growth alteration; malignant melanoma; breast cancerous condition; MADER translocation event; MADER immuno
                                                                                                                                                                                                                                                                                                                                                                                         Human melanoma associated delayed early response splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW24231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                               Johnson JP;
                                                                                 (MELC-) MELCORP
                                                                                                                   30-JAN-1996
                                                                                                                                    30-JAN-199
                                                                                                                                                                  30-JAN-1997;
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW24231 standard; Protein; 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 PHRSTP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PHRSTP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                    -1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                   96US-0593563
                                                                                                                                  97US-0593563
                                                                                                                                                                    97WO-US01586
                                                                                 DIAGNOSTICS
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Pred. No.
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96;
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                                                                                                                                                                                                                                                                                                                         MADER immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                       breast carcinoma;
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WPI; 1997-402557/37

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RESULT 123
AAW31903
ID AAW3199
XX AAW3199
XX AAW3199
XX 28-APR
XX Strept
XX Histin
KW Pneumo
KW Pneumo
KW Pneumo
KW Pneumo
XX Strept
XX W09739
XX 18-APR
XX 18-APR
XX 18-APR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
                        N-PSDB; AAT88770.
                                                             WPI; 1997-526393/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Histidyl trnA synthetase; hisS polypeptide; genetic immunisation; vaccine; antibacterial; antibiotic; otitis media; conjunctivitis; pneumonia; bacteraemia; meningitis; sinusitis; pleural emphysema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus
                                                                                                                                                                                                                                                                          18-APR-1996
                                                                                                                                                                                                                                                                                                                                     18-APR-199
                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      w09739Q17-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae histidyl tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 RSTPES
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                                                                                                                          EJ;
                                                                                                                                                                                 SMITHKLINE
SMITHKLINE
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                                                                                                                                                                                                                                                                       96GB-0007993.
                                                                                                                                                                                                                                                                                                                               97WO-US06877.
                                                                                                                                                                                 BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 369
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100.0%;
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RESULT 124
AAW24229
ID AAW242
XX AAW242
XX Human
DE Human
XX Melano
KW MADER
KW Cancer
KW MADER
XX Homo s
XX Homo s
XX Wo9228
PT Region
FT Region
XX WO9228
PM W09228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  directed towards Streptococcus pneumoniae infections causing otitis media, conjunctivitis, pneumonia, bacteraemia, meningitis, sinusitis, pleural emphysema and endocarditis. Hiss polypeptides, or vectors for their expression, can be used prophylactically in vaccines to raise an antibody and/or T cell immune response against these same diseases. Additionally, the new polypeptides allow agonists and antagonists of hiss to be identified wising standard binding assays. The compounds which are identified may have useful bacteriostatic and/or bacteriocidal activity. Antibodies against hiss can used to treat infection, isolate or identify hiss expressing clones, purify hiss and as an immunoassay reagent. More generally, the products can prevent adhesion of bacteria to wounds and in-dwelling devices, block hiss protein mediated invasion of mammalian cells and block the normal progression of infection.
                                                                                WPI; 1997-402557/37.
N-PSDB; AAT77839.
                                                                                                                                                                Johnson JP
                                                                                                                                                                                                                                                                         30-JAN-1996
                                                                                                                                                                                                                                                                                                  30-JAN-1997
                                                                                                                                                                                                                                                                                                                                                       30-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                            07 - AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MADER protein; growtl cancerous condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Melanoma associated delayed early response gene; MADER gene; MADER protein; growth alteration; malignant melanoma; breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human melanoma associated delayed early response Drop8 variant protein
                                                                                                                                                                                                                  (MELC-) MELC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₩09%28193-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MADER antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW24229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW24229 standard; Protein; 411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the histidyl tRNA synthetase (hiss) from Streptococcus pneumoniae 0100993 (NCIMB 40800). The hiss polypeptides, antagonists, antibodies and related nucleic acids can be used for diagnosis and treatment of bacterial diseases. In particular, they are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding histidyl-trna synthetase from Streptococcus pneumoniae - useful for protection against bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12;
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                                                                                                                                                                                                                                                                                                                                                                                                         1997.
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                                                                                                                                                                                                                                                                       97US-0593563
96US-0593563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 246..260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.0%; >--
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MADER translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "bipartite nuclear localisation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18; L
). 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                event; MADER immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 369
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Monoclonal antibody which binds to the MADER protein - detecting cancerous conditions, such as breast carcinon

as breast carcinoma

used for

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RESULT 125
AAU27706
ID AAU277
XX AAU277
XX AU277
XX Human
XX Human
XX Mammal
KW Mouse;
KW Cancer
KW Anglog
KW Anglog
KW Anglog
KW Anglog
KW Oytost
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KW Anglog
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XX 25-FEI
XX 28-FEI
PR 28-FEI
PR 18-MA)
PR 11-JUI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia; cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation; nervous system disorder; inflammatory disorder; cell differentiation; angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; bone regeneration; tendon; ligament; tissue repair; cytostatic; antirheumatic; antiarthritic; yulnerary; antinflammatory;
                                                                                                                                                28-FEB-2000, 2000US-0515126, 18-MAY-2000; 2000US-0577409, 17-JUN-2000; 2000US-0597707, 14-JUL-2000; 2000US-0516807
         Tang YT,
                                                                                                                                                                                                                                                                                                                                                                  07-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibacterial; immunosuppressive; vasotropic;
neuroprotective; osteopathic; antidiabetic; ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human full-length polypeptide sequence #31.
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                                                             (HYSE-) HYSEQ
                                                                                                                           19-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunostimulant; analgesic; gene therapy.
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6; Conserv
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      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411
                                                                                                                  2000US-0577409
2000US-0597707
2000US-0616807
2000US-0664641
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      Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 415
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      Asundi V,
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Pred. No.
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   Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        c; antiparkinsonian;
antiasthmatic; anti
   'n,
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      Zhao
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      QA,
      Ren
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27-OCT-2000; 2000GB-0026333. 24-NOV-2000; 2000GB-0028727. 07-MAR-2001; 2001KB-0005640.

29-OCT-2001 02-MAY-

2001WO-GB04789

Streptococcus pyogenes

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ABP27
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Best Local
                                                                                                                                                                                                       Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in arrays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xue AJ,
Drmanac
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                                                                                                                                                                                                                                                                                                                                                                         ABP27059 standard; Protein; 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSTPES
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)B; AAS44606.
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100.0%; Pr
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Pred. No.
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.3e+02;
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Best Local (
     WPI; 1998-466670/40
                                                       Gentry DR,
                                                                                                                                                      06-AUG-1997;
18-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromosography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for
                                                                                                                                                                                                                                      06-AUG
                                                                                                                                                                                                                                                                                      18-XUG-1998
                                                                                                                                                                                                                                                                                                                                        US5795758-A
                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                       Histidyl tRNA synthetase; hiss; infection; Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Histidyl tRNA synthetase of Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW70983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 3483; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus protein for the treatment or prevention of info
or disease caused by Streptococcus bacteria, such as meningitis,
for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW70983 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus
                                                                                                    (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for detecting a compound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Telford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 PESRAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PESRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-352536/38
                                                                                                                                                                                                                                   -1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conserv
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INST GENOMIC
                                                                                                       SMITHKLINE BEECHAM CORP.
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                                                       Greenwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetase; hiss; S.
                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              relates to a protein (ABP25413-ABP30895)
                                                                                                                                                      97US-0906744.
97US-0844055.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.0%;
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                                                       RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             that binds to the protein
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                                                       Lawlor EJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               equisimilis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23; I
b. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 426;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
This sequence represents a Streptococcus pneumoniae histidyl tRNA synthetase (hiss) amino acid sequence. tRNA synthetases have a primary role in protein synthesis, and inhibitors of bacterial
                                                                                   Histidyl t-RNA synthetase enzyme from streptococcus genus useful for treating diseases such as otitis media, conjunctivitis, pneumonia, bacteraemia, meningitis, sinusitis, pleural empyema and endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                            Histidyl tRNA synthetase; conjunctivitis; bacteraem:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a Streptococcus pneumoniae histidyl trNA synthetase (his5). The protein has homology to a S. equisimilis his5 protein. Fragments of hiss that retain binding and/or catalytic properties are used for research as novel targets against S. pneumoniae. The hisS nucleic acid sequence (and primers and probes derived from it) are used to isolate related genes, to diagnose disease, specifically S. pneumoniae infection (e.g. otitis media, pneumonia, conjunctivitis, osteomyelitis or especially meningitis, possibly also infections by Helicobacter pylori and associated tumours), to identify mutations or polymorphisms for serotyping, and antisense sequences are potential
                                                           Claim
                                                                                                                                               N-PSDB; AAZ98858.
                                                                                                                                                                                                                                                  06-AUG-1997;
18-APR-1997;
                                                                                                                                                                                                                                                                                           08-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                      US6040162-A
                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Histidyl tRNA synthetase (hisS) amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY85136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding Streptococcus pneumoniae histidyl tRNA synthetase - useful for recombinant production of the enzyme diagnosis, treatment and prevention of Streptococcus infecti
                                                                                                                                                                                          Lawlor EJ,
                                                                                                                                                                                                                                                                                                                         21-mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV42887
                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for screening of inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 PESRAA 176
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                                                                                                                                                            2000-270137/23.
                                                        1; Column 7-8; 16pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 429
                                                                                                                                                                                        Gentry DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              s; bacteraemia; hiss.
                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AΑ;
                                                                                                                                                                                                                                                  97US-0906744
97US-0844055
                                                                                                                                                                                                                                                                                              98US-0093134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.0%; Su
100.0%; Pr
0;
                                                                                                                                                                                          Greenwood
                                                                                                                                                                                                                                                                                                                                                                                                                          protein synthesis; otitis media; pneumonia;
ia; meningitis; sinusitis; pleural empyema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 6; DB 1; Pred. No. 1.3
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
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C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid sequence
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.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the enzyme in cus infections,
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of bacterial tRNA

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Best Local
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tRNA synthetase polypeptide sequence of the invention is useful for treating diseases such as otitis media, conjunctivitis, pneumonia, bacteraemia, meningitis, sinusitis, pleural empyema and endocarditis. The protein can also be used to treat infections of the cerebrospinal fluid. The nucleotide sequence encoding the histidyl tRNA synthetase enzyme is useful for therapeutic and prophylactic treatments, particularly for the nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU37913 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR 2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200170955-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 PESRAA 176
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                                                                                                                                                                                                                                                                                                                                                                             polynucleotides for the identification and lbiotics, comprise sequences of antisense nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-611495/70.
DB; AAS55772.
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6; Conser
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2000US-207727P.
2000US-24257BP.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                      511pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wall
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                                                                                                                                                                                                                                                                                                                                                                             nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for homologous nucleic acids which are required for cell prol a wide variety of organisms. The present sequence represents essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                 Monoclonal antibody which binds to the MADER protein detecting cancerous conditions, such as breast carcin
                                                                                                                                N-PSDB;
                                                                                                                                                              Johnson JP;
                                                                                                                                                                                                    30-JAN-1998
                                                                                                                                                                                                                                   30-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                  MADER
                                                                                                                                                                                                                                                                                                                                                                                                           Melanoma associated delayed early response gene; MADER gene; MADER protein; growth alteration; malignant melanoma; breast cancerous condition; MADER translocation event; MADER immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human melanoma associated delayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW24228 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation is
                                                                                                                                                                                  (MELC-) MELCORP
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DB; AAT77838.
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96US-0593563
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                                                                                                                                                                                                                                                                                                        /note=
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246..2
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                                                                                                                                                                                                                                                                                              "N-terminal region"
                                                                                                                                                                                                                                                                                                                 "bipartite nuclear localisation signal"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                             immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                      breast carcinoma;
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The present sequence represents a novel melanoma associated delayer early response (MADER) protein. This 55 km nuclear protein is associated growth alterations in malignant melanomas and other cancerous conditions, and is over-expressed in human malignant melanomas. Sev variants of the protein have been identified (AAW24229-31), the preprotein being the Drop9 variant. The protein contains repeat motifs are characteristic of gene regulatory NNA hinding protein.

motifs which

Several

associated

Claim 31;

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RESULT 131
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Best Local
                                                      The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rearrangement of MADER can be detected by hybridising immobilised chromosomal target DNA, that has been rendered single stranded and is obtained from a cell suspected of having undergone a MADER translocation event with a single stranded oligonucleotide probe complementary to a MADER nucleotide sequence. The probe contains a moiety capable of direct or indirect visualisation. Antibodies raised against the MADER protein can be used for detecting a cancerous condition, particularly melanoma malignancies, and especially a breast carcinoma. A composition comprising a MADER immunogen and a pharmaceutically acceptable vehicle can be used to elicit an immune response against a cell which over-expresses a MADER antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinfertility;
neuroprotective;
explessed sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated polynucleotide for treating diseases associated with encoded polypeptide such as cancer and multiple sclerosis \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABN32390
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fertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Liu C,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                             2; SEQ ID NO 472; 509pp; English.
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6; Conserv
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            479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zhou P,
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c RT;
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b. 1.4e+02;
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05-MAY-1999;
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05-MAR-1999;
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23-MAR-1999;
25-MAR-1999;
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08-APR-1999;
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23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic hypridisation assay; genetic mapping; gene expression control;
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99US-0131449.
99US-0132048.
99US-0132484.
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99US-0132486.
99US-0134218.
99US-0134218.
99US-0134219.
99US-0134768.
99US-0134768.
99US-0135124.
99US-013552.
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99US-0130077.
99US-0130449.
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Pred. No. 1.5
0; Mismatches
                                        .5e+02;
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                                                                                                                                                                                                                                                                                                                  The present sequence represents a novel melanoma associated delayed CC early response (MADER) protein. This 55 kDa nuclear protein is associated CC with growth alterations in malignant melanomas and other cancerous CC conditions, and is over-expressed in human malignant melanomas. Several CC variants of the protein have been identified (AAW2428-31), the present CC protein being able to bind erg-1 and inhibit its activity. Chromosomal CC rearrangement of MADER can be detected by hybridising immobilised CC chromosomal target DNA, that has been rendered single stranded and is CC obtained from a cell suspected of having undergone a MADER translocation CC event with a single stranded oligonucleotide probe complementary to a CC MADER nucleotide sequence. The probe contains a moiety capable of direct CC indirect visualisation. Antibodies raised against the MADER protein CC can be used for detecting a cancerous condition, particularly melanoma CC malignancies, and especially a breast carcinoma. A composition comprising the clinity and the contains a moiety capable of the can be used for detecting a cancerous condition, particularly melanoma CC malignancies, and especially a breast carcinoma. A composition comprising the contains a moiety capable of the contains a moiety capable of the capable of the contains and especially a breast carcinoma. A composition comprising the contains a moiety capable of the contains and especially a breast carcinoma.
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Best Local
ABG04560 standard; Protein; 543
                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-402557/37.
N-PSDB; AAT77840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MADER antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Melanoma associated delayed early response gene; MADER gene; MADER protein; growth alteration; malignant melanoma; breast carcinoma; cancerous condition; MADER translocation event; MADER immunogen;
                                                                                               188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnson JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MELC-) MELCORP DIAGNOSTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-1997;
30-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human melanoma associated delayed early response variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-1998 (first entry)
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                                                                                                                                                                        Local Similarity
nes 6; Conserv
                                                                                                                                   7 RSTPES 12
                                                                                                                                                                                                                                                                                                    elicit an immune response against a cell which over-expresses a
                                                                                                                                                                                                                                                    525 AA;
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 3; 69pp; English.
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96US-0593563.
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Pred. No.
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o. 1.5e+02;
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                                                                                                                                                                                                                                                                         The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
ABB93594;
                               ABB93594 standard; Protein; 614 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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N-PSDB; AAS68747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000;
23-AUG-2000;
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                                                                                                              SHLGPH
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supplement; medical imaging; diagnostic; genetic disorder.
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2000US-0649167.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                              EP1108790-A2
                                                                                                                                                                                                                                             organic acid
                                                                                                                                                                                                                                                                      Coryneform bacterium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG93019 standard;
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16-DEC-1999;
                                                18-DEC-2000
                                                                                                20-JUN-
                                                                                                                                                                                               Coxynebacterium
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                                                                                                                                                                                                                                             synthesis
                                                                                                                                                                                                                                                                                                                 protein
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                                                2000EP-0127688.
99JP-0377484.
                                                                                                                                                                                            glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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100.0%;
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                                                                                                                                                                                                                                                                      acid synthesis; vitamin;
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Pred. No. 1.8
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                                                                                                                                                                                                                                                                                                                       ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23; Le
b. 1.8e+02;
                                                                                                                                                                                                                                                                                                                         6773
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RESULT 137
ABP2714
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Best Local
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                                                                                                                               27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
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Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. 'are useful for identifying the mutation point of a gene derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifunctation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous
                                                                                                                                                                                                                                   29-OCT-2001;
                                                                                                                                                                                                                                                                                       02-MAY-2002
                                                                                                                                                                                                                                                                                                                                          WO200234771-A2
                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus agalactiae
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03-AUG-2000;
                                                (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
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DB; AAH68238.
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6; Conserv
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                                                                                                                               ; 200008-0026333.
; 2000GB-0028727.
; 2001GB-0005640.
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Senoh A, Ikeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000JP-0159162
2000JP-0280988
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da M,
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b; Pred. No. 2.1
0; Mismatches
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Ozaki A;
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40. 2.1e+02;
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Telford J, Masignani V,

Margarit Ros YI,

Grandi G,

Fraser

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RESULT 138
AAY28935
ID AAY289
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XX JPlly
PD 13-JUL
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PF 26-DEC
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PR WPI; ]
DR WPI; ]
DR WPSDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for
                                                                                                                                                                                                                                                                                                                                                           Chimera gene; chromosome translocation; t(5;14)(q33;q32); CEV14 gene; platelet-derived growth factor beta receptor; PDGFR-beta.
                                   Claim 6;
                                                                                                                                                                                           26-DEC-1997
                                                                                                                                                                                                                          26-DEC-199
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                                                                                                                                                                                                                                                                                            JP11187885-A
                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                     (MITP ) MITSÜBISHI YUKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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350 TPESRA 355
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                                                                    DNA - and sensitive method for its
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                                                                                                                       1999-451550/38
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DB; ABN68032.
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6; Conserv
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                               Page 10-13; 13pp; Japanese
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                                                                    detection
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The invention

describes a

new DNA containing

a chimera

gene

specific

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RESULT 139
AAM93437
ID AAM934
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XX AAM934
XX Human |
DT 06-NOV
XX Human;
XX Homo s
XX Ho
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Best Local
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the chromosome translocation t(5;14)(q33;q32) formed by fusing the CEV14 gene (1-287 basepairs of the present sequence) with a platelet-derived growth factor beta receptor (PDGPR-beta) gene. A method for the detection of a chimera gene produced by t(5;14)(q33;q32) in a sample by preparing cDNA from the DNA or mRNA in the sample as the template and using an oligonucleotide designed to bind the CEV14 gene region of the above chimera and an oligonucleotide designed to bind the PDGPR gene region as the primers and detecting the amplified product formed by the PCR is also provided. The method can detect a gene specific to the presence of t(5;14)(q33;q32) specifically at a high sensitivity. The present sequence represents the PDGFR-beta sequence.
                                                molecules have been determined. Primers for synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed sequence is the production of the printed sequence.
                                                                                                                                                                                                                                                                           The invention relates to primers for synthesising full length cD clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                            specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           830 Primers useful for synthesizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; full length cDNA; cDNA synthesis; oligo-capping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM93437 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SHLGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                  in genetic manipulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-524255/58
DB; AAK94358.
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                                                                                                                                                                                                                                                                                                                                                                                              8; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            821
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; 2000JP-0118774.
; 2000JP-0183765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugiyama
                               but was obtained in CD-ROM format directly
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                                                                                                                                                                                                                                                                                                                                                                                           NO 3074; 1380pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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a T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                853
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3074.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi K,
K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           full length cDNA clones and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20; L
2.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Otsuki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawai Y;
                               from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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RESULT 140
AAR3019
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XX AAR301
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                                                                                                                  Query Match
Best Local (
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Best Local :
                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                        The MDV gBh of HSV from a BamHI 13 (5.2kb) and K3 (3.6kb) fragment of MDV GA strain was cloned into pUC18. A 2.8kb BamHI-SalI subfragment from 13 fragment and a 1.1kb BamHI-ECORI subfragment from K3 fragment were ligated with EcoRI, SalI digested pUC18. The sequence of the putative MDV gBh was determined by sequencing a set of deletion mutants. The nucleotide and amino acid sequences were found to be identical with the published sequences of the gBh of MBV (Ross etal., J.Gen.Vicol., 70:179-1894, 1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marek's Disease Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fowlpox virus;
Herpes Simplex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marek's Disease Virus glycoprotein B homologue of HSV
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                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee LF,
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(USDA )
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10-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-1992;
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174 TPESRA 179
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                                                                                                                                                                                                                                    fragment contg. the entire coding region of MDV gBh was inserted nto pNZ1729R (see AAQ34774-Q34778) to produce a recombinant FPV/MDVgBh irus for immunising chickens. See also AAQ34780-Q34781.
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                                               9 TPESRA 14
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                                                                                            6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L1 Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 15-19; 30pp; English.
                                                                                                                                                                                          865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fowl pox virus contg. Marek's disease virus antigen to produce cell-free vaccine against Marek's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.0%;
ilarity 100.0%;
Conservative (
                                                                                                 Conservative
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Virus.
                                                                                                                                                                                          B
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91US-0803633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                  40.08;
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0; Mismatches
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                                                                                                                  Score 6; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ogawa R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDV; gBh; recombinant virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                              Mismatches
                                                                                                                  DB 14; L
5. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yanagida N;
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                                                                                                                                        Length 865;
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RESULT 141 AAW36051

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RESULT 142
ABG20753
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                             Fusion protein comprising herpes virus outer membrane protein and antigenic polypeptide - for prevention of infection by Mycoplasma gallisepticum, especially in poultry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen;
                     Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                  ABG20753;
                                                                                                                        ABG20753 standard; Protein; 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09738924-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hybrid Marek's disease virus/M.
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Homo sapiens
                                                     Novel human diagnostic protein #20744.
                                                                             18-FEB-2002
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 22-30; 51pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (JAPG ) NIPPON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-1996;
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                                                                                                                                                                                 174 TPESRA 179
                                                                                                                                                                                                      9 TPESRA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1997-503046/46
                                                                                                                                                                                                                           Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsuzaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marek's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marek's disease gammaherpesvirus Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                         1086 AA;
                                                                                                                                                                                                                            Conservative
                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-JP01084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96JP-0103548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "derived from Marek's disease virus 693..1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
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S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 poultry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease virus; outer membrane protein; fusion
                                                                                                                                                                                                                        40.0%; 50
100.0%; Pr
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yanagida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "derived from M. gallisepticum antigen"
                                                                                                                                                                                                                                      Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gallisepticum 40 K-C protein.
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                        DB 18; I
                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                               Length 1086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gB protein*
                                                                                                                                                                                                                            0
                                                                                                                                                                                                                            Gaps
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RESULT 143
ABB57338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags (CC for identifying expressed genes. (I) is useful in gene therapy techniques (CI). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical classified of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity amino acid sequences or other traits to assess biodiversity amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed constitution, but was obtained in electronic format directly from WIPO at the content of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
WO200188188-A2
                                         Mus musculus
                                                                                                                                                                                                07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                         Mouse; ischaemia;
                                                                                                                                                Mouse ischaemic condition related protein sequence SEQ ID NO:943.
                                                                                                                                                                                                                                             ABB57338
                                                                                                                                                                                                                                                                                ABB57338 standard; Protein; 1098 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                    vasospastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymerase chain reaction (PCR) primers, oligomers, and and gene mapping, and in recombinant production of (II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS84940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-0CT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                656 SHLGPH 661
                                                                                                                                                                                                                                                                                                                                                                                                                         1 SHLGPH 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID No 51112; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1089 AA;
                                                                                  ischaemia; ischaemic condition; ischaemic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INC.
                                                                                                         compressive ischaemia; occlusive ischaemia;
                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 6; |
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; L
.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 144
AAP90646
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                                                                                                                                                                                                                                                                                                                                             δÃ
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Best Local
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Region
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in AB57020 to AB59714) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                   Region
Region
Region
                                                                                                    Key
                                                                                                                                                  cancer;
                                                                                                                                                                                            Human platelet-derived growth factor receptor
                                                                                                                                                                                                                                           AAP90646;
                                                                                                                                                                                                                                                               AAP90646 standard; protein; 1106
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-NO
                                                                                                                            Homo sapiens
                                                                                                                                                              and antagonist
                                                                                                                                                                                                                     20-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for examining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishikawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYNI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-2
                                                                                                                                                                                                                                                                                                                         655 SHLGPH
                                                                                                                                                                                                                                                                                                                                             1 SHLGPH 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-034733/04.
DB; ABI99825.
                                                                                                                                                                        platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Page 2387-2392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -2001
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                                                                                                                                                                                                                                                                                                                                                                   Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001;
                                                                                                                                                 genetic disorders; antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00;
                                                                                                                                                                                                                                                                                                                                                                                                              1098
                                                                                                                                                                                                                                                                                                                         660
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                           (human).
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-JP04192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000JP-0145977.
                                                                                                                                                            derived growth factor receptor; drugs; wound healing; prevents a
  215
230
292
307
354
371
                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takahashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                              Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              . DB
                                                                                                                                                                                                                                                                                                                                                               2.9e+02;
0;
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                                                                                                                                                              atherosclerosis;
                                                                                                                                                                        agonist
                                                                                                                                                                                                                                                                                                                                                                                        Length 1098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishii Y;
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ischaemic
of particular
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RESULT 145
AAP90127
ID AAP901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human platelet derived growth factor receptor (see AAN90388) for features). Used to make probes and antibodies, and to evaluate drugs. The regions specified are potential N-glycosylation sites, and the domain is a transmembrane sequence.
Secreted ligand-binding receptor analogues eg - used in assays, in purifications and as, or therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP327364-A.
                                                                 Sledziewski AZ,
                                                                                                                           18-JAN-1989;
                                                                                                                                                                EP325224-A.
                                                                                                                                                                                                     Platelet derived growth factor receptor; human; ligand binding receptor analogues; isoforms; assays; antibodies; athersclerosis; wound healing; peptide dimer; cDNA.
                                                                                                                                                                                                                                           Platelet derived growth factor receptor.
                                                                                                                                                                                                                                                                01-NOV-1989
                                                                                                                                                                                                                                                                                   AAP90127;
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA encoding human platelet derived growth factor receptor useful eg for assessing agonist and antagonist drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1989-229378/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-1989
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Region
                                                                                                       22-JAN-1988;
                                                                                                                                              26-JUL-1989
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                     AAP90127 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV OF CALIFORNIA.
                                                                                    (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain .
                                                                                                                                                                                                                                                                                                                                                     656 SHLGPH
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                              1 SHLGPH 6
                                       AAN90355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 page 3; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 1106
                                                                                                                                                                                                                                                                                                                                                     661
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escobedo JE
                                                                                                       88US-0146877.
                                                                                                                           89EP-0100787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88US-0151414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89EP-0301021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         468..470
479..481
531..555
                                                                                                                                                                                                                                                                                                                                                                                                                                Α,
                                                                 Bell LA,
                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                  Kindsvogel WR;
                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                          Score 6; DB 1; Pred. No. 2.9
0; Mismatches
                                                                                                                                                                                                                                                                                                     1106
                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; L
         PDGF receptor with,
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 1106;
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RESULT 146
AAR26205
ID AAR262
XX AAR262
XX O9-FEB
XX PDGF;
XX PDGF;
XX PDGF;
XX POTtel
FT Protel
FT Protel
FT POTTEL
XX W09213
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Best Local
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The sequence given is one allele of type B human platelet-derived growth factor (PDGF) receptor (PDGF-R). This receptor is typically found on cells of mesenchymal origin. It acts while in the form of two transmembrane glycoproteins, each of which is about 180 kD. This receptor has three major regions. The first is a transmembrane region, which spans the membrane conce, separating the regions of the receptor exterior to the cell from those interior to the cell. The second region is an extracellular region which contains the domains which bind the PDGF. The third region is an intracellular region
                                                                                                                                                                                                                                                                                                                                       Platelet derived growth factor receptor (PDGF-R) poly:peptide(s) - useful as therapeutic and diagnostic agents e.g. for assaying PDGF activity in sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      details). These analogues are easily purified, produced in large quantities recombinantly, used to produce antibodies, to screen ligands as imaging agents, as (ant-)agonists, or therapeutically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Platelet derived growth factor receptor (see corresp. AAN90355). Used in the invention to make analogues that are secreted (pref. Ile-29 - Met-441, and Ile-29 - Lys-531; see specification for details). These analogues are easily provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-299970/36.
N-PSDB; AAQ27447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Type B human platelet-derived growth factor receptor.
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                                                                                                                                                                                                                                                                                      Disclosure; Page 75; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escobedo JA,
Wolf D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDGF; PDGF-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR26205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR26205 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORT-) COR THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  656 SHLGPH 661
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6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fretto LJ,
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Pred. No. 2.9
0; Mismatches
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Best Local
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                                                                             The amino acid sequence (AAR99690) of human platelet-derived growth factor receptor (PDGF-R) was deduced from a cDNA clone (AAT3452) isolated from a human diploid dermal fibroblast library. The cDNA can be used in novel constructs that allow the prodn. of secreted biologically active PDGF-R analogues. This may comprise linking a sequence coding for PDGR-R, or the ligand-binding domain of the PDGF-R extracellular region, to a protein secretion signal (e.g. SUC2) and promoter, and expression in transformed host cells, esp. Saccharomyces cerevisiae. The secreted PDGF-R analogues are used in ligand screening procedures, to screen for (ant)agonists, and in diagnostic assays.
                                                           Sequence
                                                                                                                                                                                                                                                                                           Prodn. of biologically active peptide dimers, growth factor receptor analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which posseses a tyrosine kinase activity. This tyrosine kinase domain is notable in having an insert of approx. 100 amino acids, as compared with most other receptor tyrosine kinase domains which are contiguous or have shorter insert sequences. Fragments of this sequence between 8 and 400 amino acids comprising one or more PDGF ligand binding region from the extracellular domain may be used to
                                                                                                                                                                                                                                                   Disclosure; Fig 1; 45pp; English.
                                                                                                                                                                                                                                                                              of novel (ant)agonists
                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT34552
                                                                                                                                                                                                                                                                                                                                                WPI; 1996-322833/33.
                                                                                                                                                                                                                                                                                                                                                                           Bell LA,
                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Platelet-derived growth factor receptor; PDGF-R; peptide dimer;
protein secretion; agonist; antagonist.
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Local Similarity
nes 6; Conserv
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                                                           1106
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               Score 6; 1
Pred. No.
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    Mismatches
                DB 17; L
5. 2.9e+02;
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                                                                                                                                                                                                                                                                                        esp. platelet-derived systematic designing
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                                                                                                          CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC is tensione at a sused in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC in justifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.

CC Specification, but was obtained in electronic format directly from WIPO at the printed contact of the content of the printed content of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity -
        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 34308; 103pp; English.
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food supplement; medical ir
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23-AUG-2000;
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                                                                                  ftp.wipo.int/pub/published_pct_sequences
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        1225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0540217
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maging; diagnostic; genetic disorder.
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RESULT 150
ABG15478
ID ABG154
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                                                                                                                                                                                                                                The present sequence represents the alpha 1H-2 subunit of a human CC low-voltage activated calcium channel. Alpha 1H-2 subunit cDNA CC (see AAX59082) was obtained by PCR amplification from a TT cell CC CDNA library. The invention provides calcium channel subunits, CI including 2 splice variants of alpha 1H-1 (see AAX60298 and AAY66299), CI dendisoform alpha 1H-2. Relative to alpha 1H-1, the 1H-2 isoform CC contains a 319 amino acid deletion within the intracellular loop contains a 319 amino acid deletion within the intracellular loop contains a 319 amino acid deletion within the intracellular loop contains a 319 amino acid deletion within the intracellular loop contains all cells and tissues axamined. These cleantified by PCR in all cells and tissues examined. These contained TT cels, amygdala, caudate nucleus, putamen, heart, kidney and liver cells. Cells and vectors containing nucleic calcius encoding these calcium channel subunits, and methods for cleantifying compounds that modulate the activity of calcium calcium. Channels that contain these subunits are provided by the invention. Compounds are used to treat calcium channel mediated disorders, including neurological, endocrinological, cardiovascular, curological, hepatic, respiratory and vascular disorders.
                                                                                                                                           Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calcium channel subunit 1H-2; human; neurological disorder; endocrinological disorder; cardiovascular disorder; urological disorder; hepatic disorder; respiratory disorder
ABG15478 standard; Protein; 2129 AA.
                                                                            1970 TPESRA 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-1998;
03-DEC-1997;
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                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human activated calcium channel alpha 1H-2 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                                                                             Local Similarity
mes 6; Conserv
                                                                                                             9 TPESRA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ง</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harpold M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 162-171; 171pp; English.
                                                                                                                                                                                                         2034 AA;
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0188932.
97US-0984709.
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                                                                                                                                     40.0%; 5-
100.0%; Pro
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                                                                                                                                                          Score 6; [
                                                                                                                                           Mismatches
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                                                                                                                                                     DB 20; Le
5. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respiratory disorder
                                                                                                                                                                         Length 2034;
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                                                                                                                                             Indels
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                                                                                                                                           Gaps
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ABG20749
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                                                                                                                                                                                                           RESULT 151
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                                                                                                                                        Matches
                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                        Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #15469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                     568 SHLGPH 573
                                                                                                   1 SHLGPH 6
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DB; AAS79665.
                                                                                                                                      6;
                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID No 45837; 103pp; English.
                                                                                                                                                                                                           2129 AA
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                      40.0%; Score 6; DB
100.0%; Pred. No. 5.
Live 0; Mismatches
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ABG20749;

ABG20749 standard; Protein; 2129

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RESULT 152
ABB62393
ID ABB623
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AC ABB623
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DT 26-MAR
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                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                               imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
  26-MAR-2002
                            ABB62393;
                                                     ABB62393 standard;
                                                                                                                                                                                                                              Sequence
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 51108; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
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                                                                                                                       568
                                                                                                                                         1 SHLGPH 6
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                                                                                                                     SHLGPH 573
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                                                                                                                                                                        Similarity 6; Conserv
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                                                                                                                                                                                                                              2129 AA;
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  (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                     Protein; 2139
entry)
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AAY06298
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AC AAY(
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AX
DT 23-2
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Calt
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Best Local
                                                                            urological disorde vascular disorder.
                                                                                       endocrinological disorder; cardiovascular disorder; urological disorder; hepatic disorder; respiratory
                                                                                                                 Calcium channel subunit 1H-1; human; neurological disorder;
                                                                                                                                                                                                                                                                                         1357 RSTPES 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                  Homo sapiens
                                                                                                                                           Human activated calcium channel alpha 1H-1 subunit.
                                                                                                                                                                       23-AUG-1999
                                                                                                                                                                                                 AAY06298;
                                                                                                                                                                                                                           AAY06298 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE
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                                                                                                                                                                                                                                                                                                                    7 RSTPES 12
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                                                                                                                                                                                                                                                                                                                                             Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 2139
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                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                       but was
          Location/Qualifiers 420..794
                                                                                                                                                                                                                                                                                                                                                                                                 AA.
/note= "intracellular loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                      for this patent did not form was obtained in electronic
                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                         40.0%; Sc.
100.0%; Pr
0;
                                                                                                                                                                       entry)
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Pred. No.
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.1e+02;

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Gaps

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Length 2139; Indels

n part of the printed format directly from

WIPO

respiratory disorder;

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 13971; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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AAY0629
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XC CAlciu
KW endoor
KW urolog
KW vascul
XX vascul
XX Yascul
XX Reglon
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Best Local Similarity
"hehes 6; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the the alpha 1H-1 subunit of a human low-voltage activated calcium channel. The sequence was deduced from CDNA (see AAX59080) isolated from a TT cell cDNA library.

The invention provides calcium channel subunits, including 2 splice variants of alpha 1H-1 (see also AAV6299), and isoform alpha 1H-2 (see AAV6300). The 1H-1 splice variants were detected by RT-PCR in multiple tissues. They differ only at amino acid 2230, being either Asp or Glu. 1H-2 has a 319-amino acid deletion in the lire of the AAV6400. The containing nucleic acids encoding these subunits, and methods for identifying compounds that modulate the activity of calcium channels compounds are used to treat calcium channel mediated disorders, including neurological, endocrinological, cardiovascular,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hans M,
Williams
                                                                                                                                                                                                                                                        Calcium channel subunit 1H-1; human; neurological disorder; endocrinological disorder; cardiovascular disorder; urological disorder; hepatic disorder; respiratory disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY06299 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2289 TPESRA 2294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subunits of calcium channels
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03-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-1999
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                                Region
                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                      vascular disorder.
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DB; AAX59080.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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97US-0984709
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                             /note= "intracellular loop"
520..528
                                                                                      Location/Qualifiers
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  /note= "poly-His region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 6; 1
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Urrutia A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20; L
                                                                                                                                                                                                                                                              respiratory disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2353;
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ABG30840
ID ABG3
XX
AC ABG3
XX
AC ABG3
XX
D7 07-C
XX
Huma
XX
KW Huma
KW Hype
KW volt
XX
VO Hom
OS Ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iow-voltage activated calcium channel. The sequence was deduced from cDNA (see AAX59080) isolated from a Tr cell cDNA library. The invention provides calcium channel subunits, including 2 splice variants of alpha 1H-1 (see also AAY06298), and isoform alpha 1H-2 (see AAY06300). The 1H-1 splice variants were detected by RT-PCR in multiple tissues. They differ only at amino acid 2230, being either Asp or Glu. 1H-2 has a 319-amino acid deletion in the I-II intracellular loop relative to 1H-1. Cells and vectors containing nucleic acids encoding these subunits, and methods for identifying compounds that modulate the activity of calcium channel that contain the subunits are used to treat calcium channel mediated disorders, including neurological, endocrinological, cardiovascular,
                                                                                                                                                                                                                                                        Human; calcium channel protein; prostate cancer; Parkinson's disease; CNS; central nervous system disorder; stroke; cardiovascular disorder; hypertension; angina; haematological disorder; thrombosis; pain relief voltage-dependent T-type calcium channel alpha_H subunit; asthma; inflammatory disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-371096/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hans M, Harpold M, Williams M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1998;
03-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-DEC-1998;
                             19-DEC-2001; 2001WO-EP15088.
                                                                                      04-JUL-2002
                                                                                                                                            WO200252003-A2
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human voltage-dependent T-type calcium channel alpha_H subunit protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG30840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG30840 standard; Protein; 2353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2289 TPESRA 2294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               urological, hepatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the the alpha 1H-1 subunit of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 151-161; 171pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Subunits of calcium channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SIBI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPESRA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIBIA NEUROSCIENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.0%; Silarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0188932.
97US-0984709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US25671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               respiratory and vascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stauderman K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 6; DB 2; Pred. No. 5.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Urrutia A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2353;
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0,

Gaps

0

relief;

2 splice

channels

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RESULT 156
AAW2261
ID AAW226
XX AW226
XX O2-MAR
AW D1-Yer
AW POLYKE
XX FYlact
KW POLYKE
XX Strept
XX Strept
XX Strept
XX Strept
XX Strept
XX Strept
XX DOMain
FT Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
""" ohes 6; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc human calcium channel protein polypeptide. The polypeptide, color polynucleotide and methods are useful in preventing or treating diseases crelated to calcium channel protein dysfunction, such as cancers (e.g. CC prostate), CNS (central nervous system) disorders (e.g. Parkinson's CC disease, stroke), cardiovascular disorders (e.g. hypertension, angina), CC or haematological disorders (e.g. thrombosis). The expression vector and CC reagent are useful in preparide a medicament for modulating the activity CC of the calcium channel protein in a disease. The methods are also useful in CC in detecting or producing polypeptides and polynucleotides useful CC in detecting or producing polypeptides and polynucleotides useful in CC treating the above diseases, and for screening for agents that regulate the activity of the calcium channel protein. These are also useful in CC treating inflammatory diseases (e.g. asthma, allergy) and in relieving CC pain from the above diseases. The present amino acid sequence represents CC protein. As described in the invention
                                                                                                                                                                                                                             Streptomyces
                                                                                                                                                                                                                                                                 Tylactone synthase gene cluster; tylG gene; multifunctional protein; polyKetide; tylactone synthesis; antibiotic; tylosin; hybrid protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2289 TPESRA 2294
                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                            Streptomyces
                                                                                                                                                                                                                                                                                                                                                        02-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                       AAW22611
                                                                                                                                                                                                                                                                                                                                                                                                                 AAW22611 standard; Protein; 4545 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Fig 3; 144pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotides encoding a novel calcium channel protein polypeptide, useful in preventing or treating diseases related to calcium channel protein dysfunction, e.g. cancer or CNS, cardiovascular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haematological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-575380/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smolyar A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2000;
02-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 TPESRA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to a new polynucleotide which encodes
                                                                                                                                                                                                                                                                                                                       srmG/tylG ORF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2353 AA;
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                           fradiae
                                                                                                                                                                                                                                            ambofaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-257297P.
2001US-280113P.
                   525..882
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                 /note=
                                                                                                                                                                note=
                                                                                                                                                .418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                      protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the invention.
"acyltransferase domain, AT1, from srmG"
                                                                                                                            "ketosynthase domain, KS'(s),
                                                                                                                                                           _ "encoded by GTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 6; DB 2; Pred. No. 5.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23; LC
NO. 5.6e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2353;
                                                                                             AT(s), from tylG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                           from tylG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                            from tylg'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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RESULT 157
AAW23716
ID AAW237
XX
AC AAW237
AC AAW237
XX
DT 27-FEB
XX
                                                                                                                                                                                                                                                                                                                  This sequence represents a hybrid protein of the invention. This consequence was created by replacing a EcoRI-ApaI fragment of srmG ORF1 with a EcoRI-Sful fragment from tyle ORF1. The position of the residues from the each of the two genes is not given in the specification. The srmG gene cach of the two genes is not given in the specification. The srmG gene control of the two genes is not given in the specification. The srmG gene control of the specification is the specification of the multi-functional proteins which direct the synthesis of the codes control of the multi-functional proteins which direct the synthesis of the size building block of the control of the synthase gene cluster of the invention. The tylG sequence was isolated from Streptomyces fradiae, and encodes multifunctional proteins which direct the synthesis of the polyketide tylactone. Tylactone is the basic building block of the antibiotic tylactone. Tylactone is the basic building block of the antibiotic tylactone. Tylactone is the basic building block of the antibiotic tylactone. Tylactone is the basic building block of the antibiotic tylactone. Tylactone is the basic building block of the antibiotic tylactone. Tylactone is the basic building block of the antibiotic tylactine. The hybrid sequence can be used to transform S. ambofaciens lacking the srmG ORFI sequence, so that they can produce control of the post-condensation reactions performed, thereby the post-condensation reactions performed, thereby the post-condensation reactions performed, thereby
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                               Query Match
Best Local
                  27-FEB-1998
                                                                                  AAW23716 standard;
                                                                                                                                                                         4008 PESRAA 4013
                                                    AAW23716;
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 23; Pages 198-212; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding Streptomyces fradiae tylactone synthase domain - production of tylosin-related polyketide compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-418046/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dehoff BS, Kuhstoss SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIL ) LILLY & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP791655-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
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                                                                                                                                                                                                            10 PESRAA 15
                                                                                                                                                                                                                                             hes 6; Conser
                                                                                                                                                                                                                                                                                                                                                 in novel tylosin-related polyketides.
                                                                                                                                                                                                                                                                                                                  4545 AA;
                                                                                                                                                                                                                                               Conservative
              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0012078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4083.4268
/note= "ketoreductase domain, KR2, from srmG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2232..2416
/note= "ketoreductase domain, KR1, from srmG"
/note= "acyl carrier protein domain, ACP1, from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "acyltransferase domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "dehydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "ketosynthase domain, KS2, from srmG"
                                                                                   Protein;
                                                                                                                                                                                                                                    40.0%; Pr
100.0%; Pr
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..3727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "acyl carrier protein domain, ACP2, from srmG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosteck
                                                                                                                                                                                                                                         Score 6; DB 1
); Pred. No. 9.9
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain,
                                                                                                                                                                                                                                                           DB 18; L
o. 9.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sutton
                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                          Length 4545;
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                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                       Gaps
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Platenolide

synthase

ORF1

protein.

0

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Query Match
Best Local Similarity
                                                                                                    AAW23716-W23720 represent proteins encoded by the platenolide synthase gene cluster of the invention. The gene cluster is also referred to as the srmG gene, and was isolated from Streptomyces ambofaciens. These sequences are multi-functional proteins which direct the synthesis of the polyketide platenolide. Platenolide is the basic building block of the macrolide antibiotic spiramycin. The DNA can be used to produce compounds exhibiting antibiotic activity based on the platenolide structure, including specifically the macrolide antibiotic spiramycin and spiramycin analogues and derivatives. Modifications of the platenolide synthase DNA sequence can be made so as to change the number and type of carboxylic acids incorporated into the growing polyketide chain and to change the kind of post-condensation processing that is conducted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Platenolide synthase gene multi-functional protein;
                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Pages 33-47; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-418047/39.
N-PSDB; AAT78508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burgett SG,
Rosteck PR;
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100.0%;
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Score 6; I
Pred. No.
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RESULT 158
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                                                                                             DNA encoding Streptomyces fradiae tylactone synthase domain -
production of tylosin-related polyketide compounds
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15..41
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AAW22606-W22610 represent proteins encoded by the platenolide synthase gene cluster. The gene cluster is also referred to as the srmG gene, as was isolated from Streptomyces ambofaciens. These sequences are

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Query Match
Best Local Similarity
Thickes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc multi-functional proteins which direct the synthesis of the polyketide cc platenolide. Platenolide is the basic building block of the macrolide cantibiotic spiramycin. The DNA encoding this sequence was used along cc with the tylG gene (see AAT80413) to create a hybrid ORF1 sequence (see Cc AAT80415). The tylG gene is the tylactone synthase gene cluster of the clinvention. The tylG gene is the tylactone synthase gene cluster of the cc invention. The tylG sequence was isolated from Streptomyces fradiae, and cc encodes multifunctional proteins which direct the synthesis of the cc polyketide tylactone. Tylactone is the basic building block of the cantibiotic tylosin. The hybrid sequence can be used to transform S. cc ambofaciens lacking the srmG ORF1 sequence, or S. fradiae lacking the tylG ORF1 sequence, so that they can produce polyketides. The DNA csequence can be modified so as to alter the type of carboxylic acids incorporated, the number of carboxylic acids incorporated and/or the cc post-condensation reactions performed, thereby resulting in novel xxx
            cytotoxic T lymphocyte (CTL) inducing epitope from at least one HIV-protein, and comprises examining the nucleic acid sequence in the first 24 weeks after infection, and confirming that an immune response directed against the CTL-inducing epitope is capable of selecting for viral escape variants during the acute phase of HIV infection. The method is useful for designing a rational, novel vaccine
                                                                                                                                                         The sequences given in AAB47748-50 represent epitopes derived from simian immunodeficiency virus (SIV) which were used in the method \alpha
                                                                                                                                      similan immunodericiency virus (STV) which were used in the method the invention. The method allows identification of at least one
                                                                                                                                                                                                                                                                weeks of infection
                                                                                                                                                                                                                                                                                                        Identifying CTL-inducing epitope(s) from HIV protein, useful for making an HIV vaccine, comprises determining the immune response against the
                                                                                                                                                                                                                                                                                                                                                                                                             Watkins DI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-2000; 2000US-196412P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunodeficiency virus.
                                                                                                                                                                                                                        Page 31; 85pp;
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escape variant; acute phase;
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The method is particularly useful for making
                                                                                                                                                                                                                                                                                     select viral escape
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100.0%;
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                                                                                                                                                                                                                                                                                 he immune response against variants during the first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytotoxic T lymphocyte;
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                                                                                                                                                                                                                                                                                                                                                                                                       Vogel TU;
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RESULT 160
AAB47751
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XX AAB477
XX Epitop
CTL ep
XX CTL; H
XX CTL; H
XX Simian
PN W02001
XX Watkin
XX Watkin
XX Watkin
XX Identi
PF 12-APR
XX Identi
PF 25-OCT
XX Identi
PF 25-OCT
XX Watkin
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PT 16-APR
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PT 25-APR
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PT 26-APR
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PT 27-APR
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                                                     Matches
                                                                             Query Match
Best Local
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                                                                                                                                                                                                   HIV-protein, and comprises examining the nucleic acid sequence in the first 24 weeks after infection, and confirming that an immune response directed against the CTL-inducing epitope is capable of selecting for viral escape variants during the acute phase of HIV infection. The method is useful for designing a rational, novel vaccine approach to HIV. The method is particularly useful for making an HIV vaccine. This epitope affected acute escape 4 weeks post infection.
                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                    simian immunodeficiency virus (SIV) which were used in the method the invention. The method allows identification of at least one cytotoxic T lymphocyte (CTL) inducing epitope from at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAB47751-60 represent epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying CTL-inducing epitope(s) from HIV protein, useful for making an HIV vaccine, comprises determining the immune response against the epitope in order to select viral escape variants during the first 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Epitope; simian CTL; HIV; viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watkins DI, Allen TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-2000; 2000US-196412P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-2001; 2001WO-US11502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Simian immunodeficiency virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB47751 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB47751;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 STPES 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 STPES 12
  STPES 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-049178/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of infection
                                                     5,
                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 5; Conserv
                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunodeficiency virus; SIV;
escape variant; acute phase;
                                        33.3%; 5-
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'Connor DH,
                                                %; Score 5; DB 2
%; Pred. No. 7.8
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23; ы
                                                                           23; I
.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxic T lymphocyte; vaccine.
                                                  0;
                                                                                                Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vogel TU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                             Gaps
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RESULT 162
AAG88112
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                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAB47751-60 represent epitopes derived from simian immunodeficiency virus (SIV) which were used in the method of the invention. The method allows identification of at least one cytotoxic Tlymphocyte (CTL)-inducing epitope from at least one HIV-protein, and comprises examining the nucleic acid sequence in the first 24 weeks after infection, and confirming that an immune response directed against the CTL-inducing epitope is capable of selection. The method is useful for designing a rational, novel vaccine approach to HIV. The method is particularly useful for making an HIV internal that the courter phase of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying CTL-inducing epitope(s) from HIV protein, useful for making an HIV vaccine, comprises determining the immune response against the epitope in order to select viral escape variants during the first 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 66; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-2001; 2001WO-US11502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB47758 standard; peptide;
Saccharomyces cerevisiae
                      Saccharomyces cerevisiae; complementary peptide; peptide identification; drug discovery; drug design.
                                                               Saccharomyces
                                                                                       11-SEP-2001
                                                                                                                                        AAG88112 standard; Peptide; 10
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-049178/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2000; 2000US-196412P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200178775-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Simian immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epitope; simian CTL; HIV; viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTL epitope 94004 Tat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-2002
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                                                                                                                                                                                                                                                                                                                                     Infection
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                                                                                                                                                                                                                               STPES 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of infection
                                                                                                                                                                                                                                                                                                                                                This epitope affected rapid viral escape by 4 weeks
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                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                            A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Allen TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                       (first entry)
                                                             cerevisiae peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunodeficiency virus; SIV; cytotoxic T lymphocyte;
escape variant; acute phase; vaccine.
                                                                                                                                                                                                                                                                     33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O'Connor DH,
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                                                                                                                                                                                                                                                                     Score 5;
Pred. No.
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                                                                                                                                        B
                                                                                                                                                                                                                                                         Mismatches
                                                             SEQ ID NO: 3061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mothe BR,
                                                                                                                                                                                                                                                                     DB 23; I
                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vogel TU;
                                                                                                                                                                                                                                                         Indels
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Best Local Similarity
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AAG88113
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                  nucleotide sequence databases, useful
                            Identifying complementary peptides by
                                                                     Roberts GW,
                                                                                                              13-DEC-1999;
                                                                                                                                 13-DEC-2000;
                                                                                                                                                      14-JUN-2001.
                                                                                                                                                                         WO200142276-A1
                                                                                                                                                                                              Saccharomyces
                                                                                                                                                                                                                           Saccharomyces cerevisiae; complementary peptide; peptide identification;
                                                                                                                                                                                                                                                Saccharomyces
                                                                                                                                                                                                                                                                     11-SEP-2001
                                                                                                                                                                                                                                                                                        AAG88113;
                                                                                                                                                                                                                                                                                                           AAG88113 standard; Peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 452; 488pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying complementary peptides by nucleotide sequence databases, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roberts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-DEC-1999;
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                                                                                        (PROT-) PROTEOM LTD
                                                                                                                                                                                                                                                                                                                                                                 4 RSTPE
                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                           RSTPE 11
                                                                                                                                                                                                                 discovery;
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                                                                     Heal JR;
                                                                                                                                2000WO-GB04773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-GB04773
                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                               cerevisiae peptide, SEQ ID NO: 3062
                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                              cerevisiae
                                                                                                             99GB-0029471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99GB-0029471
                                                                                                                                                                                                                  drug
                                                                                                                                                                                                                                                                                                                                                                                                  33.3%; 5-
100.0%; Pr
                                                                                                                                                                                                                  design
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 5;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                 analysis of protein and in drug design -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analysis of protein and in drug design:
                                                                                                                                                                                                                                                                                                                                                                                                                  . 59
                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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Example 5; Page 452; 488pp; English

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RESULT 164
AAR29138
ID AAR291
XX AAR291
XX DNA PO
KW DNA PO
KW Long D
XX Bacter
XX Bacter
XX Bacter
XX PN EP5162
YN 24-DEC
XX 14-JAN
PR 14-JAN
PR 14-DEC
XX WPI; 1
DR N-PSDB
XX WPI; 1
DR N-PSDB
XX Exampl
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Thehes 5; Conserv
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                      Matches ,
                                         Best Local Similarity
                                                          Query Match
                                                                                                                        This sequence represents the modified portion (aa214-224) of T7 DNA polymerase modified by the substitution of His 218 for Ser. This gives polymerase with little or no associated exonuclease activity, does not discriminate against nucleotide analogue incorporation and can utilise small oligonucleotides as specific primers. These are ideal properties for the manipulation of DNA, partic. for sequencing since the background level of radioactivity in the PACE gels is negligible, there are few or no artificial bands, and the bands are sharp. Such a polymerase allows novel methods of sequencing long DNA fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-1987;
14-DEC-1987;
                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                Example 1; Page 154; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                       Sequencing method for DNA - using T7 polymerase with no
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Richardson CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP516245-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA polymerase; DNA sequencing; base sequencing; chain termination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR29138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR29138 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 RSTPE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                             1992-400615/49
                        <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                            AAQ31619
                                                                                                                                                                                                                                                                                                                                                    activity
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                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87US-0003227
87US-0132569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87EP-0202037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tabor
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100.0%;
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                      0;
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                                       Score 5;
Pred. No.
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Pred. No.
                        Mismatches
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                               DB .
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59;
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                                                        Length 11;
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AAR94612
ID AAR946
XX AAR946
XX Prote1
XX Prote1
XX Prote1
XX Prote2
XX Synthe
PN W09609
PN C-FOS
PH Deng 7
XX Deng 7
XX C-FOS
PT Dotent
PN W01; 1
XX C-FOS
PT G1SOr(
XX C-FOS
PT Dotent
PN W01; 1
XX C-FOS
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XX C-FOS

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                                                                                                                                                                                                                                                            RESULT 166
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                       Homo sapiens
                                                                           Vascular cell
                                                                                                              N-terminal
                                                                                                                                                  17-AUG-1993
                                                                                                                                                                                      AAR34443;
                                                                                                                                                                                                                        AAR34443 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-200718/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9609835-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorder; inhibition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR94612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                         Local
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5; Conser
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                                                                                                             sequence
                                                                                                                                                (first
                                                                           adhesion molecule;
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                                                                                                              of.
                                                                                                                                              entry)
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This sequence comprises the protein binding region on c-Fos which corresponds to amino acids 226-236 of the mature protein. The peptide can be useful for the competitive inhibition of naturally occurring c-Fos in situations where it may be desirable to decrease the amount of c-Fos activation by phosphorylation by a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c-Fos regulating protein kinase phosphorylates c-Fos - acts
potentiates its activity, used to treat a cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Page 39; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein kinase binding region on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR94612 standard; peptide;
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c-Fos; activation; phosphorylation; cell proliferation;
peptide;
                                                                                                                                                                        33.3%; 5u
100.0%; Pr
0;
  12
                                                                                                                                                                              Score 5; DB 1; Pred. No. 64; 0; Mismatches
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64;
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soluble

vascular

mol.

(VCAM).

VCAM; soluble; plasma

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RESULT 167
ABJU1192
ID ABJU11
XX
AC ABJU11
XX
DT 13-SEI
XX
Human
XX
Human
XX
Human
XX
Human
XX
Homo
XX
PN W020
PN W020
YX
PD 23-M
XX
PF 13-F
XX
PF 13-F
XX
PR 16-I
XX
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soluble VCAM is naturally present in human serum and plasma. Purification of soluble VCAM from plasma on a monoclonal antibody affinity column reveals three species with mol. wt. of 100kD, 80kD and 40kD. N-terminal sequence analysis of the first 10 residues of the 100kD form (AAR34443) identified the material as being identical to the N-terminus of the published sequence of membrane bound VCAM.
                                                        Determining the presence of neoplastic molecular markers, by identifying the presence of markers in host test sample using array of neoplastic molecular marker specific reagents and analyzing the array of the reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soluble vascular cell adhesion molecule for diagnosis and prognostic(s) - useful in immunoassay as standard for detection indicating vascular damage, e.g. by diabetes or activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABJ01192 standard; Peptide; 12
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        Example 3; Page 11; 41pp;
                                                                                                                                                                                       WPI; 2002-537346/57.
                                                                                                                                                                                                                                                                                                                                           16-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-2001; 2001WO-US43461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                          (CEMI-) CEMINES LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brn-5 transcriptional regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                             2000US-249508P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91GB-0020767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-GB01791.
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100.0%;
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        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease; tumour specific marker; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14;
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        RESULT 169
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RESULT 168
AAW12798
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                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for determining the presence of neoplastic molecular markers in a host, involving the use of neoplastic molecular marker specific reagents to detect such markers and analysing the array of reagents, allowing the identification of the neoplastic disease present. This can be used to determine the best treatment for cancers, in particular neural cell, lung and prostate tumours. The present sequence is a peptide derived from a transcription factor capable of acting as a marker of the invention.
                                                                                                                        AAW12798 and AAW12799 represent antigenic peptides derived from type 0 foot and mouth disease virus. The reactivity of these peptides was examined by an indirect enzyme antibody method using bovine serum from foot and mouth disease infected cattle. The peptides were combined with horse globulin to give antigens A and B. These sequences can be conjugated to a carrier and used in the diagnosis and treatment of foot and mouth disease. Using these sequences foot and mouth disease can be sequences foot and mouth disease can be sequences foot and mouth disease can be
                                                                                                     Sequence
                                                                                                                                                                                                                                             Claim 1; Page 5; 7pp;
                                                                                                                                                                                                                                                                     Antigenic peptide for the diagnosis of foot and mouth disease derived from type 0 foot and mouth disease virus
                                                                                                                                                                                                                                                                                                             WPI; 1997-073906/07.
                                                                                                                                                                                                                                                                                                                                                              24-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                        24-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                          JP08320324-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foot and mouth disease virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigenic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW12798 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                     (NORQ ) NORINSUISANSHO KACHIKU
                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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5; Conserv
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5; Conser
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ilarity 100.0%;
Conservative (
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                     ΑA;
                                                                                                                                                                                                                                                                                                                                                              95JP-0148364.
                                                                                                                                                                                                                                                                                                                                                                                        95JP-0148364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            foot and mouth disease; bovine; cow;
                                                              33.3%;
                                                                                                                                                                                                                                            Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L
W
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Pred. No.
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Pred. No.
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                                                   Mismatches
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                                                               DB 18;
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                                                                           Length 13;
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                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           horse; globulin.
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AAM52755

III AAM5

XX AAC

AAC AAM6

XX AAC

side chain, and whose specific peptides (AAM52707-AAM32//2 hydroxymethyl), or OH.
The invention also encompasses specific peptides (AAM52707-AAM32//2 AAM52776) conforming to the above formula; esters, amides or AAM52726-AAM52776) conforming to the above formula; esters, amides or salts of peptides of the invention; and pharmaceutical agents containing these peptides of derivatives. The peptides are used as agents to control these peptides of derivatives. The peptides are used as agents to control these peptides of derivatives. The peptides are used as agents to control these peptides of derivatives.
                                                                                                                                                                                                                                        substituted in the side chain; X4 is a peptide bond, a neutral amino acid optionall side chain, or an aromatic amino acid; and X5 is an amino acid or a dipeptide (both optionally side chain, and whose C terminal carboxy may be reduced to the state of the side chain, and whose C terminal carboxy may be reduced to the side chain, and whose C terminal carboxy may be reduced to the side chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to peptides rich in arginine and proline which are recognised as ligands by the G protein-coupled receptor (GPCR) APJ (AAM52725). The peptides of the invention are at least 11 amino acids long, and contain two proline (Pro) residues, two arginine (Arg) residues, a leucine (Leu) residue and a phenylalanine (Phe) residue. The have the general formula:
                                                                                                                                                                                                                                                                                                                                                                                                           in the side chair X3 is a neutral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X1-Arg-Pro-Arg-Leu-Phe-X2-X3-Gly-Pro-X4-X5 where:
X1 is H or a chain of 1-25 amino acids all option
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-coupled receptor protein, useful for treating system, immune, digestive, metabolic and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkinson's disease; Huntington's disease; Pick's disease; circulation; heart; immune system; digestion; metabolism; diabetes; reproduction; disorder; tumour; cancer; HIV infection; human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; cardiant; vulnerary; immunostimulant; antiviral; neuroprotective; nootropic; antiparkinsonian; antialcoholic; cytostatic; antidiabetic; tranquiliser; antidepressant; anticonvulsant; antilipaemic; antirheumatic; antiarthritic; antiinflammatory; dermatological; osteopathic; antiarthritic; antiarteriosclerotic; hypertensive; hypotensive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; Page 103; 136pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides rich in arginine and proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-648386/74.
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19-SEP-2000;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is a neutral or basic amino acid residue,
                                                                                                                                                                                                                                                                                                                                                                                                                                            the side chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                side chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ligand peptide; G protein-coupled receptor; GPCR; arginine rich; line rich; central nervous system; dementia; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H or a chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human immunodeficiency virus
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2000JP-0288891
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                                                                                                                                                                                                                                                                                                                                                                                                                  aromatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Pyroglutamic acid"
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                                                                                                                                                                                                                                                                                                                                                                                                              or basic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         β
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                                                                                                                                                                                                                                                                                                                                                                                                           amino acid residue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hosoya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e are ligands
for treating
                                                                                                                                                                                                                                                                                                                                             optionally substituted in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      optionally substituted
                                                                                                                                                                                                                                                                               substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s for G
y central nervous
e disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                residue. They
                                                                                                                                                                                                                                                                                  in
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pigs

14

FMDV-specific antibodies against the disease. The

Claim

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Page 22;

27pp;

German.

AAW59073-W59119 are immunogenic peptides from a foot and mouvirus (FMDV) nonstructural protein which are immunoreactive FMDV-specific antibodies or T cells and can be used in vacci

or T cells and can be used in vaccines vaccines are used especially for immunising

foot and mouth disease

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RESULT 170
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Best Local S
Matches 5
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                                                                                                                                                                                                                                   Vaccines against foot and mouth disease virus fragments of nonstructural viral proteins
                                                                                                                                                                                                                                                                                                                                                                                Correa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   system, digestion, metabolism or reproduction. They can also be used for the prevention and treatment of human immunodeficiency virus (HIV) infection and acquired immunodeficiency syndrome (AIDS). The peptides useful for the prevention and treatment of age-related dementias and Alzheimer's, Parkinson's, Huntington's and Pick's disease; nervous disorders; anxiety or depression; epilepsy; cerebrovascular disorders, acute myocardial infarction; hypercholesterolaemia, arteriosclerosis; huntington's procession; epilepsy; cerebrovascular disorders; acute myocardial infarction; hypercholesterolaemia, arteriosclerosis; huntington's procession; epilepsy; cerebrovascular disorders; acute myocardial infarction; hypercholesterolaemia, arteriosclerosis; huntington's procession; epilepsy; cerebrovascular disorders; acute myocardial infarction; hypercholesterolaemia; arteriosclerosis; huntington's procession; epilepsy; cerebrovascular disorders; acute myocardia infarction; hypercholesterolaemia; arteriosclerosis; huntington's procession; epilepsy; cerebrovascular disorders; acute myocardia infarction; hypercholesterolaemia; arteriosclerosis; huntington's procession; epilepsy; cerebrovascular disorders; acute myocardia infarction; hypercholesterolaemia; arteriosclerosis; hypercholesterolaemia; arteriosclerosis; hypercholesterolaemia; acute myocardia infarction; hypercholesterolaemia; arteriosclerosis; hypercholesterolaemia; acute myocardia infarction; hypercholesterolaemia; arteriosclerosis; hypercholesterolaemia; hypercholesterolaemia; hypercholesterolaemia; hypercholesterolaemia; hy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foot and Mouth disease; FMDV; immunogenic; viral nonstructural protein; immunoreactive; antibody; T cell; vaccine; pig; cattle.
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                                                                                                                                                                                                                                                                                                                                                                                                                             (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FMDV non-structural viral
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5; Conserv
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100.0%; Pr
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Saalmueller
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lmueller A, Wiesmueller
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74;
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                                                                                                                                                                                                                                                            comprising
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RESULT 171
AAW59109
ID AAW591
XX AAW591
XX 10-AUG
DT 10-AUG
DT 10-BUDV n
XX FOOt a
KW Immuno
XX DE1963
XX 19-MAR
XX 18-SEP
XX 18-SEP
XX COrrea
PR 18-SEP
XX CFARB
XX FOOT a
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XX CORRE
PF FR 18-SEP
XX CORREA
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XX CORREA
XX CRAW590
CC FMDV-g
CC SPMDV-g

RESULT 172
AAR47671
ID AAR476
XX
AC AAR476
XX
DT 27-JUL
XX
DE HIV ep
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HIV-sp
KW Outer
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Best Local Similarity
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Matches
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW59073-W59119 are immunogenic peptides from a foot and mouth disease virus (FMDV) nonstructural protein which are immunoreactive with FMDV-specific antibodies or T cells and can be used in vaccines against the disease. The vaccines are used especially for immunising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Correa R, Pauly T,
HIV-specific; principal neutralisation; epitope; antigen; outer membrane proteosome; Neisseria; AIDS; vaccine; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccines against foot and mouth disease virus - fragments of nonstructural viral proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foot and Mouth disease; FMDV; immunogenic; viral nonstructural protein; immunoreactive; antibody; T cell; vaccine; pig; cattle.
                                                      HIV epitope #4
                                                                                            27-JUL-1994
                                                                                                                               AAR47671;
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        pigs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE19638044-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FMDV non-structural viral protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW59109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW59109 standard;
                                                                                                                                                                 AAR47671
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nes 5; Conserv
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| RSTPE 7
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                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Froehlich Pfaffe E,
                                                                                                                                                                                                                                                                                                                                                                                                      14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27pp; German
                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide;
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                                                                                                                                                                                                                                                                                                                                              33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B, Glatthaar-Saalmueller B, Saalmueller A, Wiesmueller
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                                                                                                                                                                                                                                                                                                                           Score 5; DB 1; Pred. No. 78; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 5; DB 1
Pred. No. 78;
0; Mismatches
                                                                                                                                                                 Å
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). 78;
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. 78;
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                                                                                                                                                                                                                                                                                                                                                             Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising peptide
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 conjugate;
infection;
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Matches
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20-JUL-1992;
20-JUL-1992;
20-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAR47668-788 are HIV-specific selected principal neutralisation epitopes which may be used in an antigenic conjugate linked to purified outer membrane proteosome of Neisseria. This conjugate may be used in an AIDS vaccine which may be used pre-and post-exposure to prevent or treat HIV infection or disease. The vaccine is capable of eliciting specific HIV neutralising antibodies and bind the broadly neutralising human monoclonal antibody (447)
                                                                                                                                                                                                                Tumour supressor protein 63; cytostatic; virucidal; immunmodulator; antiinflammatory; haemostatic; gene therapy; tumour; breast carcinoma; Wilm's tumour; haemopathy; HIV infection; immunological disease; inflammation; developmental disorder.
                                     17-MAR-2000; 2000CN-0114977.
                                                                       16-MAR-2001; 2001WO-CN00331.
                                                                                                            04-OCT-2001
                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                            Tumour supressor protein 63 peptide fragment
                                                                                                                                                                                                                                                                                                                                                17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                   AAG78901;
                                                                                                                                                                                                                                                                                                                                                                                                                   AAG78901 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 93; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New conjugates for treating or preventing HIV infection - comprising HIV-specific neutralisation epitopes covalently linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-048884/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arnold BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MERI ) MERCK & CO INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease; antibody; human; monoclonal antibody; 447 antibody.
 (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
                                                                                                                                                WO200172786-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 GPHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                              (first entry)
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92US-0917215.
92US-0917217.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Neisseria
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Mismatches

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0

Gaps

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DB 15; . 83;

Length 15 Indels

Shaw AR;

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RESULT 174
AAEO1628
ID AAEO16
XX
AAEO166
XX
AC AAEO16
XX
DI 17-JUI
XX
Human
XX
KW Human
XW infl;
KW eard
KW limin;
KW eard
KW card
KW card
KW eelj
KW eelj
XX
FT Pef
FT Pef
FT Pr
YX
YX
PF WC
XX
PF WC
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PF O
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XX
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; pscriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary;
                                                                                   05-NOV-1999;
30-JUN-2000;
                                                                                                                                             01-NOV-2000; 2000WO-US30037
                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                      binding
                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 foetal abnormality; developmental abnormality; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE01628 standard; Protein; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breast carcinoma and Wilm's tumour, haemopathy, HIV infection, immunological diseases, inflammation and developmental disorders present sequence is an N-terminal peptide fragment of the tumour suppressor protein, which was used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to tumour suppressor protein 63 (see AAG78900). The tumour suppressor protein and its coding sequence are useful in the diagnosis and treatment of malignant tumours including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene 28 encoded secreted protein HBHME51, SEQ ID NO:178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide for the diagnosis and treatment of malignant neoplasm, hemopathy, HIV infection, immunological disease and inflammations,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises the tumor suppressor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-616469/71
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mes 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TPESR 6
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  , MS
                                                                                                                                                                                                                                                                                                                                                                                                                                      culture; chemotaxis; food additive; gene therapy;
ing partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secreted protein; proliferative disorder; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Page 13; 38pp; Chinese
    Komatsoulis GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
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                                                                               99US-0163577
2000US-0215137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA,
                                                                                                                                                                                                                                                                     /label= Human_mature_secreted_protein
                                                                                                                                                                                                                                                                                            /label= Signal_peptide
19..21
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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    Moore PA;
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83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due t sunburn, to maintain organs before transplantation, for supporting cel culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be use as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, an in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.
                                                                                                                                                                   Albumin fusion protein; therapeutic protein %; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; disorder; immune disorder; nedocrine disorder; hatematopoietic disorder; neural disorder; connective disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 29 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
                      Synthetic
                                                                                   osteopathic;
                                                                                                       cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; noo neuroprotective; antiparkinsonian; antimicrobial; neurole
                                                                                                                                                                                                                                                                             Human albumin fusion protein #479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders,
                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                       27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                 ABG63804;
                                                                                                                                                                                                                                                                                                                                                                                                       ABG63804 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding 29 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD05389-AAD05473 represent cDNAs corresponding to 29 human secreted protein genes, and AAE01546-AAE01630 represent the proteins they encode. AAE01631-AAE01660 represent human secreted protein fragments or variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 510; 535pp; English.
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DB; AAD05471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AA;
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                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                   antiarthritic
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100.0%;
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). 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 21;
                                                                                                       ric; nootropic;
neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT 176
ABB39746
ID ABB397
XX ABB397
XX ABB397
XX ABB397
XX Peptid
XX Peptid
XX Human:
XX Homo s
XX WO2001
XX O9-AUG
XX O9-AUG
XX O1-AUG
PR 30-JUN
PR 30-JUN
PR 31-SEP
PR 27-SEP
PR 27-SEP
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Best Local
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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to albumin fusion proteins comprising a therapeutic protein x and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein x. The albumin extends the shelf-life of protein x, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. alzahelmer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders feedom proteins of the invention. ABG63326-ABG65518 represent albumin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2000;
25-APR-2000;
21-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
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                                                                                                                                               WO200157277-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                           30-JAN-2001; 2001WO-US00669.
                                                                                                                     09-AUG-2001.
                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                Human; foetal liver; gene expression; single exon nucleic acid probe
                                                                                                                                                                                                                          Peptide #7252 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                 ABB39746;
                                                                                                                                                                                                                                                                                                            ABB39746 standard; Peptide; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fusion
                                                                                                                                                                                                                                                                                                                                                                                        1 SHLGP 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion protein for treating disease e.g. diabetes comprises whin fused to a therapeutic protein - % \left( 1\right) =\left( 1\right) ^{2}
                                                                                                                                                                                                                                                                                                                                                                           SHLGP
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                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
5; Conserv
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; 2000US-199384P.
; 2000US-256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                       (first entry)
                                                                2000US-0180312.
            2000US-0632366
2000US-0234687
                                      2000US-0207456.
2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
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Pred. No.
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RESULT 177
AAM60466
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Best Local
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                                                                                                                                         04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                            03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exonucleic acid probe of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2000; 2000GB-0024263
         Single exon nucleic acid probes for analyzing gene expression in human brains -
                                       WPI; 2001-483446/52
                                                                                                                                                                                  30-JAN-2001;
                                                                                                                                                                                                       09-AUG-2001
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                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                  epilepsy;
                                                                                                                                                                                                                                                                           microarray; Alzheimer's disease;
                                                                                                                                                                                                                                                                                       Human; brain expressed exon; gene expression analysis; probe
                                                                                                                                                                                                                                                                                                           Human brain expressed single
                                                                                                                                                                                                                                                                                                                               05-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-)
                                                                               (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                   7 RSTPE 11
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                                                           SG,
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5; Conserv
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                                                                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                  cancer
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                                                           Hanzel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 AA;
                                                                                                            2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.3%; Sullarity 100.0%; I Conservative 0;
                                                                                                                                                                                  2001WO-US00667
                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                    2000GB-0024263
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                                                           Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 5;
Pred. No.
                                                                                                                                                                                                                                                                                                           exon probe encoded protein SEQ
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                                                           Rank
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                                                                                                                                                                                                                                                                             multiple sclerosis;
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5. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                             schizophrenia;
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RESULT 178
AAM7311
XX AAM731
XX AAM731
XX AAM731
XX Human
DT 06-NOV
XX Human;
KW Human;
XX Homo s
YX Homo s
YX Human
PT 20-AUG
YX 10-JUN
PR 21-SEP
PR 30-JUN
PR 21-SEP
PR 30-JUN
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Query Match
Best Local S
Matches '5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0632366.
21-SEP-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236559.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                 probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00668
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                                                                                                                                                                                                                                                                    present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSTPE
                                                                                                                                                                                                                                                                                                                                                                 genome-derived single exon nucleic acid probes useful zing gene expression in human bone marrow \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone marrow expressed exon; gene expression analysis; probe
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  Similarity
5; Conser
                                                                                                                                             encoded by one of the probes of the invention
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                                                                                                                                                                                                                                                                                                                         SEQ ID NO:
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer;
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                                                                                               ΑĄ;
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                      33.3%;
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0,
Score 5; DB 2; Pred. No. 1.7
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 5; |
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lymphoma; myeloma.
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                      DB 22; Loo, 1.7e+02;
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                                          Length 34;
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Indels
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Gaps
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RESULT 179
AAM33328
ID AAM3333
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XX Probe;
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ABG42957
ID ABG
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AC ABG
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                                                                                                                                                                                 RESULT 180
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Best Local Similarity 100
Matches 5; Conservative
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26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                19-AUG-2002
                                                                                            ABG42957;
                                                                                                                                   ABG42957
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analyzing
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                                                                                                                                   standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID No
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                              (first entry)
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100.0%; Pr
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes useful
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Human peptide

encoded by genome-derived

single exon

probe

SEQ ID

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The invention relates to a spatially-addressable set of single exon CC nucleic acid probes for measuring gene expression in a sample derived CC from human lung comprising single exon nucleic acid probes having one of CC 12614 nucleic acid sequences mentioned in the specification, or their CC complements or the 12387 open reading frames derived from the 12614 CC probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a CC nucleic acid expressed in the human lung; measuring the next sequences comprise derived from human lung; measuring the array with the carray identifying exons in a eukaryotic genome, comprising the array; identifying exons in a eukaryotic genome, comprising coff the array; identifying exons in a eukaryotic genome, comprising coff the eukaryote; and (b) measuring the label detectably bound to each probe of the eukaryote; and (b) detecting specific hybridisation of detectably coff in the above mentioned microarray; assigning exons, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, and (b) measuring the expression of each of the exons in the tissues and/or cell types using hybridisation to a single exon probe with exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the exons should be assigned to a single gene; a peptide comprising one coff 12011 sequences, mentioned in the specification, or encoded by the exons human lung derived mRNA and for the study of lung diseases (COPD), interstitial lung disease (IID), familial idiopathic pulmonary diseases. Hermansky-Pudlak syndrome, sarcoidosis, pulmonary disease, croman protensis, pulmonary disease. The proses are sequence is a peptide/protein and hyaline membrane disease. The present sequence is a peptide/protein
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03-AUG-2000;
21-SEP-2000;
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26-MAY-2000;
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2000US-060840B.
2000US-0632366.
2000US-234687P.
2000US-236359P.
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RESULT 181
ABG22649
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              The invention relates to isolated polynucleotide (I) and (C) polypeptide (II) sequences. (I) is useful as hybridisation probes, (C) polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags (C) polynucleotides are also used in diagnostics as expressed sequence tags (C) polynucleotides are also used in diagnostics as expressed sequence tags (C) polynucleotides are also used in tiasues expressed sequence tags (C) in tissues to restore normal activity of (II) or to treat disease states involving (C) (II). (II) is useful for generating antibodies against it, detecting or (C) (II). (II) is useful for generating antibodies against it, detecting or (C) (II). (II) and its binding partners are useful in medical activation of sites expressing (II). (I) and (II) are useful for treating (C) imaging of sites expressing (II). (I) and (II) are useful for treating (C) the polypeptide and polypucleotide sequences have applications in (C) the polypeptide and polypucleotide sequences have applications in (C) the polypeptide and polypucleotide sequences have application of mutations (C) and to produce other types of data and products dependent on DNA and (II) and control action of the forestic manner of the forestic manner of the forestic movel human (C) therefore the forestic manner of the forestic movel human (C) the forestic manner of the forestic movel human (C) the forestic manner of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
amino acid sequences. diagnostic amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
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23-AUG-2000;
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Considers involving aberrant protein expression or biological activity. The polymers biodivers in the superior of diagnostics as expressed sequence tags of the restore normal activity of (II) or to treat disease states involving control and its binding partners are useful in gene therapy techniques (II). (II) is useful in gene therapy techniques (II). (II) and its binding squinst it, detecting or consistent expressing (II). (I) and (II) are useful in medical consistent expression or biological activity. (II) and (III) are useful for treating (III) and (III) are useful for treating (III) are useful for treating (III) are useful for treating (III). (II) and (III) are useful for treating (III) are useful activity. (III) are useful activity. (III) are useful activity. (III) are useful for medical activity. (III) are useful for medical activity. (III) are useful for treating (III) are useful for medical activity. (III) are useful for treating (III) are useful for treating (III) are useful for medical activity. (III) are useful for treating (III) are useful for treating (III) are useful for medical activity. (III) are useful for treating (III) are useful for treating (III) are useful for medical activity. (III) are useful for medical for medical for other traits to assess biodivers
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                                                                                                                                                                                                                                                        AAW79463-67 represent Staphylococcus aureus WCHU (NCIMB 40771) proteins that have homology to a Cowpea extensin-like protein fragment. The S. aureus proteins are used to generate antibodies and to screen for antimicrobials. The products are used to treat or prevent bacterial infections, particularly where caused by S. aureus but also against Helicobacter pylori. Particular applications are to treat subjects before surgery or insertion of an in-dwelling device (alternatively the device itself is impregnated before placement). The nucleic acid sequence is used as sources of antisense sequences (for therapeutic use) or regulatory elements for controlling expression of bacterial genes, and for antibacterial screening. The protein can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity nes 5; Conserv
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                                            HRSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Page 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RL;
                                                                                           Similarity
5; Conserv
                                                                                                                                                                                                                                         used
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al infection; Helicobacter pylori; vaccine.
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                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114pp;
                                                                                    33.3%; 50
100.0%; Pr
0;
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prevention and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                         Score 5; DB 1; Pred. No. 2.2
0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                               19; L
.2e+02;
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                                                                                                                                        Length 47;
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RESULT 184
ABB40766
ID ABB407
XX ABB407
XX ABB407
XX Pept1d
XX Human;
XX Homo g
YX WO2001
XX HO2001
XX HO2
ARESULT 185
AAM61626
ID AAM616
AC AAM616
XX O5-NOV
XX U5-NOV
XX Human;
KW Human;
KW microa
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Best Local s
Matches 5
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
    epilepsy; cancer.
                     Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                         Human brain expressed single
                                                                                                                                           05-NOV-2001
                                                                                                                                                                                                                                  AAM61626 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analyzing gene expression
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les 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome-derived single exon nucleic acid probes zing gene expression in human fetal liver -
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ilarity 100.0%;
Conservative (
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO 33401; 639pp + sequence listing;
                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide;
                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression; single exon nucleic acid probe
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                                                                                           probe encoded protein SEQ ID NO: 33731.
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AAM74418
ID AAM7
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AC AAM7
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Home
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Matches 5
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001
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27-SEP-2000;
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03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                 Human; bone
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                                                                                                                                         30-JAN-2001; 2001WO-US00668
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                                                                                                                                                                                                                                                                              sapiens.
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2000US-0180312.
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2000US-0608408.
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2000US-0234687.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                              cancer;
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                    Human bone marrow expressed probe encoded protein SEQ ID NO: 34724.
                                                                                                                                                                                                                     AAM74418 standard; Protein; 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.3%; Silarity 100.0%; Conservative 0;
                     marrow expressed exon; gene expression analysis; probe;
leukaemia; lymphoma; myeloma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT 187
AAM34532
ID AAM345
XX AAM345
XX Probe;
XX Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR XXX PR XX PR XXX PR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM34532 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #8569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM34532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 GPHRS 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GPHRS 8
                                                                                                                                                                                                                                            2001-488897/53
                                                                                                                                      genome-derived single exon nucleic acid zing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microarray;
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                  Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoded by probe for measuring placental gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression in
                                                                                                                                                                                                                                                                                                               DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.3%;
                                                                                                                                                                                                                                                                                                           Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34724; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  placenta;
                                                                                                                                                                                                                                                                                                               ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Į.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 5;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a number of single exon
                                                                                                                                                                                                                                                                                                               Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antenatal diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; LC
NO. 2.3e+02;
O;
                                                                                                                                                                  probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic
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present

relates

single

exon

nucleic acid

probes

(SENP

antipsoriatic; antiparkinsonian;

ian; nootropic; antiarthritic;

27;

SEQ

ID .No 34801;

654pp; English.

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RESULT 188
AAB42306
ID AAB423
XX Human;
KW Human;
KW Ullner
KW Inmunno
KW Inm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1999;
02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; hypotensive; dermatological; imfliently antiheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypotrension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism, SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                     AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                          Claim 11;
                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               see AAI31315-AAI57546). The present sequence is a peptide encoded leach probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples deficed human placenta. The probes are useful for antenatal diagnosis human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                WPI; 2000-602362/57.
N-PSDB; AAC76515.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB42306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GPHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    damage; cartilage damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFX ORF2070 polypeptide sequence SEQ ID NO:4140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 5; Conserv
                                                                                                                                                                        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0127636.
99US-0127728.
2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Leach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0127607
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100.0%; Pr
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                                                                                                                                                                        5507pp;
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                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 5;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; L
.3e+02;
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RESULT 189
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                                                                                                                                                          Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
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                                                                                               Disclosure;
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29-AUG-2000;
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antidiabetic; hypotensive; dermatological; immunosuppressive;
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les 5; Conserv
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DB; ABN21410.
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                                                                                           SEQ ID 11298; 1037pp; English.
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2000US-228716P.
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3. 2.3e+02;
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1

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09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
01-APR-1999
06-APR-1999
08-APR-1999
116-APR-1999
119-APR-1999
21-APR-1999
23-APR-1999
23-APR-1999
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23-APR-1999
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                                                                                                                                                                                                                          25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                                                                          25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                      termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 74532.
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990S-0129845.

990S-0130077.

990S-0130449.

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990S-0130891.

990S-0131449.
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99US-0127462.
99US-0128234.
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990S-0145919 990S-0145919 990S-0145919 990S-0146386 990S-0146388 990S-0147303 990S-0147303 990S-0147303 990S-0147303 990S-0147303 990S-0147416 990S-0147416 990S-0148341 990S-0149368 990S-0149368 990S-0149368 990S-0149368 990S-0149369 990S-0150566 990S-0150566 990S-0151066 990S-0151066 990S-0151066 990S-0151086 990S-0151086 990S-0151086 990S-0151086 990S-0151086 990S-0151086 990S-0155465 990S-0155465 990S-0155865	9US-01450 9US-01450 9US-01450 9US-01450 9US-01451 9US-01451 9US-01452 9US-01452
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RESULT 191
ABP10197
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KW Hyperp
KW degene
KW cardio
KW hypert
KW immune
KW autoim
KW hypert
KW immus
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KW ocardio
KW hypert
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The present invention describes substantially purified human (referred to as open reading frame, ORFX, where X is 1-11491
                                                                       Disclosure;
                                                                                                               Novel human polypeptides and polynucleotides useful for diagnosing preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders -
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29-AUG-2000;
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13 TPESR 17
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DB; ABN25949.
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99US-0161361.
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99US-0160768.
99US-0160770.
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99US-0161993.
99US-0162142.
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                                                                  ID 20376; 1037pp;
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0; Mismatches
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psoriasis; benign tumour; haemorrhage;
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                                                                    English
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NO. 2.5e+02;
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proteins
(see Tab
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Table
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RESULT 192
AAUGO387
ID AAUGO3
AC AAUGO3
AC AAUGO3
AC APPOPIO
KW SAPHO
KW UVeiti
KW Inflam
KW dermat
XX

POPI 01-NOV
XX
PPOPIO
PN WO2001
XX
PPOPIO
PN WPI;
PN WPI;
PN WPOPIO
PT VACCOI
PT V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC in the specification). ABN15762 to ABN27252 encode the human ORFX CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for CC treating or preventing a pathology associated with an ORFX-associated CC disorder in humans, and in the manufacture of a medicament for treating a cc sequences can be used in gene therapy. ORFX sequences can be used in the cc treatment of cancer, hyperproliferative disorders, cirrhosis of liver, cc psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, cc steoarthritis, neurodegenerative disorders, disorders, haemorrhage, cc steoarthritis, neurodegenerative disorders, cirrhosis of liver, cc psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, cc steoarthritis, neurodegenerative disorders, cirrhosis or organ cransplantation, cardiovascular diseases, diabetes mellitus, systemic cc lupus erythematosus, hypertension, hypothyroldism, cholesterol ester cc storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host clisease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, chemical disease, and for gut corporative disorders, or periodontal disease, and for gut creperfusion injury in various tissues and conditions resulting from cc systemic cytokine damage.
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Best Local :
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2001.
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                                                                                                                            N-PSDB;
                                                                                                                                                                                                                      L'maisonneuve
                                                                                                                                                                                                                                                         Skeiky YAW,
                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
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| HRSTP 34
                                                                                                                            2001-616774/71.
DB; AAS59609.
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5; Conserv
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e J, Zhang Y,
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100.0%; Pr
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Pred. No.
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S, Carter [
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Propionibacterium acnes polypeptides and nucleic acids useful vaccinating against and diagnosing infections, especially usefureating acne vulgaris -

seful for y useful 1

2000US-0225268. 2000US-0225270. 2000US-0225447. 2000US-0225757. 2000US-0225757. 2000US-0225759. 2000US-0225759.

2000US-0220964. 2000US-0224518. 2000US-0224119. 2000US-0225213. 2000US-0225214. 2000US-0225266. 2000US-0225267.

2000US-0217496. 2000US-0218290. 2000US-0220963.

2000US-0216647. 2000US-0216880. 2000US-0217487.

2000US-0227009. 2000US-0228924. 2000US-0229287. 2000US-0229343.

2000US-0226681. 2000US-0226868. 2000US-0227182.

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RESULT 193
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Best Local
                               04-FEB-2000
24-FEB-2000
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (BLISA).

Note: The sequence data for this patent did not form part of the printed as pecification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunoger polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
                                                                                                                                                                                                          17-JAN-2001;
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                                                                                                                                                                                                                                                                             WO200155313-A2
                                                                                                                                                                                                                                                                                                                                               excretory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
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 7-JUN-2000;
8-JUN-2000;
0-JUN-2000;
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                                                                                                                                                                                                                                                                                                             sapiens
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5; Conser
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2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-0214886.
2000US-0215135.
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                                                                                                     2000US-0186350.
2000US-0189874.
                                                                                                                                      2000US-0180628
2000US-0184664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide SEQ ID NO 345.
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2.6e+02;
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s caused by
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21-SEP-2000

21-SEP-2000

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29-SEP-2000

21-SEP-2000

29-SEP-2000

20-CCT-2000

20-CC
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05-SEP-2000;
05-SEP-2000;
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30-AUG-2000;
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14-AUG-2000;
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07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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14-SEP-2000;
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08-SEP-2000;
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06-SEP-2000;
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2000US-0229344
2000US-0229349
2000US-0229513
2000US-0230438
2000US-0231243
2000US-0231414
2000US-0231414
2000US-0232881
2000US-023298
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2000US-0232883
2000US-0232883
2000US-0238836

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20-OCT 2000
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20-OCT 2000
01-NOV 2000
08-NOV 2000
017-NOV 2000
17-NOV 2000
17-NO
The invention relates to novel excretory system related human polynucleotides (AAI98507-AAI99503) and the encoded proteins (AAM995913) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy, especially disorders related to the excretory system. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                 2001-465569/50.
DB; AAI98581.
                                                                                                                                                                                                                                                                                                                        CA,
                                                                                                                                                                                                       d nucleic acid molecule encoding excretory system antigen preventing, treating or ameliorating a medical condition
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2000US -0251988.

2000US -0251988.

2000US -0256719.

2000US -0251479.

2000US -0251866.

2000US -0251868.

2000US -0251869.

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2000US-0249297.
2000US-0249299.
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2000US-0246528
2000US-0246532
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2000US-0246611
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2000US-0246523.
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2000US-0250160.
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RESULT 194
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; antiallergic; hepatotropic; antidiabetic;
                                                                                                                                                                                                                                        17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              opthalmological; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antipagene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
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14 - AUG - 2000; 14 - AUG - 2000; 14 - AUG - 2000; 14 - AUG - 2000; 14 - AUG - 2000; 14 - AUG - 2000;

2000US-0225270. 2000US-0225447. 2000US-0225757. 2000US-0225758.

2000US-0225267

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The invention relates to novel kidney related polynucleotides (AAM52971-AAM63793) and the encoded polypeptides (AAM2417-AAM42691) CC collectively known as kidney antigens and the use of such kidney antigens CC for detecting disorders of the kidney, especially kidney cancer and CC kidney cancer metastases. The polynucleotides and proteins are also CC useful for preventing, treating or ameliorating medical conditions CC e.g. by protein or gene therapy. The genes are isolated from a range CC proteins, antibodies and (ant)agonists are useful in the diagnosis, CC treatment tand prevention of: (a) cancer, e.g. breast and ovarian cancer, CC and other cancers of the adrenal gland, bone, bone marrow, breast, CC gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple csclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases useh as viral, bacterial, fungal and CC parasitic infections.
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N-PSDB; AAI62977.
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2000US-0249208.
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2000US-0249211.
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2000US-0249218.
2000US-0249218.
2000US-024929.
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2000US-0232401. 2000US-0233063. 2000US-0233064. 2000US-0233065. 2000US-0234223.

2000US-0232397. 2000US-0232398. 2000US-0232399. 2000US-0232400.

2000US-0232080. 2000US-0232081. 2000US-0231968.

14-AUG-2000 18-AUG-2000 22-AUG-2000 22-AUG-2000 23-AUG-2000 30-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 06-SEP-2000 08-SEP-2000
2000US-0229509 2000US-0229513 2000US-0227009. 2000US-0228924. 2000US-0229287.

2000US-0229343 2000US-0229344 2000US-0225759. 2000US-0226279. 2000US-0226681. 2000US-0226868. 2000US-0227182.

2000US-0230437. 2000US-0230438. 2000US-0231242.

2000US-0231243

08-SEP-2000
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29-SEP-2000
20-OCT-2000
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2000US-0236368. 2000US-0236369. 2000US-0236370. 2000US-0236802.

2000US-0236327 2000US-0236367

2000US-0235484 2000US-0235834 2000US-0235836

2000US-0241809 2000US-0241826 2000US-0244617 2000US-0246474 2000US-0246475 2000US-0246475 2000US-0246477 2000US-0246477 2000US-0246478

2000US-0240960. 2000US-0241721. 2000US-0241785. 2000US-0241786. 2000US-0241787. 2000US-0241808.

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                       CC AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
CC sequences, corresponding to human secreted proteins. AAX64651 to
CC AAX65438 represent the EST-related proteins corresponding to AAZ42265 to
CAAX3052. The 5' ESTS can be used for producing secreted human gene
CC products. They can be used to identify and isolate 5' untranslated
CC regions (UTRs) and upstream regulatory regions which control the
CC location, development stage, rate, and quantity of protein synthesis, as
CC well as stability of mRNA. The ESTs are also useful as probes for
CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can
CC diagnostic procedures to identify individuals, or in
CC diagnostic procedures to identify individuals having genetic diseases
CC resulting from abnormal gene expression. The products may also be used in
CC used for directing extracellular secretion of a polypeptide or the
CC insertion of a polypeptide into a membrane, or importing a polypeptide
CC into a cell. The proteins encoded by the EST sequences may be useful in
CC treating a variety of human conditions. Secreted proteins have
CC valuable. AAZ42249 to AAZ42264 and AAX64644 to AAX64650 represent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 704; 837pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
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28-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                  diagnostic,
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               of the present
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                                         CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II), (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC specification, but was obtained in electronic format directly from WIPO

Cc specification, but was obtained in electronic format directly from WIPO
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                                at ftp.wipo.int/pub/published_pct_sequences
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ESRAA 15
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                                                                                                                                                                                                                                                                                                                                                         invention relates to isolated polynucleotide (I) and
ypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-639362/73
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
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2000US-0649167
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100.0%; Pred. No.
Live 0; Mismatcl
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D. 2.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutations
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RESULT 197
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Best Local
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
                                                                                                                                                              The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM/8323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny, inhibit activity and may be useful in the diagnosis and/or treatment of career leverage activity and may be useful in the diagnosis and/or treatment of career leverage activity.
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Zhao QA,
     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic
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                                                  were missing
                                                                         Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages
                                                                                                                                             treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
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                                                                                                                           inflammation.
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nes 5; Conserv
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DB; AAK51919.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                acids encoding polypeptides with cytokine-like activities in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Liu C,
, Wang D,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                 Page 3715; 6221pp; English
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2000US-0560875.
2000US-058075.
2000US-0520325.
2000US-062325.
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2000US-0633561.
2000US-0693325.
2000US-0728422.
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                                                  at the time of publication
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     B
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, Wang J, zl
Wejhrman T,
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                                                                         as the relevant pages
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J, Zhang J, rc..
T, Goodrich J
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ang J, Ren
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5. 2.7e+02;
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F, (
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from
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                                                                         (AAK52582) and 3666 the sequence listing
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R, ₩
                                                                         sequence listing
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Query Match

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RESULT 198
AAU46591
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                                        pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Matches 5; Conserv
Sequence
                                                                                                                                                                                                                                                                                        the treatment, prevention and diagnosis of medical conditions of P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                         Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in
                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
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uveitis; endoph
                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID No 7786; 1069pp; English
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DB; AAS59534.
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, Jen S, Carter
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Mismatches 0;
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                                             part of the printed directly from WIPO
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                                                                         Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in CC the treatment, prevention and diagnosis of medical conditions caused by CP acnes. The disorders include SAPHO syndrome (synovitis, acne, CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the CC presence or absence of P. acnes in a patient comprises contacting a CC sample with a binding agent that binds to the proteins of the invention CC and determining the amount of bound protein in the sample. The CC polypeptides may be used as antigens in the production of antibodies CC specific for P. acnes proteins. These antibodies can be used to CC downregulate expression and activity of P. acnes polypeptides and CC therefore treat P. acnes infections. The antibodies may also be used as CC diagnostic agents for determining P. acnes presence, for example, by CC enzyme linked immunosorbent assay (ELIAA).
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02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes polypeptides and nucleic acids useful vaccinating against and diagnosing infections, especially usestreating acne vulgaris -
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Sequence
                                              Note: The sequence data for this patent did not specification, but was obtained in electronic for
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                               at ftp.wipo.int/pub/published_pct_sequences
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ve J, Zhang
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02-JUN-2000;
07-JUL-2000;
                                                                                   presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by
                                                                                                                                                                                                                  Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by p. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky YAW, Persing DH, P
                           at ftp.wipo.int/pub/published_pct_sequences
                                            Note: The sequence data for this patent did not specification, but was obtained in electronic for
                                                                            enzyme
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-52-322-2
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5212-68-484-258-4
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                          ADDRESSEE TESTA, HURWITZ & THIBEAULY
STREET: High Street Tower - 125 High;
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver:
COMPUTER APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION NUMBER: 08/592,541
APPLICATION NUMBER: 08/592,541
FILING DATE: 10-NOV-1997
CLASSIFICATION NUMBER: 08/592,541
APPLICATION NUMBER: 08/592,541
FILING DATE: 10-NOV-1997
CLASSIFICATION NUMBER: 08/592,541
FILING DATE: 10-NOV-1997
CLASSIFICATION NUMBER: 08/592,541
FILING DATE: 617) 248-7100
TELEPHONE: (617) 248-7100
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LEEGTH: 15 amino acids
TYPE: Amino acids
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US-08-967-101-170
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Patent No.
GENERAL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 TYPE: amino a STRANDEDNESS: TOPOLOGY: lin
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                         amino acid
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High Street Tower - 125 High Street
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US-08-469-537A-98
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US-09-124-698-170
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                                                                             Sequence 170, Application US/09124698 Patent No. 6117978
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                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: ST. GEORGE-HYSI
APPLICANT: ROMMENS, JOHANII
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENET.
TITLE OF INVENTION: TO AL.
                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: [617] 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/592,541 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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es 15; Conservative
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                                                                  INFORMATION:
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High Street Tower - 125 High Street
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                                                    ST. GEORGE-HYSLOP, PETER H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ST. GEORGE-HYSLOP,
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 GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
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Pred. No.
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 248-700
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
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APPLICANT:
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NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High:
                                          CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                APPLICANT: FRASER, PAUL E TITLE OF INVENTION: GENET TITLE OF INVENTION: TO AL
                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                             COMPUTER READABLE FORM:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                           COUNTRY:
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                             APPLICATION NUMBER:
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et Tower -
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RESULT 5
US-08-496-841C-167
US-08-496-841C-167
Sequence 167, Application 6210919
Patent No. 6210919
GENERAL INFORMATION:
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-127-480-170
                                                                                                                                   US-08-496-841C-167
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                                                                                                                                                                                                                           APPLICATION NÜMBER: US/08/496,841C FILING DATE: 28-Jun-1995 CLASSIFICATION: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D. REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPHONE: (212) 527-7700
TELEPHONE: (210) 53-6337
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                   Matches
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                             MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 167:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                             SHLGPHRSTPESRAA 15
SHLGPHRSTPESRAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHLGPHRSTPESRAA 15
                                                                 15;
                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pitcher,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08496841C
                                                              100.0%; ilarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROMMENS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248-7100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOHANNA M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                            Score 15; DB 4;
Pred. No. 1e-09;
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Pred. No.
                                                               Mismatches
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Mismatches
                                                                                                DB 4;
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                                                                                             Length 15;
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                                                               Indels
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                                                                                                                                                                                                                                                                                                                            RESULT 7
US-08-875-972-4
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US-09-124-523-170
                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08875972 Patent No. 5985564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6395960 GENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS,
                                                                                                                                                                                                      APPLICANT: Huntington Potter and Jinhue Li
TITLE OF INVENTION: ASSAY FOR IDENTIFYING GENES
TITLE OF INVENTION: CHROMOSOME NON-DISJUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/124,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES
TITLE OF INVENTION: TO ALZHEIMER'S DIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: "-"
STREET: "-"
Yassac
                                                             COUNTRY: USA
ZIP: 02173-4799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                STATE: Massachusetts
                                                                                                                       CITY:
                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SHLGPHRSTPESRAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                     SHLGPHRSTPESRAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 100.0%;
1 Similarity 100.0%;
15; Conservative 0
                                                                                                                     Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   READABLE FORM:
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                                                                                                                                   Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09124523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15; DB Pred. No. 1e-
); Mismatches
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1e-09;
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RESULT 8
US-08-788-231A-15
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                      TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/002,4
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Granahan Esq., Yatricia
REGISTRATION NUMBER: 3X-227
REFERENCE/DOCKET NUMBER: HU95-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10FORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (781) 861-95.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SENERAL INFORMATION:
                                                                                                   NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 60.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                             APPLICATION NUMBER: US 6 FILING DATE: 26-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          PRIOR APPLICATION NATA:
PRIOR APPLICATION NUMBER, US 60/010,672
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
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                            SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPETIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 5370 M
CITY: Boulder
STATE: Colorad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 SHLGPHRSTPESRAA 300
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                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 24-JAN-1997
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STRANDEDNESS:
                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         80303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L'Hernault, Steven W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 15; DB 2; ilarity 100.0%; Pred. No. 1.7e-08; Conservative 0; Mismatches 0;
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                 acto
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08-AUG-97
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                                                                                                                                                                                                                                                                                                                                             Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                            US/08/788,231A
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                                                                                                                                             60-95
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HYPOTHETICAL: YES
US-08-788-231A-15
          δ.
                                                                                      ANTI-SENSE: NO; FRAGMENT TYPE: 1; ORIGINAL SOURCE: US-08-670-479-18
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US-08-670-479-18
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Best Local Similarity 100.
Matches 15; Conservative
                                     Best Loc
Matches
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                                                             Query Match
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                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,500
FILING DATE: 18-JUL-1996
APPLICATION NUMBER: 60/001,800
FILING DATE: 02-NG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hardy, John A. APPLICANT: Goate, Alison M.
                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                   TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 SHLGPHRSTPESRAA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: //>
CITY: King of Prussia
                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/670,479 FILING DATE: 26-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19406-0939
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1 SHLGPHRSTPESRAA 15
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                                                                                                                                                                                                     ENGTH:
                                     Similarity 100 15; Conservative
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                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                       Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08670479
                                                                                                                                                                                                 463 amino acids
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                                                                                                                                                               linear
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9 Swedeland Road
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                                                                                                               N-terminal
                                                                                                                                                   peptide
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                                    Score 15; DB 2; Pred. No. 1.9e-08; Mismatches 0;
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Pred. No. 1.9e-08;
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                                                           Length 463;
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342 SHLGPHRSTPESRAA 356

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US-08-888-077A-4
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                                                                                                                                                                                                                                                           RESULT 11
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                                                                                                                                                                                  Sequence 4, Applicati
Patent No. 6020143
GENERAL INFORMATION:
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Best Local S
Matches 15
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APPLICANT: Hardy, John A.
TITLE OF INVENTION: EARLY ONSET ALZHEIMER'S DISEASE
TITLE OF INVENTION: GENE AND GENE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                   APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES
TITLE OF INVENTION: TO ALZHEIMER'S DIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino I sing STRANDEDNESS: sing Type Inear
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road - UW2220; P.O.
                                                               NUMBER OF SEQUENCES: 4
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
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ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                             342 SHLGPHRSTPESRAA 356
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                                 STREET:
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OPERATING SYSTEM: DOS
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CITY: Philadelphia
                                                   ADDRESSEE:
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WESTFIELD
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                               E: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK 600 SOUTH AVENUE WEST
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JUL-1995
                                                                                                   GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE AND USES THEREFOR
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Pred. No. 1.9e-08;
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RESULT 12
US-08-788-231A-17
; Sequence 17, Application US/08788231A
; Patent No. 6019974
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Best Local Similarity
Thehes 15; Conserve
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APPLICANT: L'Hernau
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (908) 654-7866 INFORMATION FOR SEQ ID NO:
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                               FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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LENGTH: 463 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 654-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NATA:
APPLICATION NAMEE: US 08/592,541
FILING DATE: 26 JAN 1996
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 SHLGPHRSTPESRAA 356
                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 24-JA
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ZIP: 07090-1497
                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                  COUNTRY:
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: Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 amino acids
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                                                                                                                                                           umber: US/08/788,231A
24-JAN-1997
                                                                                                MBER: US 60/010,672
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Pred. No.
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS

17:

LENGTH:

465 amino acids

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                                                                                                                       ; TOPOLOGY: 1; MOLECULE TYPE: US-08-967-101-2
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; HYPOTHETICAL:
US-08-788-231A-17
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                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0;
                                                          Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                            TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC FOOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                           NAME: Pitcher, Edmund R. TELECOMMUNICATION: INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US FILING DATE: 10-NOV-19 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
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346 SHLGPHRSTPESRAA 360
                                                                                                                                                                  STRANDEDNESS:
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STRANDEDNESS: sir
TOPOLOGY: not rel
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                            1 SHLGPHRSTPESRAA 15
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High Street Tower - 125 High Street
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ROMMENS, JOHAI
FRASER, PAUL 1
                                                          100.0%; ilarity 100.0%; Conservative 0
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Pred. No.
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                                                                                    Length 467;
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RESULT 14

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US-08-967-101-134
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ANTORNEY/AGENT INFORMATION:

NAME: Pitcher, Edmund R.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEPAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: ST. GEORG
APPLICANT: ROMMENS,
APPLICANT: FRASER, P
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08967101 Patent No. 5840540
                                                                                                                                                                                                                                                                                                     Sequence 134,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 10-NOV-1997 CLASSIFICATION: 415 PRIOR APPLICATION DATA:
                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                        346 SHLGPHRSTPESRAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lir
                                                                                                    STREET: High
CITY: Boston
                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                         1 SHLGPHRSTPESRAA 15
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                                                       02110
                                                                                                                                                                                                                                                                                         5840540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino.acid
                                                                   Massachusetts: U.S.A.
                                                                                                                     E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 amino acids
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High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                       Application US/08967101
                                                                                                                                                                                                                    FRASER, PAUL E
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                                                                                                                                                                                                                                                      ST. GEORGE-HYSLOP, PETER H
                                                                                                                                                                                                                                     ROMMENS, JOHANNA M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Pred. No.
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PatentIn

Query Match

DB 2;

Length 467;

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; TOPOLOGY: 11; MOLECULE TYPE: US-08-592-541-2
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                                                                                                          TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
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APPLICANT: ST. GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                       NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                   CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: TESTA, HU
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PRIOR APPLICATION DATA:
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                                            TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
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TYPE: amino acid
STRANDEDNESS: single
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les 15; Conserv
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TELEFAX: (617) 248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 10-NOV-1997
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SOFTWARE: Patent:
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                                                                                                                                                                                                                                                                                                                                                                                                        E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
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FRASER, PAUL
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linear
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                                linear
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n Release #1.0, Version #1.30
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Pred. No.
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Query Match
Best Local Similarity
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US-08-592-541-134
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US-08-592-541-4
                                          GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PI
APPLICANT: ROMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Patent No.
                                                                                                                                                 Patent No.
                                                                                                                                                  Sequence 134, Application US/08592541 Patent No. 5986054
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APPLICANT: FRASER, E
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        346 SHLGPHRSTPESRAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 SHLGPHRSTPESRAA 360
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Boston
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                ADDRESSEE:
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5. 5986054
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E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
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(617) 24
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                                                                                                                    ST. GEORGE-HYSLOP, PETER H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRASER, PAUL
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                                                                                                                                                                                                                                                                                               Conservative
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                                          GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
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Pred. No. 2e-08;
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Pred. No. 2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THIBEAULT
125 High Street
                                                                                                                                                                                                                                                                                                Mismatches
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RESULT 19
US-08-923-454A-10
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Best Local Similarity 100.0%;
Matches 15; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08923454A Patent No. 6004794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08X592,541

FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: F
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LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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ADDRESSEE: Smithkline Beecham Corporation STREET: 709 Swedeland Road
                                                                      APPLICATION NUMBER: 60/02
FILING DATE: 06-SEPN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                    CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER 60/025436
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                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: King of Prussia
STATE: PA
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   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                   Baumeister, Kirk
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Clinkenbeard, Helen
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APPLICANT: Hardy, John
TITLE OF INVENTION: EA
TITLE OF INVENTION: GR
NUMBER OF SEQUENCES: (
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                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: 26-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road - UW2220; P.O.
                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                          FILING DATE: 18-JUD-1995
ATTORNEY/AGENT INFORMATION:
NAME: Han, william T
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
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LENGTH: 467 amino acids
 MOLECULE TYPE:
                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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HYPOTHETICAL:
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TYPE: amino acid
STRANDEDNESS: single
                              STRANDEDNESS:
                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/00 FILING DATE: 13-JUL-1995 APPLICATION NUMBER: 60/00
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CO
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Philadelphia
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les 15; Conserv
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TELEFAX: 610-270-5090
                TOPOLOGY:
                                                                                                          TELEPHONE: 610-270-5090
                                                                                                                                                                     REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
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protein
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Pred. No.
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Query Match

100.0%;

Score 15;

DB 3;

Length 467;

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                   Sequence 17, Application US/08888077A Patent No. 6020143
                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: ST. GE
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Matches 15; Conser
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/888,077A
FILING DATE: 03-7UL-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
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                             TITLE OF INVENTION:
                                                                                          APPLICANT:
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APPLICANT:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: SYSTEM: PC-DOS/MS-DOS
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ZIP: 07090-1497
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SEQUENCES:
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600 SOUTH AVENUE
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ROMMENS, JOHANNA M
FRASER, PAUL E
                                                                                                                    ROMMENS,
                                                                                       FRASER, PAUL E
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Conservative 0;
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                                                                                                                    GEORGE-HYSLOP, PETER H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                654-5000
                   GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE AND USES THEREFOR
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Pred. No.
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RESULT 23
US-09-124-698-2
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Matches
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Patent No. (
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                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                 PRIOR APPLICATION DANG
                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAGUT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                           APPLICANT: FRASER, PAUL
TITLE OF INVENTION: GENE
TITLE OF INVENTION: TO A
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FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: PALISI, THOMAG M
REGISTRATION NUMBER: 36,629
REFERENCE/DOCKET NUMBER: SCHERING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (908) 654-5000
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                                               APPLICATION NUMBER: FILING DATE:
                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                   CLASSIFICATION:
                                                                                                                                                                                                        STATE:
APPLICATION NUMBER:
                                                                                                                                                                                       COUNTRY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 07090~1497
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                                                                                                                                                                                                                     Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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   V08/592,541
                                                              US/09/124,698
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Pred. No.
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ATTORNEY/AGENT INFORMATION:

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346 SHLGPHRSTPESRAA 360

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Best Local Similarity
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                               Query Match
Best Local Similarity
Matches 15; Conserv
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE 467 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                            TYPE: amino acid
STRANDEDNESS: signopology: linear
                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
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             1 SHLGPHRSTPESRAA 15
Boston
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FRASER, PAUL E
                                          Conservative
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125 High Street
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RESULT 26
US-09-127-480-2
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US-09-124-698-134
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GENERAL INFORMATION:
                                                                                                                                                                              Patent No. 6194153
                                                                                                                                                                                          Sequence 2,
                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                         CORRESPONDENCE ADDRESS:
                                                                                                                  APPLICANT:
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APPLICANT: FRASER, PAUL E
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                                                                         NUMBER OF SEQUENCES:
                                                                                        TITLE OF INVENTION:
                                                                                                                                                APPLICANT:
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MEDIUM TYPE: Floppy disk
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Massachusetts
                          E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
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High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 amino acids
                                                                                                                  FRASER, PAUL E
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                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                ROMMENS, JOHANNA M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                     GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134:
                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                            Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETER H
                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                            2e-08;
                                                                                                                                                                                                                                                                                                                                                          Length 467;
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-127-480-2
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Patent No.
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Best Local Similarity
Matches 15; Conserv
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 248-710 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 SHLGPHRSTPESRAA 360
                   TELEFAX:
                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                STREET: High
CITY: Boston
                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SHLGPHRSTPESRAA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/127,480 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H: 467 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                 E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
              (617) 248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (617) 248-7100
(617) 70 NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 15; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                      183
                                                                                                                US/08X592,541
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RESULT 29
US-08-496-841C-2
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US-09-127-480-134
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                                                                                                                                                 Query Match
                                                                                                                      Matches
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Best Local Similarity
                                                                                                                                                                                                                                    TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: RRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                            NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08X592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
                                                              346 SHLGPHRSTPESRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 SHLGPHRSTPESRAA 360
                                                                                                                    Match 100.0%;
Local Similarity 100.0%;
les 15; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                          1 SHLGPHRSTPESRAA 15
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                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: High
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/127,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Massachusetts
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High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09127480
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                                                                                                                                   Score 15; DB 4;
Pred. No. 2e-08;
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Pred. No.
                                                                                                                    Mismatches
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                                                                                                                                                 DB 4; Length 467;
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                                                                                                                    Indels
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                                                                                                                    Gaps
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Sequence 2, Application US/08496841C Patent No. 6210919

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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-496-841C-2
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                                                                                                                                                                                                                                                                                                                                                                            RESULT 30
US-08-496-841C-4
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Patent No. 6210919
GENERAL INFORMATION:
GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
ROMMENS, JOHANNA M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 100.0%; Score 15; Local Similarity 100.0%; Pred. No.
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE NUMBER OF SEQUENCES: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ST.
                                                                                                                          CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                             STREET:
                                                                                                            ZIP: 10022
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APPLICATION NUMBER: US/08/496,841C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Darby & Darby, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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ROMMENS, JOHANNA M
FRASER, PAUL E
                                                                                                                                                                                                                                                                                FRASER, PAUL
                                                                                                                                                                             805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    805 Third Avenue
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                              Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 31
US-08-496-841C-134
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GENERAL INFORMATION:
Query Match 100.0%; 9
Best Local Similarity 100.0%; 9
Matches 15; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                     TELEFAX: (212) 7:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: U.S.A.
2IP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Uh-1995
CLASSIFICATION: <UNROWN>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION 1NFORMATION:
TELEPHONE: (212) 757-7700
TELEPAX: (212) 759-6237
NEORRATION FOR SCOT IN NO. 134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 SHLGPHRSTPESRAA 360
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CLASSIFICATION: <UNKNown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby,
STREET: 805 Third Avenue
                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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TELEPHONE: (212) 527-7700
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OMMUNICALL...
TELEPHONE: (212) 527-//
                                                                                                                                                                                    LENGTH: 467 amino acids
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                                                                                           SEQ ID NO: 134:
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Pred. No.
Score 15; DB 4; 1
Pred. No. 2e-08;
; Mismatches 0;
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                                  Length 467;
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346 SHLGPHRSTPESRAA 360

SHLGPHRSTPESRAA 15

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RESULT 33
US-08-706-344C-2
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                                                                                                                                                                                  Sequence 2, Application Patent No. 6248555
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              Matches
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GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 527-71
TELEPAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
                                                                                           APPLICANT: TANZI, RUDOLPH
APPLICANT: WASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related
TITLE OF INVENTION: Alzheimer's Disease
NUMBER OF SEQUENCES: 32
                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-7un-1995
CLASSIFICATION: <Unknown>
ATTORNEY,AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
REGISTRATION UNFORMATION:
TELEPHONE: (212) 527-7700
                                                                                                                                                                                                                                                                                                            346 SHLGPHRSTPESRAA 360
                              CITY: WASHINGTON
                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
COUNTRY:
                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                          1 SHLGPHRSTPESRAA 15
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compati
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ADDRESSEE: Darby & Darby,
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein SEQ ID NO: 136:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                      Application US/08706344C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
                g
                                                E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08496841C
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                    To Familial
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RESULT 34
US-08-706-344C-4
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INFORMATION FOR SEQ ID NO: 2:
                                                                                      APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT ENFORMATION:
                                                                                                                              APPLICATION NUMBER: US/01
FILING DATE: 30-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/01
                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN &
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/00 FILING DATE: 31-ANG-1995 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Genetic Alterations Related To Familial TITLE OF INVENTION: Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TANZI, RUDOLPH APPLICANT: WASCO, WILMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 SHLGPHRSTPESRAA 360
                                  NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1100 NEW CITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100 les 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SHLGPHRSTPESRAA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467 amino acids
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100.0%; Pred. No. 2e
cive 0; Mismatches
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                                        0609.4180001
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RESULT 36
US-08-706-344C-30
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US-08-706-344C-28
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING CLASSIFICATION: \536
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 60/003,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Genetic Alterations Related To Familial TITLE OF INVENTION: Alzheimer's Disease NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/00
APPLICATION NUMBER: 60/00
FILING DATE: 31-AUG 1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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APPLICANT: WASCO, WILMA
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                                                                                      346 SHLGPHRSTPESRAA
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ZIP: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/01 FILING DATE: 30-AUG-1996
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                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                       1 SHLGPHRSTPESRAA 15
                                                                                                                                                    Local Similarity
es 15; Conserva
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o. 6248555
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                                                                                                                                                                     Score 15;
Pred. No.
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                                                                                                                                                    Mismatches
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                                                                                                                                                                                     Length 467;
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RESULT 37
US-08-706-344C-32
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                                                                                                                                                                                                                                           Patent No. 6248555
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
APPLICANT: WASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related To Familial
TITLE OF INVENTION: Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                           Sequence 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/00:
APPLICATION NUMBER: 31-AUC 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                            NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: STERRE, KESSLER, GO
STREET: 1100 NEW YORK AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Genetic Alterations Related To Familial TITLE OF INVENTION: Alzheimer's Disease NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TANZI, RUDOLI
APPLICANT: WASCO, WILMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM FC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                            COUNTRY:
                                                                                                                                                             CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 30-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SHLGPHRSTPESRAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100 es 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                           Application US/08706344C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                              KESSLER, GOLDSTEIN & ORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Release #1.0, Version #1.30 (EPO)
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Pred. No.
                    Version
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                                                                                                                                                                                                 FOX P.L.L.C
                  #1.30 (EPO)
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30-AUG-1996

US/08/706,344C

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GENERAL INFORMATION:

APPLICANT: St. George-Hyslop, Peter H.

APPLICANT: Rommens, Johanna

APPLICANT: Fraser, Paul E.

TITLE OF INVENTION: Alzheimer's Related Prot
TITLE OF INVENTION: of Use

FILE REFERENCE: 1034/IF810-US1

CURRENT APPLICATION UMBER: US/09/227,725A

CURRENT FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
""" hes 15; Conserve
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; TYPE: PRT
; ORGANIZM: Caenorhabditis elegans
US-08-832-867-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: BAUMEISTER, RAIf
APPLICANT: BAUMEISTER, RAIf
TITLE OF INVENTION: DNA MOLECULES COMPRISING A PROMOTER CAPABLE OF
TITLE OF INVENTION: CONFERRING EXPRESSION OF A HETEROLOGOUS DNA SEQUENCE
TITLE OF INVENTION: ALL NEURAL CELLS AT ALL STAGES OF DEVELOPMENT IN C.
TITLE OF INVENTION: ELECANS AND USES THEREOF
FILE REFERENCE: 674503 2004
                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09227725A Patent No. 6383758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08832867C Patent No. 6376239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/832,867C CURRENT FILING DATE: 1997-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver.
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LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
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ATTORNEY/AGENT INFORMATION
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PRIOR APPLICATION DAMA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 SHLGPHRSTPESRAA 360
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les 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TORNEY/AGENT TORNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                               Alzheimer's Related Proteins and Methods
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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RESULT 41 US-09-124-523-4

; Sequence 4, Application US/09124523

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GENERAL INFORMATION:
APPLICANT: ST. GEO
APPLICANT: ROMMENS
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US-09-124-523-2
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                                                                                                           US-09-124-523-2
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SEQ ID NO 1
LENGTH: 46
TYPE: PRT
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Matches
                                                      Matches
                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                   TELEFAX: (617) 248-71
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                     STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Relicuration DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                         1 SHLGPHRSTPESRAA 15
                                                                                                                                                                           LENGTH:
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SHLGPHRSTPESRAA 360
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                                                                 Similarity
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                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts
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High Street Tower - 125 High Street
                                                                                                                                                                           467 amino acids
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROMMENS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                     S: single
linear
                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEORGE-HYSLOP, PETER H
                                                                                                                                                                                                                   7) 248-7000
248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                   US/08X592,541
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                                                                Score 15;
Pred. No.
                                                    Mismatches
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                                                                 DB 4;
2e-08;
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2e-08;
                                                                              Length 467;
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; MOLECULE TYPE: protein US-09-124-523-4
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US-09-124-523-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                      Sequence 134, Application US/09124523 Patent No. 6395960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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APPLICANT: ROMMENS, JOHANNA
APPLICANT: FRASER, POUL E
TITLE OF INVENTION: GENERIC
TITLE OF INVENTION: TO AL2H
NUMBER OF SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 248-71 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                      SENERAL INFORMATION:
                                                                                                                                                                             CORRESPONDENCE ADDRESS: ADDRESSEE: TESTA, HU
                                                                                                                                                                                                                       APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: PICCHEF, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,523
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                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Mar
                                                                                                                        STREET: High
CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: Patentin Release #1.0, Version #1.30
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 100.0%;
Local Similarity 100.0%;
les 15; Conservative 0
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STREET: High Street Tower - 125 High Street
                                                                                                      COUNTRY:
                                                                                                                                                                           ADDRESSEE:
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                                                                                       02110
                                                                                                                          Massachusetts
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High Street Tower - 125 High Street
                                                                                                       U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOHANNA M
                                                                                                                                                                                                                 183
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Pred. No.
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   Version #1.30
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Best Local Similarity
Matches 15; Conserve
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US-09-375-318-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO:
                                                                           INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
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                                                                                                                                                                                                        CURRENT APPLICATION DAMA:
APPLICATION NUMBER US/09/375,318
FILING DATE: 16-Aug 1999
CLASSIFICATION: <UNKNOWD>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levy-Lahad, Ephrat
Bird, Thomas D.
Galas, David J.
TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO
ALZHEIMER'S DISEASE
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                               NAME: Verna, James M.
REGISTRATION NUMBER: 33,287
REFERENCE/DOCKET NUMBER: 92/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tanzi, Rudolph E.
                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SEED and BEERY LLP
STREET: 701 Fifth Ave, Suite 6300
                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schellenberg, Gerard D.
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Pred. No.
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NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Win
SEQ ID NO 57
LENGTH: 256
TYPE: PRT
ORGANISM: Pinus radiata
US-09-325-932A-57
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Best Local Similarity
"~+~hes 6; Conserve
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US-09-325-932A-57
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 76, Application US/07857224B Patent No. 5958784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Flinn, Barry APPLICANT: Lasham, Anne
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPLICANT: Lasham, Annette ITLE OF INVENTION: Compositive Of INVENTION: death a
                                                                                                                                                                                             ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                   PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION:
                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 PESRAA 189
                                                                                                                                                Apple MacIntosh
OPERATING SYSTEM: MacIntosh
SOFTWARE: Micro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 SHLGPHRSTPESRAA 360
                                                                                                 APPLICATION NUMBER: US/07 FILING DATE: 03/25/92 + CLASSIFICATION: 436
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                                          TELEFAX:
                                                         TELEPHONE:
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                                                                                                                                                                                                                                                                        CITY: Zurich
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Local Similarity 100.0%;
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Hadlaubstrasse 151
                                      : (International) 41 1 632 2830 (International) 41 1 262 2437
                                                                                                                                                                                                                                           Switzerland
                                                                                                                                                       SYSTEM: MacIntosh 7.0 Microsoft Word
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100.0%;
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Pred. No.
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Pred. No.
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             ; MOLECULE TYPE: US-08-844-055-2
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; DATE: 1988
US-07-857-224B-76
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                                         TOPOLOGY:
                                                   STRANDEDNESS:
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                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
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Query Match
Best Local Similarity
"~+ches 6; Conserv
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Patent No. 5747313
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                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                             SEQUENCE CHARACTERISTICS
                                                                                                                   TELEPHONE: 610-270-4478
                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 18-APR 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lawlor, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
                                                                                        TELEPHONE: 610-270-5090
                                                                                                                                                                                             APPLICATION NUMBER: 9607 FILING DATE: 18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                          19406-0939
                                                                                                                                                                                                                                                                                                                                                                                        King of Prussia
                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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Protein kinase;
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                                             369 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Quinn, A. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science
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             linear
                                                                                                                                                                                                                                                                                                           IBM Compatible
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                                                                                                                                                                                                                                                                                                                        Diskette
protein
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                     single
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No. 5747313el Compounds
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                                                                                                                                                      38,891
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Pred. No.
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Length 369;

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; MOLECULE TYPE: protein US-09-006-849-2
                                                                                                                        RESULT 48
US-08-906-744A-2
                                                                                           sequence 2, Application US/08906744A
Patent No. 5795758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 2, Application US/09006849 Patent No. 6071731
                                                                                                                                                                                                                                                    Matches
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Matches 6; Conserv
                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
         APPLICANT: Gentry, Daniel
APPLICANT: Greenwood, Rebecca
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: NOVEL hiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 9607:
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 18-ARR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                       171 PESRAA 176
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                   10 PESRAA 15
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 709 Swedeland CITY: King of Prussia STATE: PA
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                                                                                                                                                                                                                                                  Local Similarity es 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 38
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRY: USA
19406-0939
                                                                                                                                                                                                                                                    Conservative
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gentry, Daniel
APPLICANT: Greenwood, Rebecca
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: NOVEL hiss
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR AFFICIATION NUMBER: 08/844, APPLICATION NUMBER: 18 APR-1997
APPLICATION NUMBER: 960799; FILING DATE: 18 APR-1996
ATTORNEY/AGENT INFORMATION: Gimmi, Edward R
NAME: Gimmi, Edward R
NAME: MINMER: 38,89
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MEDIUM TYPE: Diskette
                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
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nes 6; Conserv
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TOPOLOGY: 111
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OPERATING SYSTEM:
CLASSIFICATION:
                                                                         COMPUTER: IBM CON OPERATING SYSTEM:
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                             APPLICATION NUMBER:
                                                                                                                                                  COUNTRY:
                                                                                                                                        19406-0939
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                                                                          IBM Compatible SYSTEM: DOS
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100.0%; Prv
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                             US/09/093,134
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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06-AUG-1997
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Gaps

PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:

08/906,744

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RESULT 50
US-08-810-116-11
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Patent No. 5766860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
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APPLICANT: Terman,
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NAME: Gimmi, Edward n
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P314
TELECOMMUNICATION: TOORNATION:
TELECOMMUNICATION TOORNATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/930,548
FILING DATE: 23-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-831-3244
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/844,055
FILING DATE: 18-APR-1997
APPLICATION NUMBER 9607993.4
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 PESRAA 176
                                                                 NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                             STATE: New Jersey
                                                                                                                                                                                                         APPLICATION NUMBER: US/08/810,116 FILING DATE: 25-FEB-1997
                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 07470
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                                                                                                                                                                                          CLASSIFICATION:
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                                                                    31,298-01
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US-07-930-548A-11
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; PAGES: 3435-3439
; DATE: 1988
US-08-810-116-11
             Matches
                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/07930548A Patent No. 5861301
                                              Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 201-831-32.
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide PUBLICATION INFORMATION: AUTHORS: Gronwald, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS: LENGTH: 566 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 201-831-3244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREE: Cone Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Terman, Bruce I.
APPLICANT: Carrion, Miguel E.
TITLE OF INVENTION: Identification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                    AUTHORS:
JOURNAL:
          Local Similarity
nes 6; Conserv
                                                                                                                                                                      VOLUME: 85
PAGES: 3435-3439
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/930,548A FILING DATE: 23-NOV-1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Gordon, Alan M. REGISTRATION NUMBER: 30,637 REFERENCE/DOCKET NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Wayne
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100 les 6; Conservative
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             Conservative
                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A.
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SYSTEM: PC-DOS/MS-DOS
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100.08; r.
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          40.0%; Score 6; DB:
100.0%; Pred. No. 49;
ive 0; Mismatches
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                                                                      DB 2;
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          0; Indels
                                                                         Length 566;
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          Gaps
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1 SHLGPH 6

RESULT 52 US-07-803-633A-13

103 SHLGPH 108

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; LENGTH: 865 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-803-633A-13
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                                                                                                                                                                                                                                                              US-08-180-195-2
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/803,633A
FILING DATE: 19911210
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1644-103P
TELEPHONE: (703) 241-1300
TELEPHONE: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703) 241-284
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                           TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: INVENTION: IT
                                                                                                                                                     APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 No. 5369025th Washington Street
CITY: Falls Church
                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: RECOMBINANT FOWLPOX VACCINE FOR TITLE OF INVENTION: PROTECTION AGAINST MAREK'S DISEASE NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                       174 TPESRA 179
  ADDRESSEE:
STREET: 63
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ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 6; Conserva
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                                                                 Bell, Lilian A.

Bell, Lilian A.

Kindsvogel Ph.D., Wayne R.

Kindsvogel Ph.D., Wayne R.

KINDSVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS

NVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
3: Seed and Berry
6300 Columbia Center
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                          Sledziewski Ph.D., Andrzej
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100.0%; Pred. No
tive 0; Misma
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US-08-168-917-2
                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                 TOWNSEND AND TOWNSEND STREET: Steuart Street Tower, 20th Floor \ One Market STREET: Plaza CITY: San Francisco STATE: California COUNTRY: US

ZIP: 94105
COMPUTER ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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APPLICATION NUMBER: US 07/147,291
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/347,291
FILING DATE: 02-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: MAKI J.D., David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 3723836
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                            APPLICANT:
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APPLICANT:
APPLICANT:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR TITLE OF INVENTION: PLATELET-DERIVED GROWTH NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1106 amino acids
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MEDIUM TYPE: Flopp disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 98104-7092
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TELEFAX: 206-682-6031
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                                                                                                                                                                                                                                                                                                                                               Fretto,
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                                                                                                                                                                                                                                                                                                                                                               Tomlinson, James
                                                                                                                                                                                                                                                                                                                                               Larry J.
                                                                                                                                                                                                                                                          DOMAINS OF EXTRACELLULAR REGION OF HUMAN PLATELET-DERIVED GROWTH FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.0%;
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                Version
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RESULT 55
US-08-477-329-2
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REFERENCE/DOCKET NUMBER: 1241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08477329 Patent No. 5750375
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                                                                                                                        TELEX: 3723836
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 9900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: S
                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/477,329
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1106 amino aci
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                              TOPOLOGY: 1i
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NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/650,793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        656 SHLGPH 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6300 c
                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                             amino acid
                                                                                                                                            3723836
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                                                                                          1106 amino acids
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Kindsvogel Ph.D.,
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                                                             linear
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                                               protein
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Pred. No.
Score 6;
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RESULT 57
US-08-460-510-2
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Best Local Similarity
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                                                                                                                                                    Sequence 2, Application US/08460510 Patent No. 5872218
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICANT:
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LENGTH: 1106 amino aci
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       APPLICANT:
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NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990
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CURRENT APPLICATION DATA:
                                                APPLICANT:
                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
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TELEX: 3723836
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                                                                                                                                                                                                                                                                         1 SHLGPH
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98104-7092
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                                           Fretto, Larry J.
Giese, Neill A.
Escobedo, Jaime A.
Williams, Lewis T.
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                                                                                                       Tomlinson, James E.
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Kindsvogel Ph.D.,
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               DOMAINS OF EXTRACELLULAR REGION OF HUMAN PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
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100.0%; Pred. No.
Live 0; Mismatc
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CORRESPONDENCE ADDRESS:

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Query Match
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REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 0124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2420
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5891652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW
                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,490
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,510
FILING DATE: 02-UNN-1995
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
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LENGTH: 1106 amino aci
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MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  ATTORNEY/AGENT INFORMATION: NAME: Dow, Karen B.
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CITY: San Francisco
STATE: California
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STATE: California
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REGISTRATION NUMBER:
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Pred. No.
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US-08-980-400-2
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                             Query Match
Best Local S
Matches 6
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TELEX: 3723836
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 99
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/4 FILING DATE: 07-JUN-1995 ATTORNEY_AGENT INFORMATION: NAME: Maki, David J. REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TYPE: amino acid
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TOPOLOGY: linear
                                                                                                                                     TYPE:
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                                                                                                                                                LENGTH:
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                             6; Conserv
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98104-7092
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                               Conservative
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                                                                                                                        linear
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                                                                                                       protein
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100.0%; Pro
                          40.0%; Score 6; DB. 100.0%; Pred. No. 87 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHODS
                                                                                                                                                                                                                                                                                                                                   US 08/477,329
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wayne R.
OF PRODUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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5. 87;
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                                                           Length 1106
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656 SHLGPH 661

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                                                                                                                                                                                                               Sequence 2,
Patent No. (
                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Sledzie
APPLICANT: Bell, L
APPLICANT: Kindsvo
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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Patent No.
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APPLICANT: WILLIAMS, Lewis T.
APPLICANT: ESCOBEDO, Jaime A.
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415/326-2422 INFORMATION FOR SEQ ID NO:
                                                   CORRESPONDENCE ADDRESS
                                                                  APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
TITLE OF INVENTION: FUSIONS
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/309,322
FILING DATE: 10-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/151,414
FILING DATE: 02-FEB-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/309,322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market, Steuart Street Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,684
REFERICE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1106 amino acids TYPE: amino acid
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                               1 SHLGPH 6
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Seattle
                                                                                                                                                                                                                                  Application US/09583459A
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             6300 Columbia Center
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SYSTEM: PC-DOS/MS-DOS
                                  Seed and Berry
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                        TITLE OF INVENTION: A
TITLE OF INVENTION: A
TITLE OF INVENTION: H
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
             SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/583,21
FILING DATE: 30-MAY-2000
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
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NAME: Maki J.D., David J.
REGISTRATION NUMBER: 31,3
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CLASSIFICATION:
PRIOR APPLICATION DATA:
US
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                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                               STATE:
                                                                                                                                                                                             CITY: Seattle
                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 200 ---
206-682-6031
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APPLICATION NUMBER: US 0
FILING DATE: 02-MAY-1989
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FILING DATE: 22-JAN-1988
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CLASSIFICATION:
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GY: linear
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6300 Columbia Center
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Kindsvogel Ph.D., Wayne R.
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                                                                                                                                                                                                                                                           FUSIONS
36
                                                                                                                                                                                                                                                                                          METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.0%; Score 6; I
100.0%; Pred. No.
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APPLICATION NUMBER: US 0 FILING DATE: 27-DEC-1990 APPLICATION NUMBER: US 0

US 07/634,510

FILING DATE: 22-JAI APPLICATION NUMBER:

MBER: US 0 22-JAN-1988

07/146,877

US 07/347,291

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US-09-583-449A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MAK1 J.D., DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 9900
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BIM PC COMPATIBLE
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                    APPLICATION NUMBER: US 07/146,877
FILING DATE: 22-JAN-1988
APPLICATION NUMBER: US 07/347,291
FILING DATE: 02-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Maki J.D., David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D.
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: AND BIO
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                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 99
FELECOMMUNICATION INFORMATION:
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                                                                                                                                                       APPLICATION NUMBER: US 07 FILING DATE: 27-DEC-1990
                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 30-MA' CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 98104-7092
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IVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
IVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
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                      990008.446C3
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RESULT 65

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-09-435-059-2
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Patent No. 6323323
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                                                                                     Query Match
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Matches 6; Conserv
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                                                                                                                                                                                                           TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGI
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1106 amino aci
                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 206-622-4900 TELEFAX: 206-682-6031
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ADDRESSEE: Seed and Berry
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                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 99
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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656 SHLGPH
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ZIP: 981
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                                                        Local Similarity es 6; Conserv
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                             1 SHLGPH 6
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661
                                                        40.0%; Solitarity 100.0%; Solitarity 100.0%; Solitarity 0;
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                                                        %; Score 6; DB 4
%; Pred. No. 87;
0; Mismatches
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                                                                          DB 4;
                                                                                      Length 1106;
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                                                           Indels
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Query Match
Best Local Similarity
Watches 6; Conserve
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                                                                                                                                                                                                                                                                                                 -US92-00730-2
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ADDRESSEE: Townsend and Townsend and Crew STREET: One Market, Steuart Street Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/309,322
FILING DATE: 10-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/151,414
FILING DATE: 02-FEB-1988
                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                  TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR TITLE OF INVENTION: PLATELET-DERIVED GROWTH
                                                                                                                                                          APPLICANT:
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                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                             APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ESCOBEDO, TITLE OF INVENTION: F
                STREET: Steuar
STREET: Plaza
CITY: San Fran
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                                                                                                                                                                                                                                                                                                                                                                   656 SHLGPH 661
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CITY: San Francisco
STATE: California
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REGISTRATION NUMBER: 29,684
                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                    1 SHLGPH 6
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San Francisco
California
                                                                                                                                                                                                                                                                               Application PC/TUS9200730
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                                              Steuart Street Tower, 20th Floor \ One Market
                                                                                             GLESE, .....
ESCOBEDO, Jaime A.
Williams, Lewis T.
WILLIAMS, Lewis T.
VENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
VENTION: TOWNS OF EXTRACELLULAR REGION POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415/326-2422
                                                                                                                                                                                          Giese, Neill A.
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ESCOBEDO, Jaime A.

ENTIRE PLATELET-DERIVED GROWTH FACTOR RECEPTORS
                                                                                                                                                                                                         Fretto, Larry
                                                                                                                                                                                                                           Tomlinson, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
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                                                                  TOWNSEND and TOWNSEND
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Query Match
Best Local Similarity
Grandes 6; Conserve
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GENERAL INFORMATION:
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INFORMATION FOR
                            NAME: Ching, Edwin P.
REGISTON NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 230
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 326-2400
                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/151,141
FILING DATE: 02-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/309,322
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ESCObedo, Jaime A.
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24
               TELEFAX:
                                                                                                                                                                                                                                                           APPLICATION NUMBER: POFILING DATE: 19920131
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                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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: California
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                 (415)
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100.0%; Pr
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%; Pred. No. 87;
0; Mismatches
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Best Local :
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                                                                                                                                                                                                                                               TELEFAX: (619) 587-53
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2289
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
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LENGTH: 1106 amino acids
TYPE: AMINO ACID
                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, Suite 700
                                                                                                                                           ANTI-SENSE:
                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 450-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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TOPOLOGY: ] 1 **--
DLECTOr **
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nes 6; Conserv
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OPERATING SYSTEM:
                                                 Local Similarity es 6; Conserv
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                                                                                                                                                                                                                                                                                                                          NAME: Seidman, Stephanie L.
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0
FILING DATE: 02-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: La Jolla
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TPESRA 2294
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NO: 50:
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                                                 Score 6; DB;; Pred. No. 1.
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                                                              DB 4; Length 2353; 1.7e+02;
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US-08-804-227C-8
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APPLICANT: DeHoff,
APPLICANT: Kuhstos,
APPLICANT: Rosteck
APPLICANT: Sutton,
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Patent No. 58/07.
Patent No. 58/07.
Patent No. 58/07.
Patent No. 58/07.
Patent No. 58/07.
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SEQUENCE CHARACTERISTICS:
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                                                                             COMPUTER READABLE FORM:
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ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                 APPLICANT: Knhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                         4008 PESRAA 4013
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NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCI(DOS) TE CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: THOMAS G. PLANT 1501
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APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLKKETIDE S
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
CURRENT APPLICATION DATA:
        MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text
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                                                                                                                                   CITY: INDIANAPOLIS STATE: IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: unknown
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OPERATING SYSTEM:
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                                                                                                                 COUNTRY:
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Query Match
Best Local Similarity
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; MOLECULE TYPE: peptide
US-08-804-198-2
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Best Local Similarity
""" 6; Conserve
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                                                                                                                                                                                       NAME: CANTRELL, PAUL R.
REGISTRATION UNMBER: 36,470
REFERENCE/DOCKET NUMBER: P911
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 4550 amino aci
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                                                                                                                                                                                                                                                                                                                                 COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
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LENGTH: 4550 amino acids
                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: PAUL R. CANTRELL 1138
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TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
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10 PESRAA 15
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STATE: IN
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                                                                                                                                    amino acid
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                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burgett, Stanley G. Kuhstoss, Stuart A.
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N: 435
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                          Score 6; DB 2; Pred. No. 3e+0; Mismatches
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No. 3e+02;
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                                          DB 2; 1
o. 3e+02;
                                                        Length 4550;
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RESULT 73
US-08-707-874-1
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US-08-707-873-1
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                                                                        GENERAL INFORMATION:
APPLICANT: KARIN, MICHAEL
APPLICANT: DENG, TILIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: KARIN, MICHAEL
APPLICANT: DENG, TILIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 619/455-5110 INFORMATION FOR SEQ ID NO:
                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PITELECOMMUNICATION INFORMATION: 619/455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/315
FILING DATE: 29-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAILE PH.D., LISA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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TOPOLOGY: li
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OPERATING SYSTEM: PC-DOS/MS-DOS
 ADDRESSEE:
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SPENSLEY HORN JUBAS & LUBITZ
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100.0%; Pr
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                                                             NOVEL MITOGEN ACTIVATED PROTEIN KINASE,
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Query Match
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US-08-707-874-1
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US-08-315-067-1
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                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  APPLICANT: KARIN, MICHAEL
APPLICANT: DENG, TILIANG
TITLE OF INVENTION: NOVEL MITOGEN ACTIVATED PROTEIN KINASE,
TITLE OF INVENTION: FRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/315,067
FILING DATE: 29-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAILE PH.D., LISA A.
REGISTRATION NUMBER: P-38,347
REGISTRATION NUMBER: P-38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
NAME: HAILE PH.D., LISA A.
                                   APPLICATION NUMBER: US/0 FILING DATE: 29-SEP-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                               ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                   COUNTRY: U
ZIP: 90067
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REFERENCE/DOCKET NUMBER: PD3743
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1..11
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                                                                        US/08/315,067
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US-09-193-797-1
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Best Local s
Matches 5
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                   TELEFAX: 619/455-5110 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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                                            FEATURE:
                                                            MOLECULE TYPE:
                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 619/455-5100
                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: HAILE PH.D., LISA A.
REGISTRATION NUMBER: P-38,
REFERENCE/DOCKET NUMBER: P
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
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STRANDEDNESS: sir
TOPOLOGY: linear
                              NAME/KEY:
                                                                           TOPOLOGY:
                                                                                      STRANDEDNESS:
                                                                                                   TYPE: amino acids
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619/455-5110
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DENG, TILIANG
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SYSTEM: PC-DOS/MS-DOS
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100.0%; Pred. No. 17
Live 0; Mismatches
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RESULT 77
US-08-630-897-1
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Best Local Similarity
Thes 5; Conserve
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PCT-US95-01770-1
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                                                                                             Sequence 1, Application Patent No. 5639601
GENERAL INFORMATION:
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                    APPLICANT: SAEKI, TA
APPLICANT: SAKAMOTO,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
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ADDRESSEE: ROBBINS, BERLINER & CARSON
STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
           NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: FEATURE:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA TITLE OF INVENTION: NOVEL MITOGEN ACTIVATED PROTEIN KINASE, TITLE OF INVENTION: FRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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NAME: BERLINER, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/01770 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: LOS ANGELES
STATE: CALIFORNIA
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                                                                                                                             Application US/08630897
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SAKAMOTO, KENICHI
VENTION: PEPTIDE FOR DIAGNOSIS OF FOOT-AND-MOUTH
VENTION: DISEASE, AND ANTIGENS CONTAINING THE PEPTIDE FOR DIAGNOSIS
VENTION: OF FOOT-AND-MOUTH DISEASE
EQUENCES: 2
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1..11
                                                                                 SAEKI, TAKAKIYO
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100.0%; Pred. No.
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Pred. No.
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; MOLECULE TYPE:
US-08-630-897-1
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 413-222
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06751
FILING DATE: 19930719
                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold TITLE OF INVENTION: Immunological Conjugates of OMPC and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
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APPLICATION NUMBER:
FILING DATE: 24-MAY-
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR CITY: ARLINGTON
STATE: VIRGINIA
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STREET: P.O.
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REGISTRATION NUMBER: 24,
REFERENCE/DOCKET NUMBER:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSTPE 11
                                                                                                                                                                                                                                                                                                                                                    OF SEQUENCES:
                                                                                                                                                                                                                                                                             Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 amino acids
                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                 Merck & Co., Inc.
O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: JP 148364/1995
24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.3%; 5c.
100.0%; Pr
0;
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Pred. No.
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                                                                                                       ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-751-767A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-751-767A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; IMMEDIATE SOURCE: Random Epitope Library Alpha PCT-US93-06751-4
                                                  Query Match
Best Local S
Matches 5
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 138825
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                       TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: pe
HYPOTHETICAL: NO
ANTI-SENSE: NO
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LENGTH: 15 amino acid:
                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/00
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ANDERSO APPLICANT: GRANT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: NIXON
STREET: 1100 NOR'
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 138825
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GPHRS 8
                                                   Local Similarity es 5; Conserv
                                                                                                                                                         LENGTH:
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              4 GPHRS 8
GPHRS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                             26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MACDONALD, IAN D.
VENTION: INTERLUKIN-12 FUSION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                   Conservative
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                                            33.3%; 5--
100.0%; Pre
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                                                               Score 5;
Pred. No.
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                                                   Mismatches
                                                           DB
37;
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5. 23;
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                                                  Gaps
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RESULT 80
US-07-743-518-18
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local :
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TELEFAX: 202 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION UNMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/
TELECHMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
                                                                                                                                                                              GENERAL
                                                                                                                                               APPLICANT: APPLICANT:
                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/743,518
FILING DATE: 19910812
CLASSIFICATION: 424
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                    36 HLGPH 40
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   ADDRESSEE:
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ZIP: 20036-5601
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                                                                                                                                                                                                                                                                                                                  2 HLGPH 6
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5; Conserv
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                                            INVENTION:
                                                                                                                                                                                                            Application US/08466886
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                                                                     Riordan, John R.
Rommens, Johanna M.
Kerem, Bat-Sheva
Collins, Francis S.
Iannuzzi, Michael C.
Drumm, Mitchell L.
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IVENTION: PAPUA NEW GUINEA HUMAN T-LYMPHOTROPIC
IVENTION: VIRUS
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                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                      Buckwald, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YANAGIHARA,
                                                                                                                                                            Isui, Lap-Chee
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STERNE, KESSLER, GOLDSTEIN & FOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                           Cystic Fibrosis Gene
                                                                                                                                                                                                                                                                                                                                                             33.3%;
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; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-466-886-41
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US-08-469-617-41
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INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/466
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JOTGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1329
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PS C COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Cystic Fibrosis Gene
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W.
                 ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Drumm, MAPPLICANT: Buckwald TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                    FILING DATE: 00 CLASSIFICATION:
                                                                                                                                                                                                                                            CITY: Washington
STATE: DC
                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 PESRA 62
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Collins, Francis S.
Iannuzzi, Michael C.
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Rommens, Johanna M.
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                                                       06-JUN-1995
N: 800
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Jorge A.
ER: 29,021
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100.0%; Pr/
0;
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US-09-069-896-1
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Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4265
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US-09-134-001C-4265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMÁTION:

APPLICANT: Lynn DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4265
LENGTH: 161
TYPE: PRI
TYPE: 
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Best Local Similarity 100.
Thes 5; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hillman, Jennifer L. APPLICANT: Patterson, Chandra APPLICANT: Corley, Neil C.
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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TITLE OF INVENTION: DELAY!
TITLE OF INVENTION: CHANNE
NUMBER OF SEQUENCES: 4
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                  COUNTRY: UZIP: 94304
                                                                                                                           CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 SHLGP 103
                                                                                                                                                                                             STREET:
                                                                                                                                                                                             ADDRESSEE: Incyte Pharmaceuticals, Inc STREET: 3174 Porter Drive
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STRANDEDNESS: not
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                                                                                                                                                                                                                                                                                                                            CHANNEL HOMOLOG
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100.0%;
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b; Pred. No. 1.3
0; Mismatches
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o. 1.8e+02;
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US-09-471-468-1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hillman, Jennifer L.
APPLICANT: Patterson, Chandra
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: DELAYED RECTIFIER POTASSIUM
TITLE OF INVENTION: CHANNEL HOMOLOG
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: CETTODE, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/471,468
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: BRSTNOT03
CLONE: 637471
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                    CLASSIFICATION:
                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
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STRANDEDNESS: sir
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                                                                                 FILING DATE:
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3174 Porter Drive
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RESULT 87
US-09-530-058-6
; Sequence 6, Application US/09530058
; Patent No. 6379938
; GENERAL INFORMATION:
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; LIBRARY: BRSTNOT03
; CLONE: 637471
US-09-471-468-1
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                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-98
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Best Local Similarity
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 98, Application US/09413814
Patent No. 6225064
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide TITLE OF INVENTION: heteropolyketide compounds FILE REFERENCE: PCT/US 99/23535 CURRENT APPLICATION NUMBER: US/09/413,814 CURRENT FILING DATE: 1999-10-07 EARLIER APPLICATION NUMBER: DE 198 46 493.2 EARLIER FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 107
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SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
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APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
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les 5; Conserv
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TELEFAX: 650-845-4166
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                            APPLICANT: <Unknown>
TITLE OF INVENTION: Epoxide hydrolase
NUMBER OF SEQUENCES: 11
              CORRESPONDENCE
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Goldberg, Steven L
Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brandt, Petra
Cino, Paul M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reichenbach, Hans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bloecker,
                                                                                                                                                                                                                                                Conservative
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linear
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100.0%; Pr
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                                                                                                                                                                                                                                                            Score 5;
Pred. No
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Martens, Olson & Bear
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o. 2.5e+02;
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b. 1.9e+02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 40,637
REFERENCE/DOCKET NUMBER: VAI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-0176
INFORMATION FOR EGO ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/699,092
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 page Mill Road
CITY: Palo Alto
                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 PHRST 169
                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 5; Conserv
              NAME: Glaister, Debra
REGISTRATION NUMBER: 3
 REFERENCE/DOCKET NUMBER:
                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 PHRST 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/530,058 FILING DATE: 03-Jul-2000 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                        CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 501 Wes
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hart, Danie]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                California
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                                                                                                                                           US/08/911,853
33,888
IR: GC361-2
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                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM FOR ALTERED LEVELS
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o. 2.6e+02;
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                                                                                                                                                                                                                                                                           ; TOPOLOGY: US-09-479-409-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: US-08-911-853-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-479-409-37
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                                                                                                                                     Matches
                                                                                                                                                                     Best
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-845-6504 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gerritse, Gijsbert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION LEVELS
TITLE OF INVENTION: EXPRESSION LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 RSTPE 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
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                                                                  RSTPE 11
RSTPE
                                                                                                                                                                 Similarity
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24
                                                                                                                                                                                                                                                                                                                                                                                                      282 amino acids
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                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                       SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
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                                                                                                                           33.3%; Score 5; 1
100.0%; Pred. No.
Live 0; Mismatcl
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Pred. No.
                                                                                                                                     Mismatches
                                                                                                                                                                 DB 4; Length 282;
5. 2.9e+02;
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b. 2.9e+02;
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                                                                                                                                  Gaps
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RESULT 90

US-09-479-453-37

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Query Match
Best Local Similarity
Watches 5; Conserve
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US-09-479-453-37
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APPLICANT: Gerritse, Gijsber
APPLICANT: Quax, Wilhelmus J
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 37:
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            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                           APPLICANT: Moosa Mohammadi, Joseph Schlessinger, APPLICANT: and Stevan R. Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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ZIP: 94304-1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                       20 RSTPE 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Glaister, Debra J
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                   COUNTRY:
COMPUTER:
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                                                          90071-2066
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                                                                        U.S.A
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IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                33.3%;
                                                                                                                                                                                              CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN RECEPTOR TYROSINE KINASE
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Pred. No.
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No. 2.9e+02;
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RESULT 92
US-09-323-872A-34
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                                                                                                                                                                                                                                                   RESULT 93
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APPLICANT: COSChiqano, Peter
TITLE OF INVENTION: Compositions and Methods for Bioremediation
FILE REFERENCE: OHU-03640
CURRENT PELLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US/09/323,872A
CURRENT FILING DATE: 09/072,433
PRIOR FILING DATE: 1998-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 34
LENGTH: 308
                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                     Sequence 23, Application US/09199637A Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/09323872A Patent No.: 6395539
                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 30
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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TELEX: 67-3510
PMATION TO STANDARD TO STAN
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                                                                                                                                                                                                                                                                                                                                           44 PESRA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                                                                                                                                                                                                                                                                                                                                                                                                  10 PESRA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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Ausubel, Frederick
Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
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N: 530
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100.0%; Pro
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100.0%; Pred. No.
tive 0; Mismatc
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-23
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SEQ ID NO 23
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                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/231
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Date: I
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NFORMATION FOR SEQ ID NO: 2:
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HYPOTHETICAL:
ANTI-SENSE: NO
FRAGMENT TYPE:
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TITLE OF INVENTION: SEQUENCES AND USES THEREOF
TLE REFERENCE: 00786/361002
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           NAME: Pabst, Patrea L.
REGISTRAEN NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Korsmeyer, Stanley J.
TITLE OF INVENTION: HOX11 Gain and Loss of Function Murine
TITLE OF INVENTION: Models
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                                                                      TOPOLOGY:
                                                                                   STRANDEDNESS: single
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100.0%; Pred. No
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RESULT 95
US-08-712-948-1
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Best Local Similarity
~~+~hes 5; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08712948 Patent No. 5850002
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,948
         TELEFAX: (404)-815-655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                      REFERENCE/DOCKET NUMBER: WU
TELECOMMUNICATION INFORMATION:
                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KOTSMEYE TITLE OF INVENTION:
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PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL: 253
                                                                                                    NAME: Pabst, Patrea L. REGISTRATION NUMBER: 31,284
                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                  FILING DATE:
                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 30309-4530
                                                                                                                                                                                                                                                                                                                                                                  CITY: Atlanta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS: Korslmeyer,
TITLE: Deregulation of a Homeobox gene,
TITLE: the t(10;141) in T Cell Leukemia
                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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RELEVANT RESIDUES IN SEQ ID
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ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                 1100 Peachtree Street, Suite 2800
                                         : (404)-815-6508
(404)-815-6555
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Pred. No.
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                                 Matches
                                                              Query Match
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GENERAL INFORMATION:
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Matches 5; Conserv
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                                                                                                                                                                                        REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 263:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO FRAGMENT TYPE: N ORIGINAL SOURCE: ORGANISM: MUT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
 11 ESRAA 15
                              Local Similarity
nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 HLGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 HLGPH 6
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch. 1.44mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Blattner, Frederick R.
Burland, Valerie
Perna, Nicole T.
                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: No. 6365723el Sequences of NUMBER OF SEQUENCES: 265
                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 53701-2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Madison
                                                                                                                                                                                                                                                                                                                          NAME: Seay, Nicholas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                              33.3%; So ilarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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100.0%; Pr
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                                score 5; DB 4
s; Pred. No. 3.5
0; Mismatches
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                                                  DB 4;
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o. 3.3e+02;
                                               .5e+02;
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                                                              Length 348;
                                Indels
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US-08-239-431A-4
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LENGTH: 350
TYPE: PRT
ORGANISM: MOUSE
FEATURE:
NAME/KEY: UNSURE
LOCATION: (167)
                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08239431A Patent No. 5716835
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Patent No. 6323317
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                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NICHOLSON, Sandı
APPLICANT: METCALF, Donald
APPLICANT: NICOLA, NICOS A
TITLE OF INVENTION: THERAPE
FILE REFERENCE: 109762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                              APPLICANT: Regan, L.A...APPLICANT: Gil, Daniel W.
APPLICANT: Gil, Daniel W.
APPLICANT: WOOdward, David F.
APPLICANT: WOOdward, David F.
APPLICANT: WOODWARD EP PROSTAGLANDIN RECEPTOR
APPLICATION NUMBER: US/0 FILING DATE: 05-MAY-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                          SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 HRSTP 162
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                                                                                                                                                                               STREET: 620 Newport
CITY: Newport Beach
STATE: CA
                                                                                                           COMPUTER:
                                                                                        OPERATING SYSTEM:
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                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                 ADDRESSEE:
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ANT: HILTON, Douglas J
                                                                                                                                                          92660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09302769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RICHARDSON, Rachael T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WILLSON,
                                                                                                                                                                                                                 620 Newport Center Drive 16th Floor
                                                                                                                                                                         USA
                                                                                                        IBM Compatible
                                                                                                                                                                                                                                 Knobbe, Martens, Olson and Bear
                                                                                                                             Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.3%; Score 5; DB (100.0%; Pred. No. 3.5)
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                                              US/08/239,431A
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ATTORNEY/AGENT INFORMATION:

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FRAGMENT TYPE: Internal ORIGINAL SOURCE: US-08-239-431A-4
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Best Local Similarity
watches 5; Conserva
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                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/8/463,081B
FILING DATE: 5-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: VIVITAL PARAFION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Smith,
                                 NAME: Viviana Anzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEPHONE: (213) 489-4210
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide, TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 29,655
REFERENCE/POCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 PESRA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower St. - Suite 1900
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 PESRA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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Pred. No.
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RESULT 101
US-08-462-390B-6
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Best Local Similarity
"---hes 5; Conserv
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                                                                                                                               Matches
                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILLING DATE: 5-UNET-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                           TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: 607/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 6 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
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                                                                                                                                                                                                                                                                                                                         TELEPHONE: (610)470-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                104 PESRA 108
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                                                                                             10 PESRA 14
                                                                                                                             Local Similarity les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Valley Forge
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                                                                                                                                                                                                                                                            358 amino acids
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(610)470-0701
(610)470-0701
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                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratner & Prestia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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Nucleic Acids Encoding CR5 Polypeptide,

Vector and Transformed Cell Thereof, and
Expression Thereof
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100.0%; Pr
                                                                                                                           33.3%; Score 5; DB 2; Le
100.0%; Pred. No. 3.6e+02;
tive 0; Mismatches 0;
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Pred. No. 3.6e+02;
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                                                                                                                                                             Length 358;
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                                                                                                                               Gaps
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Sequence 6, Application US/08462390B Patent No. 5882894

GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling,

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                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08463074B Patent No. 6020155 GENERAL INFORMATION:
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:
APPLICATION DATA:
INCOMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: VIVIana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOKET NUMBER: 30,930
REFERENCE/DOKET NUMBER: 30,930
                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compactable

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

SOFTWARE: Version #1.25

CURRENT APPLICATION DATA:
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COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS'
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acid
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 PESRA 108
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nes 5; Conserv
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                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Ratner & Prestia

(B) STREET:One Westlakes-Berwyn
APPLICATION NUMBER: US/08/463,074B FILING DATE: 5-JUN-1995
                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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PENTION: Nucleic Acids Encoding CR1
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Pred. No.
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                                                                                                                                                                                                                                                                                                                            Fusion Protein, Vector an
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US-08-465-585C-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                               TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                  FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Arrani
                                                                                                                                                                                                                     FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
                                                                                 REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acid
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REFERENCE/DOCKET NUMBER: P6
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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nes 5; Conserv
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               LENGTH:
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Californiaa
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amino acid
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                                                                                                                                  Viviana Amzel, Ph. D. RATION NUMBER: 30,930
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               358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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VENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
VENTION: Transformed Cell Thereof, and Expression Thereof
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. (B) STREET:
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100.0%; Pr
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                                                                                                                    38149 (DART-050)
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3.6e+02;
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Patent No. 6057427
GENERAL INFORMATION:
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                                                                                                                                       APPLICATION NUMBER: 08/4
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 08/463,0/4
ETLING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/462,337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP APP. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, SOFTWARE: Version #1.25 CURRENT APPLICATION DATA:
                                                                                  APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
                                                                                                                                                                                                  FILING DATE: 5-JUN-1995 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
RELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release "1" SOFTWARE: Version Release "1" RREPUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 PESRA 108
                                                    NAME: Viviana Amzel, REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/465,585 FILING DATE: 5-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                     APPLICATION NUMBER:
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nes 5; Conserv
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: Nucleic Acids Encoding CR5
: Polypeptide, Vector and Transformed Cell Thereof, and
: Expression Thereof
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                                                                                                                                                                                                                                     08/463,081
                                                                                                                                                                               08/461,379
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-652-446-6
                                                                                                                                                                                                                                                                                                                                                                 US-09-552-322-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4
FENGTH: 358
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gould-Rothberg
APPLICANT: Rastelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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Best Local Similarity
                                                    SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09552322 Patent No. 6436642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09267423 Patent No. 6395878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
LENGTH: 384
TYPE: PRT
ORGANISM: Homo:
                                                                                                    CURRENT APPLICATION NUMBER: US/09/552, CURRENT FILING DATE: 2000-04-19 PRIOR APPLICATION NUMBER: 60/130,123 PRIOR FILING DATE: 1999-04-20 PRIOR APPLICATION NUMBER: 60/193,203 PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                 APPLICANT: RASTELLI TITLE OF INVENTION: METHOD OF CLASSIFYING A THYROID CARCINOMA USING TITLE OF INVENTION: DIFFERENTIAL GENE EXPRESSION FILE REFERENCE: 15966-548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 17023 DIV CIP
CURRENT APPLICATION NUMBER: US/09/267,
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: 09/019,393
EARLIER FILING DATE: 1998-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Regan, John W. APPLICANT: Gil, Daniel W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Woodward, David F.
TITLE OF INVENTION: No. 6395878el Human Prostaglandin EP Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Regan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO:
                                                                                         NUMBER OF SEQ ID NOS: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 08/239,431 EARLIER FILING DATE: 1994-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                      104 PESRA 108
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TOPOLOGY: linear
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es 5; Conser
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100.0%;
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100.0%; Pred. No. 3.
Live 0; Mismatches
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Pred. No.
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b. 3.6e+02;
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; SOPTWARE: PatentIn v
; SEQ ID NO 6
; LENGTH: 386
; TYPE: PRT
; ORGANISM: E. coli
US-09-390-326-6
                                        Query Match
Best Local Similarity
Watches 5; Conserva
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                                                                                                                                                                                              APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                            Patent No. 5171840
                                                                                                                                            SEQ ID NO:5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MCTIGÜE, MICHELE A.
APPLICANT: WICKERSHAM, JOHN A.
APPLICANT: PYMKO, CHRIS
APPLICANT: SHOWALTER, RICHARD
APPLICANT: SHOWALTER, RICHARD
APPLICANT: TEMPCYZK-RUSSEL, ANNA
APPLICANT: GEHRING, MICHAEL R.
APPLICANT: MROCZKOWSKI, BARBARA
APPLICANT: MROCZKOWSKI, BARBARA
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VILLAFRANCA, J. ERNEST
APPLICANT: APPELT, KRZYSZTOF
TITLE OF INVENTION: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND
TITLE OF INVENTION: METHODS OF USE
TILE REFERENCE: 0125-0016US
CURRENT FILLOTION NUMBER: US/09/390,326
CURRENT FILLING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KAN, CHEN-CHEN
                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19-JAN-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 PESRA 278
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53
                                                                                                                             LENGTH: 386
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
mes 5; Conserv
                                                                                                                                                                                                                                                                                                                                    75 HLGPH 79
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RSTPE 57
                            RSTPE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                      Conservative
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0; Mismatches
                                                      Score 5; DB 6; Pred. No. 3.8
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Pred. No. 3.8e+02;
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                                                 DB 6; L., No. 3.8e+02; 0;
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5. 3.8e+02;
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Best Local Similarity
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                                                                                                                                                                    APPLICATION NUMBER: US 07/938
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 1960
REFERENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
IFNORMATION CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:5:
     Query Match
Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
FOR HUMAN B CELL STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: JAGENDORF, ANDRE
APPLICANT: CERUTTI, HERIBERTO
TITLE OF INVENTION: CDNA ENCOU
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Relea
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 16-JUN-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/:
FILING DATE: 02-UTL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 298,694
FILING DATE: 19-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                    TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 RSTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP STREET: CLINTON SQUARE, P.O. BOX 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 386
                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 RSTPE 11
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   h 33.3%; So Similarity 100.0%; I 5; Conservative 0;
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                                                                                                                                                           388 amino acids
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100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                    US 07/938,332
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     Score 5; DB; Pred. No. 3. 0; Mismatches
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DB 1; L-
40. 3.8e+02;
0;
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o. 3.8e+02;
                                   Length 388;
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Query Match
Best Local Similarity
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US-08-725-758A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Patent No. 5212296
; APPLICANT: DEAN, CAROLINE;HARDER, PATRICIA A.;LETO, KENNI;J.; O'KEEFE, DANIEL P.;OMER, CHARLES A.;ROMESSER, JAMES A.;TEPPERMAN, JAMES M.
;TEPPERMAN, JAMES M.
;TEPPERMAN, JAMES M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 111
5212296-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08725758A Patent No. 6160108
                                NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0543
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPAX: 617-542-8906
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                              CURRENT AFFLUCTION NUMBER: US/UB//2//,
FILING DATE: 04-CCT-1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/005,074
                                                                                                                                                                                                                                            SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/725,758A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 23-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reed, Guy
APPLICANT: Clement, Christophe Y.
TITLE OF INVENTION: NOVEL PLATELET ACTIVATION PROTEIN
                                                                                                                                               APPLICATION NUMBER: 60/0 FILING DATE: 06-OCT-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 RSTPE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 HRSTP 364
                     TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 225 |
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                      DOS
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100.0%; Pred. No.
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                                                                                            05433/020001
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o. 3.9e+02;
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US-08-725-758A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Glycine max US-09-362-473-14
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US-09-362-473-14
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Best Local Similarity 100.
The Strong Strong Conservative
                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08725758A Patent No. 6160108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 421
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Sequence 14, Apr-
No. 6218169
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APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
FITLE OF INVENTION: Aromatic Amino Acid Catabolism Enzymes
FILE REFERENCE: BB-1197
CURRENT APPLICATION NUMBER: US/09/362,473
CURRENT FILING DATE: 1999-07-28
EARLIER APPLICATION NUMBER: 60/094,783
EARLIER FILING DATE: JULY 31, 1998
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Falco, S. Carl
APPLICANT: Morgante, Michele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cahoon, Edgar B.
APPLICANT: Cahoon, Rebecca E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                            ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       APPLICANT: Reed, Guy
APPLICANT: Clement, Christophe Y.
APPLICANT: CLEMENT, Christophe Y.
TITLE OF INVENTION: NOVEL PLATELET ACTIVATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                   361 PESRA 365
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                                                                                                             COUNTRY:
                                                                                                                                                     CITY:
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                  SOFTWARE:
                                OPERATING SYSTEM:
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                                                                                                                                                   Boston
                                                                                                                                  MA
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                 FastSEQ Version 2.0
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internal
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100.08; F1
0;
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100.0%; Pred. No.
tive 0; Mismatc
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b; Pred. No. 4e+
0; Mismatches
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b. 4.1e+02;
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APPLICATION NUMBER: US/08/725,758A FILING DATE: 04-OCT-1996 PRIOR APPLICATION DATA:

APPLICATION NUMBER:

60/005,074

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Query Match
Best Local Similarity
Them 5; Conservi
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US-08-845-258-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0543
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                    TELEFAX: (206)682-6031 INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 211
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-Lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 C
CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 STPES 284
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                  STRANDEDNESS
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                                                  LENGTH:
                                                                                                                        TELEPHONE:
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                                 : 431 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6300 Columbia Center, 701 Fifth Avenue
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linear
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                                                                                                                          (206) 622-4900
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Pred. No. 4.1e+02;
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US-08-723-142A-34
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Best Local S
Matches 5
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                                                                                                                                                     Patent No. 6306396 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Si
                                                                                                                                                                                     Sequence 34,
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                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEOUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 11-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Washington
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                                                                                                                                                                                     Application US/08723142A
E: SEED AND BERRY
6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                  74
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                                                                                                      Houghton, Raymond
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                                                                                                                        Reed, Steven G.
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                         linear
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100.0%; Pred. No.
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 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                       DB 4; L. NO. 4.2e+02; 0;
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), 4.2e+02;
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RESULT 119
US-08-261-110A-2
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; TYPE: PRT
; ORGANISM: Babesia microti
US-09-528-784A-34
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Sequence 2, Application US/08261110A Patent No. 5674992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Paul R.
APPLICA
                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 34
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CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
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TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 34:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/723,142A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 STPES 12
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Washington
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Pred. No.
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lo. 4.2e+02;
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b. 4.2e+02;
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US-07-872-678A-47
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Patent No. 5541060
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REFERENCE/DOCKET NUMBER: 19603/10231(D-1292A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION: BETECTION OF EARLY-ONSET
TITLE OF INVENTION: DETECTION OF EARLY-ONSET
TITLE OF INVENTION: NO. INSULIN-DEPENDENT DIABETES MELLITUS
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           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/261,110A FILING DATE: 16-JUN-1994
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
Addresse: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICATION NUMBER: US 07/938,332
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J
REGISTRATION NUMBER: 34,103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: CLINTON SQUARE, P.O. BOX 1051
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: JAGENDORF, ANDRE
APPLICANT: CERUTTI, HERIBERTO
TITLE OF INVENTION: COMA ENCODING A recA HOMOLOG IN
TITLE OF INVENTION: EUKARYOTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 HRSTP 414
                                                                                                                               COUNTRY: USA
ZIP: 77210
                                                                                                                                                                                    CITY:
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CITY: ROCHESTER
STATE: NEW YORK
                                                                                                                                                                                                        STREET:
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APPLICATION NUMBER:
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SYSTEM: PC-DOS/MS-DOS
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N: 536
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100.0%; Pr
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US/07/872,678A
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b. 4.2e+02
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Query Match
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Thes 5; Conserve
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Patent No. 5854067
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                                                                                                                                                                                                    APPLICATION NUMBER: US/08/588,983
FILING DATE: Concurrently herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:424/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
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TELEX: 79-9924
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Meth
TITLE OF INVENTION: for
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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NAME: Coughlin, Daniel F
REGISTRATION NUMBER: 36,
                                                                                                                                                                                            TELEFAX:
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ZIP: 77210
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STATE: TX
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REFERENCE/DOCKET NUMBER: ARCD016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Arnold,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Christopher B. Newgard, et al.
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                     Conservative
                                                                                                  linear
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100.0%; Pr
              33.5°,
100.0%; Pr
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                                33.3%; Score 5; DB 2; Le 100.0%; Pred. No. 4.5e+02;
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Pred. No. 4.5e+02;
                     Mismatches
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                                               Length 465
                   Indels
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US-08-588-976-20
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                                                                                                                                                                                                                                                                                                                                                                                  Matches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Sequence 20, Application US/08588976
Patent No. 5891717
GENERAL INFORMATION:
APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions for TITLE OF INVENTION: Inhibiting Hexokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08588983 Patent No. 5854067 GENERAL INFORMATION:
APPLICANT: Christopher B. Newgard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: n/a
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,983
FILING DATE: CONCULTENTLY herewith
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: FUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:424/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: for Inhibiting Hexokinase
                                                                                                          NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        63 RSTPE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 465 amino acid
TYPE: amino acid
STRANDEDNESS: single
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ZIP: 77210
                                                   STREET: P.O. I
COUNTRY: US
ZIP: 77210
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                                                                          ADDRESSEE: Arnold, Wh
STREET: P.O. Box 4433
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                                     ΤX
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100.0%; Pr/
0;
                                                                                                                                 43
                                                                                          White & Durkee
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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o. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 465;
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RESULT 124
US-08-588-976-22
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                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,976
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22, Application US/08588976 Patent No. 5891717
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENCE 465 amino acids
                                                                                         TELEFAX: (512) 474-75;
TELEX: n/a
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                         NAME: FUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/FOCKET NUMBER: UTSD:481/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Inhibiting Hexokinase
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:481/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 77210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
                                                      LENGTH: 465 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 RSTPE 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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US-08-249-112-4
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-878-44
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Best Local Similarity 100.
The Strong S
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08249112 Patent No. 5527703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ. ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                  TELEFAX: (908) 594-47 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/249,112
FILING DATE: 25-MAY-1994
CLASSIFICATION: 514
CLASSIFICATION: 514
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W.
REGISTRATION NUMBER: 35,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cully, Doris F.
APPLICANT: Arena, Joseph P.
APPLICANT: Liu, Ken K.
APPLICANT: Vassilatis, Demetrics
TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE
TITLE OF INVENTION: CHANNELS
SEQUENCE CHARACTERISTICS:
                                                                                                                                              TELECOMMUNICATION INFORMATION:
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STATE: New Jersey
                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 RSTPE 67
                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 RSTPE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
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                                                                                                               (808)
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100.0%;
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s; Pred. No. 4.5
0; Mismatches
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b. 4.5e+02;
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Query Match
Best Local Similarity
Them 5; Conserve
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RESULT 128
US-09-426-568A-2
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                                                                                                                               Query Match
Best Local :
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                                                                                                                Matches
                                                                                                                                                                                                                                                                            TELEFAX: (908) 594-47 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06556
                                                                                                                                                                                                                                                                                                     NAME: Wallen, John W.
REGIZION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
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APPLICATION NUMBER: US 08/249,112
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE:
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                                                        432 STPES 436
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STATE: New J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 487 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                              / Match 33.3%;
Local Similarity 100.0%;
les 5; Conservative
                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                   8 STPES 12
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                                                                                                                                                                                                                                amino acid
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Vassilatis, Demetrios
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cully, Doris F.
Arena, Joseph P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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1594-4720
1594-4720
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                                                                                                                Score 5; DB 5; Pred. No. 4.7
0; Mismatches
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                                                                                                          DB 5; L., NO. 4.7e+02; 0;
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US-09-431-470-4
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                                                                                                        RESULT 130
US-08-399-646-2
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                                                                                                                                                                                                                                                                                              ; TYPE: PRT; ORGANISM: Zea mays; US-09-431-470-4
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APPLICANT: DUVICK, Jon
APPLICANT: Simmons, Ca
APPLICANT: Crasta, Osw
APPLICANT: Folkerts, O
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                                                         Sequence 2, Application Patent No. 5556781
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 563
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Best Local S
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Best Local Similarity
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                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Simmons, Carl R.
APPLICANT: Crasta, Oswald R.
APPLICANT: Folkerts, Otto
TITLE OF INVENTION: The Use of Beta-Glucosidase to Enhance
TITLE OF INVENTION: Disease Resistance to Insects in Crop Plants.
FILE REFERENCE: 5718-43
CURRENT APPLICATION NUMBER: US/09/431,470
CURRENT FILING DATE: 1999.11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance FILE REFERENCE: 008105/195497
CURRENT APPLICATION NUMBER: US/09/426,568A
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/106,239
PRIOR FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/107,920 PRIOR FILING DATE: 1998-11-10 NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 491
TYPE: PRT
ORGANISM: Arabidopsis sp.
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 PESRA 181
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                                                                                                                                                                      19 SHLGP 23
                                                                                                                                                                                                                                  Local Similarity es 5; Conserv
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                                                                                         Application US/08399646
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Hu, Weiming
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TSUSAKI, Keiji
HATTORI, Kazuko
SUGIMOTO, Toshiyuki
                                                                                                                                                                                                                                   Conservative
                              KUBOTA, Michio
TSUSAKI, Keiji
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Colleen
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100.0%; Pr
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0; Mismatches
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Pred. No.
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No. 5.3e+02;
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RESULT 131
US-08-607-321-2
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Best Local S
Matches 5
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/399,646
FILING DATE: 07-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 59840
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Keiji
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS
NUMBER OF SEQUENCES: 18
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS.
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CORRESPONDENCE ADDRESS
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: EN
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 RSTPE 515
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                                                                                              COUNTRY:
                                                                                                                  STATE:
                                                                                                                                                      STREET:
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                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 RSTPE 11
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5. 5716813
                                                                                                              Washington : D.C.
                                                                                 20004
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                                                                                                                                                  E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
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419 Seventh Street, N.W., Suite 300
                                                                                            USA
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 compatible
PC-DOS/MS-DOS
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version #1.30
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                                                                                                                                                      Suite 300
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-607-321-2
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US-08-961-240-2
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Best Local S
Matches 5
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FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: KU TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      511 RSTPE 515
                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                  FILING DATE: 30-
CLASSIFICATION:
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                                                                                                                                                  APPLICATION NUMBER: US/08/961,240 FILING DATE: 30-OCT-1997
                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                          STREET: 419 Seventh Street, N.W., Suite 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 26-FEB-1996
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100.0%; Pred. No. 5.
Live 0; Mismatches
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5.5e+02;
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FILING DATE: 07-MAR-1994 ATTORNEY/AGENT INFORMATION:

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                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/605,501
FILING DATE: 26-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
1D 50040
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                                                                                                                                                                                                                                                                                                                                                           ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

CURRENT APPLICATION UMBER: US/08/605,501
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SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acid
                                                                                                                                      APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TYPE: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 511 RSTPE 515
                                                     TELEFAX: 202-
TELEX: 248633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
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nes 5; Conserv
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                                                                                      TELEPHONE:
                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 RSTPE 11
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419 Seventh Street, N.W., Suite 300
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100.0%; Pre
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                                                                                                                              KUBOTA-5
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Pred. No.
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518 RSTPE 522

7 RSTPE 11

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Query Match
Best Local Similarity
"~+~hes 5; Conserve
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                                                                         ; TOPOLOGY: 15; MOLECULE TYPE: US-08-399-646-12
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US-08-399-646-12
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: JP 598
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 598
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERRNEZ/DOCKET NUMBER: KU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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APPLICANT:
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APPLICATION NUMBER: US/08/399,646
FILING DATE: 07-MAR-1995
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ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
NUMBER OF SEQUENCES: 18
                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
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                                                                                                                                                                                    TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TSUSAKI, Keiji
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                  Conservative
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100.0%; Pred. No. 5.
Live 0; Mismatches
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                               DB 1; Le
). 5.5e+02;
                                           Length 596;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-607-321-12
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                                                                                                                                                Sequence 12, Application US/08961240 Patent No. 5830715
                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                             GENERAL INFORMATION:
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                 APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, Toshi;
TITLE OF INVENTION: DNA ENC
TITLE OF INVENTION: ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KUBOTA=5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 08/399,646
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: UP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-MAR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             518 RSTPE 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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419 Seventh Street, N.W., Suite 300
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HATTORI, Kazuko
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                              KUBOTA, Michio
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26-FEB-1996
), TOShiyuki
DNA ENCODING ENZYME, RECOMBINANT DNA AND
ENZYME, TRANSFORMANT, AND THEIR PREPARATI
18
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100.0%; Pred. No. 5.9
tive 0; Mismatches
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No. 5.5e+02;
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                   AND THEIR PREPARATIONS AND USE
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; MOLECULE TYPE:
US-08-961-240-12
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                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: KUBOTA,
APPLICANT: TSUSAKI
APPLICANT: HATTORI
APPLICANT: SUGIMOT
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08605501 Patent No. 5834287
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CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: UP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 596 amino acts
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                         NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                     APPLICANT: SUGIMOTO, TOShiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rele
CURRENT APPLICATION DATA:
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ADDRESSEE: BROWDY AND NEIMARK
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                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KU
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                 20004
                                                                                                                                                     Washington
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                                                                                                                                     D.C.
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                                                                                                                                                                           419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        596 amino acids
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                                                                                                                   USA
                                                                                                                                                                                                                                                                                                             TSUSAKI, Keiji
HATTORI, Kazuko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                       KUBOTA, Michio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.3%; Score 5; DB 2; Le
100.0%; Pred. No. 5.5e+02;
tive 0; Mismatches 0;
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   Version #1.30
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PRIOR APPLICATION DATA:

FILING DATE: 20 CLASSIFICATION: CURRENT APPLICATION DATA:

APPLICATION NUMBER:

26-FEB-1996

US/08/605,501

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TELEFAX: (312) 715-1234
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
                                       CLASSIE ...
ATTORNEY/AGENT INFORMATION.
ATTORNEY/AGENT INFORMATION.
NAME: MCNIcholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 92,306-A; D001 CIP PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
(312) 715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: UP 59
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Osborn, Laurelee
APPLICANT: Benjamin, Christopher D.
TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE FOURTH
TITLE OF INVENTION: IMMUNOGLOBULIN-LIKE DOMAIN OF VCAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 59840 FILING DATE: 07-MAR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            518 RSTPE 522
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CITY: Chicago
STATE: IL
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                                                                                                                                                                            APPLICATION NUMBER: POFILING DATE: 19930112 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BROWDY, ROGER L.
REGISTRATION UMBER: 51,618
REFERENCE/DOCKET NUMBER: KU
LECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100 es 5; Conservative
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10 South Wacker Drive
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b; Pred. No. 5.5
0; Mismatches
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PCT-US93-00031-21; Sequence 21, Applicat; GENERAL INFORMATION:
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US-09-009-490A-91
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                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein PCT-US93-00031-21
                                                                                                            Sequence 91, Application US/09009490A Patent No. 6300491
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                          GENERAL INFORMATION:
APPLICANT: Bennett and Mirabelli
TITLE OF INVENTION: Oligonucleotide Modulation
TITLE OF INVENTION: of Cell Adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (312) 715-123
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US93/00031
FILING DATE: 19930112
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Benjamin, Christopher D.
TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE FOURTH
TITLE OF INVENTION: IMMUNOGLOBULIN-LIKE DOMAIN OF VCAM1
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 644 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                               30 TPESR 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
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CITY: Chicago
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10 South Wacker Drive
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Law Office of Jane Massey Licata
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715-1234
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Pred. No.
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o. 5.9e+02;
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b. 5.9e+02;
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66 East Main Street

ADDRESSEE:

Fish & Neave

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RESULT 141
US-08-482-073-5
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                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                           Sequence 5,
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                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 939,855
FILING DATE: September 2, 1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: 567,286
FILING DATE: August 14, 1990
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Amino Acid
STRANDEDNESS: Sinc
TOPOLOGY: Linear
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (609) 810-1454 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                            TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 007,997
FILLING DATE: January 20, 1993
PRIOR APPLICATION DATA:
                                                                                APPLICANT:
                                                                                             APPLICANT:
                                                                                                               APPLICANT:
                                                                                                                              APPLICANT:
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OPERATING SYSTEM: Windo
SOFTWARE: WORDPERFECT (
SOFTWARE) APPLICATION DATA:
CORRESPONDENCE ADDRESS:
                  NUMBER
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APPLICATION NUMBER:
FILING DATE: May 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: May 12, 1995 PRIOR APPLICATION DATA:
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nes 5; Conserv
                                                                                                                                                                                                                                                                                           30 TPESR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 969,151 FILING DATE: February 10, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 063,167 FILING DATE: May 17, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/009,490A FILING DATE: January 20, 1998 CLASSIFICATION: 514
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               OF SEQUENCES:
                                                                                                                                                                                              , Application US/08482073
6307025
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                                                                                        Osborn, Laurelee
Benjamin, Christopher D.
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                             Goelz, Susan E.
                                                                              Rosa, Margaret D.
                                                                                                                                          Lobb, Roy R.
                                                                                                                                                            Hession, Catherine
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                          ENDOTHELIAL CELL-LEUKOCYTE ADHESION MOLECULES (ELAMS) AND MOLECULES INVOLVED IN LEUKOCYTE ADHESION (MILAS)
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100.0%;
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Query Match
Best Local Similarity
Watches 5; Conserve
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TOPOLOGY:
US-08-482-073-5
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                                                                                                                                                                                                                                       RESULT 142
                                                                                                                                                                                    Sequence 11, Application PC/TUS9300031 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 596-900
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                         APPLICANT: Benjamin, Christopher D.
TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE FOURTH
TITLE OF INVENTION: IMMUNOGLOBULIN-LIKE DOMAIN OF VCAM
                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07
FILING DATE: 01-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 31-OCT-1550
PRIOR APPLICATION DATA:
PRIOR TOWNTON NUMBER: WO PCT/US 90/02357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                            CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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                                                                                                         NUMBER OF SEQUENCES:
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                             STATE:
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 ZIP:
                                               CITY:
                                                            STREET:
                                                                                                                                                                                                                                                                                     30 TPESR 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Haley Jr., Jar
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
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                                                                         ADDRESSEE:
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TRY: US
60606
                                            Chicago
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                                                              10 South Wacker Drive
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                                                                           Allegretti & Witcoff, Ltd
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31-OCT-1990
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08261304 Patent No. 5708147 GENERAL INFORMATION:
                                                                                                                                                                                   CLASSITETC: IBM PC compatible operating system: PC-DOS/MS-DOS SOFTWARE: Ascii CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/261 30.
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/649,565

FILING DATE: 01-FEB-1991

APPLICATION UMBER: U.S. 07/487,038

FILING DATE: 02-MAR-1990

ATTORNEY/AGENT INFORMATION:

NAME: POTTER, Jane E. R.

REGISTRATION NUMBER: 3,332

REFERENCE/DOCKET NUMBER: 0627.2100004

TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 647 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MCNIcholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 92,306-A; D001 CIP PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00031
FILING DATE: 19930112
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cybulsky, Myron I.
APPLICANT: Gimbrone, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Collins, Tucker
                                                                                                                                                                                                                                                                                                                                                                       STATE: District of Columbia COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1225 Conn
STREET: Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 TPESR 34
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SOFTWARE: PatentIn Release #1.0, Version #1.25
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1225 Connecticut Avenue, N.W.
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SYSTEM: PC-DOS/MS-DOS
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100.0%;
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US-08-205-018-2
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Best Local Similarity
Matches 5; Conserv
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                                                                             Query Match
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                  TYPE: amino acids
TYPE: amino acid
TOPOLOGY: lin-
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                                                                                                                                                                                                                  REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: CH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
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TITLE OF INVENTION:
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                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Gaumond, Rebecca R
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CITY: Philadelphia
STATE: PA
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65 PESRA
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ses 5; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
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69
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Pleasure, David
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                                             33.3%; >--
100.0%; Pr
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Pred. No.
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b. 6.1e+02
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US-08-424-424B-2 US-08-424-424B-2 ; Sequence 2, Application US/08424424B ; Patent No. 5759854

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Query Match
Best Local Similarity
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GENERAL INFORMATION:
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TOPOLOGY: LIN
MOLECULE TYPE:
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NFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 727 AMINO ACIDS
                                              COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                             APPLICANT: LI, ET AL.
TITLE OF INVENTION: Neurotransmitter Transporter
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
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OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,424B
FILLING DATE: APPLIC 21, 1995
CLASSIFICATION: 435
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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MEDIUM TYPE: 3.5 INCH DISKETTE
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APPLICATION NUMBER: PCT/US94/05363
FILING DATE: MAY 25, 1996
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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                  APPLICATION NUMBER: FILING DATE: SUBMI
                                                                                                                                                                                                             STREET: 6 BECKER FARM ROAD CITY: ROSELAND
CLASSIFICATION:
                                                                                                                                                           COUNTRY: USA
ZIP: 07068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UZIP: 07068
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                SUBMITTED HEREWITH
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                                 PCT/US94/05363A
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Pred. No. 6.6e+02;
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Query Match
Best Local Similarity
"hes 5; Conserva
                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-696-944-20
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US-08-696-944-20
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Best Local Similarity
Thes 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08696944
Patent No. 5981831
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 9
FILING DATE: 23-FEB-1994
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                         FILING DATE: 23-FEB-1732
FILING DATE: 23-FEB-1732
PRIOR APPLICATION DATA: GB 9403423.8
                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00372
FILING DATE: 23-FEB-1995
                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: FERRARO, GREGORY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 721 STPES 725
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APPLICATION NUMBER:
                                                                                                     TYPE:
                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 23-AUG-1996 CLASSIFICATION: 435
                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 STPES 12
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                                                                                                               731 amino acids
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             Conservative
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/ENTION: No. 5981831el Exo-(1-4)-Beta-D Galactanase
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201-994-1744
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          b; Score 5; DB 2
b; Pred. No. 6.6
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      DB 2; L.,
No. 6.6e+02;
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                                   Length 731;
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            Indels
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7 RSTPE 11

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RSTPE

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; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
LENGTH: 734 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-706-216-2
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                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Kerry E. Quinn
APPLICANT: Curagen Corporation
APPLICANT: Curagen Corporation
TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids
TITLE OF INVENTION: encoding Same
FILE REFERENCE: 15966-581
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Patent No
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PRIOR APPLICATION NUMBER: 60/159,613
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: 60/175,534
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/224,086
PRIOR FILING DATE: 2000-08-09
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                                                                                                                           CURRENT APPLICATION NUMBER: US/09/641,741
CURRENT FILING DATE: 2000-08-18
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REFERENCE/DOCKET NUMBER: DXI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,216
FILING DATE: 30-AUG-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: MAMMALIAN PROTEASES; RELATED REAGENTS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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nes 5; Conserv
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ZIP: 94304-1104
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100.0%;
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b. 6.6e+02;
tches 0; Indels
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-641-741-2
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Best Local Similarity
Ymthes 5; Conserva
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                                                                                 RESULT 151
PCT-US93-00031-15
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                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US93-00031-13
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PCT-US93-00031-13
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SOFTWARE: Pate
SEQ ID NO 2
FRIGTH: 734
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                                                   Sequence 15, Application PC/TUS9300031 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 92,306-A; D001 CIP PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 735 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
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MEDIUM TYPE: Floppy disk
APPLICANT: Osborn, Laurelee
APPLICANT: Benjamin, Christopher D.
TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE FOURTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Benjamin, Christopher D.
TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE FOURTH
TITLE OF INVENTION: IMMUNOGLOBULIN-LIKE DOMAIN OF VCAM1
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
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ZIP: 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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o. 6.6e+02;
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Query Match
Best Local Similarity
Watches 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Osborn, L
APPLICANT: Benjamin,
APPLICANT: Rosa, Mar-
TIPLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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LENGTH: 736 amino acids
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NAME: MCNIcholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: United States of America
                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: POFILING DATE: 19930112 CLASSIFICATION:
  CLASSIFICATION:
                             FILING DATE:
                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                       STREET:
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ZIP: 60606
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                                                                                                                                                                                                                                                                                                                                    1251 Avenue of the Americas
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10 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosa, Margaret D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osborn, Laurelee
Benjamin, Christopher D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goelz, Susan E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hession, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                               Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (312) 715-1000
312) 715-1234
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ADHESION (MILAS)
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                                                    US/08/482,073
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; L. do. 6.6e+02; 0;
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PCT-US93-00031-9
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Best Local :
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                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
               ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 92,306-A; D001 CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OSBORN, Laurelee
APPLICANT: Benjamin, Christon
TITLE OF INVENTION: ANTIBODJ
TITLE OF INVENTION: IMMUNOGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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FILING DATE: 01-7UN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/354151
FILING DATE: 28-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 18-DEC-PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA: APPLICATION NUMBER: WO DOTE FILING DATE: 27 FILING DATE: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 27-APR-PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                         APPLICATION NUMBER: POFILING DATE: 19930112
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CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 596-90
TELEFAX: (212) 596-9090
TELEX: 14-8367
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(312)
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18-DEC-1989
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Christopher D.
ANTIBODIES RECOGNIZING THE
                                                                                                                                                                                                PCT/US93/00031
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RESULT 155
US-09-342-648-2
Sequence 2, Application US/09342648
Patent No. 6248584
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
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Best Local Similarity
"~+~hes 5; Conserva
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Best Local Similarity
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                                                                                                                                                                                                                                                      PCT-US93-00031-17
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00031
FILING DATE: 19930112
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 92,306-A; D001 CIP PCT
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INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Benjamin, Christopher D.
APPLICANT: Benjamin, Christopher D.
TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE FOURTH
TITLE OF INVENTION: IMMUNOGLOBULIN-LIKE DOMAIN OF VCAM1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 740 amino acids
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MEDIUM TYPE: Floppy disk
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LENGTH: 739 amino acid
                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 715-1000
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30 TPESR 34
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                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
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Pred. No.
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lo. 6.7e+02;
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o. 6.7e+02;
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; MOLECULE TYPE: US-08-696-944-19
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SOFTWARE: Microsoft Of
SEQ ID NO 2
LENGTH: 755
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Best Local (
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APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Transcription Coactivators
FILE REFERENCE: BB-1169-B
CURRENT APPLICATION NUMBER: US/09/342,648
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,659
EARLIER FILING DATE: July 13, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: UNSURE
LOCATION: (185)
                                                                                                     FILING DATE: 23-FEB-1994 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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ORGANISM: Zea mays
FEATURE:
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                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: PCT/GB95/00372
FILING DATE: 23-FEB-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      SOPTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,944
FILING DATE: 23-AGG-1996
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: John S. REID
APPLICANT: Jacqueline DE SILVA
TITLE OF INVENTION: No. 5981831el Exo-(1-4)-Beta-D Galactanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 STPES 496
                                  LENGTH: 838 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
SOFTWARE: MS Word
                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.0%; local Similarity 100.0%; les 5; Conservative '0;
                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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Susan S. REID
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Susan A. HELLYER
                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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b; Pred. No. 6.8
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Best Local Similarity
'atches 5; Conserv
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                                                                                                   Sequence 2, Application PC/TUS9502792 GENERAL INFORMATION:
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/20:
FILING DATE: 01-MAR-1994
FILING DATE: 101-MAR-1190:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 35,152
REFERENCE/DOCKET NUMBER: GH-0488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3420
FORMATION FOR
                         APPLICANT: Usharani R. Reddy, David Pleasure and the Children's
APPLICANT: Hospital of Philadelphia
TITLE OF INVENTION: Novel Protein Kinase, Nucleic Acid
TITLE OF INVENTION: Sequences Encoding the Same and Methods Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US,
FILING DATE: herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NO TITLE OF INVENTION: See NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Usharani R. Reddy, David Pleasure and the Children's APPLICANT: Hospital of Philadelphia TITLE OF INVENTION: No. 5676945el Protein Kinase, Nucleic Acid TITLE OF INVENTION: Sequences Encoding the Same and Methods Related Thereto
                NUMBER
                                                                                                                                                                                                                                                                                Local Similarity hes 5; Conserv
                                                                                                                                                                                                             65
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                                                                                                                                                                                                                                             10 PESRA 14
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                OF SEQUENCES:
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One Liberty Place - 46th Floor
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1. 7.4e+02;
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RESULT 159
US-09-150-460B-7
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                                                                      US-09-150-460B-7
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APPLICANT: Lee, Chei
APPLICANT: Albrecht
APPLICANT: Eichele,
 Best Loc
Matches
                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/150,460B
CURRENT FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 60/058,256
PRIOR FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 7
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09150460B Patent No. 6190882
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Best Local 9
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                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205
APPLICATION NUMBER: 01-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca L. Ralph (for REGISTRATION NUMBER: 35,15
                                                                                      OTHER INFORMATION: Peptide sequence of largest deduced open reading OTHER INFORMATION: frame from RIGUI 6.6
                                                                                                                                       ORGANISM: artificial sequence
                                                                                                                                                            TYPE: PRT
                                                                                                                        FEATURE:
                                                                                                                                                                           LENGTH: 875
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SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US
FILING DATE: herewith
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LENGTH: 859 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
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MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
 Local Similarity les 5; Conserv
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Eichele, Gregor
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 Conservative 0;
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DN: _Mammalian Circadian Rhythym-Like Gene
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 33.3%; Score 5; DB 4; Let 100.0%; Pred. No. 7.7e+02; ive 0; Mismatches 0;
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100.0%; Pred. No.
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35,152
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RESULT 161
US-09-357-014-9
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US-08-574-959A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 905 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09357014
Patent No. 6291645
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/574,959A
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617,227-7400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: 962 POLYPEPTIDES, RELATED POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CITY: Boston
STATE: Massac
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COUNTRY: USA
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                             NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                         APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi and Jack L. Strominger
TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES
AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02109-1875
                                                                                                                            STATE: Massachusetts
                                                                                                                                            CITY: Boston
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100.0%; Pr
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5. 8e+02;
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US-08-588-983-9
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FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: MANDIAGENT INFORMATION:
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application Patent No. 5854067
GENERAL INFORMATION:
APPLICANT: Christo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                       TELEX: n/a
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                             NAME: FUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/588,983
FILING DATE: Concurrently herewith CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Fussey, Shellev P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        429 GPHRS 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100 tes 5; Conservative
                                 TYPE: amino acid
STRANDEDNESS: Si
                                                     TYPE:
                                                                                                                               TELEX:
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                                                                       ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08588983
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                                                                     919 amino acids
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                 linear
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                               single
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o. 8e+02;
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US-08-588-976-9; Sequence 9, Application US/08588976; Patent No. 5891717
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; Sequence 12, A
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Best Local Similarity
Thehes 5; Conserve
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                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                          APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Inhibiting Hexokinase
                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NAME: FUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:424/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHAX: (512) 474-7577
                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: for Inhibiting Hexokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    517 RSTPE 521
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                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/588,983 FILING DATE: Concurrently herewith CLASSIFICATION: 424
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ZIP: 77210
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STATE: TX
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STREET: P.O. Box 4433
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Houston
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5854067
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100.0%;
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0; Mismatches
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Pred. No.
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No. 8.1e+02;
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US-08-588-976-12
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                                                                                                      COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,976
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FUSSEY, Shelley P.M.
REGIGTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:481/FUS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 TELEX: n/a
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 919 amino acids
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CITY: H
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                                                                          TELEPHONE: (512) 418-30
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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TOPOLOGY: li
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Query Match
Best Local Similarity 100.
5; Conservative
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                                             COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Inhibiting Hexokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:481/FUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/588,976
FILING DATE: Concurrently herewit:
CLASSIFICATION: 435
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                                                                                                                                                                    P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                919 amino acids
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                                                       Floppy disk
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Version #1.30
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US-09-651-656-101
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US-09-078-347A-1
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                                                                                                                                                                                                                                                                                                                           US-09-078-347A-1
GENERAL INFORMATION:
APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
APPLICANT: LAWRENCE NIVERNAL NATIONAL LABORATORY
                                                                        Sequence 101, Application US/09651656 Patent No. 6340566
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                                                                                                                                                                                                                                                                                        Query Match
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION UNUBER: US/09/078,347A
FILING DATE: 13-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAITOIL PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UALB-03283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Le, Xiao-Chun
APPLICANT: Weinfeld, Michael
APPLICANT: Xing, James Z.
TITLE OF INVENTION: Methods for Quantitating Low Level
TITLE OF INVENTION: Modifications of Nucleotide Sequences
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 940 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 RSTPE 521
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                                                                                                                                                                                                                                                     Local Similarity
mes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
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es 5; Conserv
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8 1e+02;
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FILE REFERENCE: IL-10689
CURRENT APPLICATION NUMBER: US/09/651,656
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOOTWARR: Patentin Ver. 2.1
SEQ ID NO 101
LENGTH: 940
TYPE: PRT
ORGANISM: Escherichia coli
US-09-651-656-101
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Best Local Similarity
5; Conserve
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US-08-006-676B-1
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TYPE: PRT
; ORGANISM: Escherichia coli
US-09-650-855-101
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US-09-650-855-101
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                                                                                                                                                                                       Sequence 1, Application US/08006676B Patent No. 5411865
GENERAL INFORMATION:
APPLICANT: Reed, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 101, Appl Patent No. 6365355
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF
TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND I
TITLE OF INVENTION: MISMATCHES
FILE REFERENCE: IL-10284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS, TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
                                                                                                                                  TITLE OF INVENTION: DI
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                               STREET: 8339 SE 57th Street CITY: Mercer Island STREE: Washington
                                                                                                                                                                                                                                                                                                                               719 PESRA 723
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                                                    STATE: Washington COUNTRY: USA
                                     98040-4906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09650855
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100.0%; Pr
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100.0%;
                                                                                                                                                                     Diagnosis of Leishmaniasis
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                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 940;
. 8.2e+02;
ches 0; Indels
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Query Match
Best Local Similarity
Thems 5; Conserv
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US-08-282-845-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                            TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: Reed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 236 020
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                         SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acid
                                                                                                        REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                   COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh Operating System 7.1
SOFTWARE: Microsoft Word for Macintosh 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,845
FILING DATE:
                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/006,676
FILING DATE: JANUARY 15, 1993
CIASTELLATION: 425
                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT. TITLE OF INVENTION: A 23Unu Species
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Seattle
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APPLICATION NUMBER: US/08
FILING DATE: 15-JAN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 ESRAA 482
                                                                                                                                                     NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
                TOPOLOGY:
                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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REGISTRATION NUMBER: 32,585
REFERENCE/DOCKET NUMBER: REI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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51 University Street
                                         955 amino acids
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              linear
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N: A 230Kd Antigen Present
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Pred. No.
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US-08-428-414A-3
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                                                                                                                 Sequence 1, Application PC/TUS9400324
GENERAL INFORMATION:
APPLICANT: Reed, Steven
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                                                                                                                                                                                                                                                                                                  Query Match
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TELEX: 3723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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STREET:
STREET:
CITY: Seattle
CITY: Washington
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                      NUMBER OF SEQUENCES:
                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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ADDRESSEE: SEED and BERRY
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                                                                                                                                                                                                                    478 ESRAA 482
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                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kadlecek, Ann T. REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washing
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                                            51 University Street
                                                                                                                                                                                                                                                                                                                                                                                       955 amino acids
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                                                                                                                                                                                                                                                                                                                                              linear
                                                         Immunex Corporation
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100.0%; pr
                                                                                                    Diagnosis of Leishmaniasis
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100.0%;
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Pred. No.
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Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                       Mismatches
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b. 8.3e+02;
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COMPUTER READABLE FORM:

98101

COUNTRY:

MEDIUM TYPE: Floppy disk

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US
FILING DATE:
CLASSIFICATION:
APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 15-7AN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 5004 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Apple System 7.1 SOFTWARE: Microsoft Word, version 5.1a CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                      STREET: ...
CTTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                   PRIOR APPLICATION DATA:
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OPERATING SYSTEM: Apple S
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mes 5; Conserv
                             APPLICATION NUMBER: FILING DATE: 22-JAN
                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                    CLASSIFICATION: 435
                                                                                                                                  APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                     COUNTRY:
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   amino acid

GY: linear
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Kindsvogel Ph.D.
                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                             22-JAN-1988
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                        AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE FUSIONS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                             METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
                                               US 07/146,877
                                                                                                                                                  US/08/180,195
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                                                                                US/07/634,510
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US 07/347,291
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; Pred. No. 8.3e+02;
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RESULT 174
US-08-168-917-4
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Patent No. !
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Best Local :
                                                                           TELEFAX: (415) 326-24:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1089 amino act
                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 1241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
TOPOLOGY: li
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mes 5; Conserv
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REFERENCE/DOCKET NUMBER: 99
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                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                            LENGTH:
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                               amino acid
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                                             1089 amino acids
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Giese, Neill A.
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                Linear
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100.0%; Pr
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5. 9.3e+02;
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Query Match
Best Local Similarity
"~+~hes 5; Conserv?
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US-08-477-329-36
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Patent No. 5843725
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Matches 5; Conserv
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                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 9900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
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SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
APPLICANT: Sledziewski rn.u., Amarica APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
NUMBER OF SEQUENCES: 36
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
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TELEFAX: 3723836
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                                                                                                                                                                                                                              650 HLGPH 654
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                Application US/08475458
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6300 Columbia Center, 701 Fifth Avenue
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Kindsvogel Ph.D.,
                                                                                                                                                                                                                                                                                                Conservative
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100.0%; Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                           DB 1; Le
o. 9.3e+02;
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No. 9.3e+02;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,
                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,510
                                                                                                                                                                                                                                                    STREET: Une CITY: San Francisco
STATE: California
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fretto, Larry J.
APPLICANT: Giese, Neill A.
APPLICANT: Escobedo, Jaime A.
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSE: TOWNSEND and CREW
ADDRESSEE: TOWNSEND and TOWNSEND and CREW
STREET: One Market Plaza, Steuart Street Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wolf, David APPLICANT: Tomlinson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 206-622-4900
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/mb ...
OPERATING Patentin Release #1.24
OPERATING DATA: OPERATING AF
                                                         FILING DATE: 02
CLASSIFICATION:
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les 5; Conserv
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TOPOLOGY: linear
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/475,458 FILING DATE: 06-JUN-1995
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                                                               02-JUN-1995
N: 435
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Best Local Similarity
"-*rhes 5; Conserv
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                                                                                                                                                                                                                                                                     GROUP OF CONTROL 
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Patent No. 589165
                                                                                                                                                               Query Match
Best Local :
                                                                                                                               Matches
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:

NAME: DOW, KATEN B.

REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 0124

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2420

TELEPAX: (415) 326-2422
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ESCOBEDO, Jaime A.
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW
STREET: One Market Plaza, Steuart Street Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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650 HLGPH 654
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                                                                                                                           Local Similarity hes 5; Conserv
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                                      11111
9 HCGPH 8
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amino acid
GY: linear
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Giese, Neill A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Larry J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326-2400
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                                                                                                                        33.3%; Score 5; DB:
100.0%; Pred. No. 9.
Live 0; Mismatches
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No. 9.3e+02;
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5. 9.3e+02;
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US-08-462-728-2
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TELEX: 3723836
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
FUNGTH: 1089 amino acids
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                                                                                                                                                                                                  Patent No. 6043211
GENERAL INFORMATION:
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APPLICANT: Bell, Lil
APPLICANT: Kindsvoge
TITLE OF INVENTION:
                                                                            APPLICANT: WILLIAMS, Lewis T.
APPLICANT: ESCOBEDO, Jaime A.
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR REC
UNMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market, Steuart Street Tower, 20th Floor
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MEDIUM TYPE: Floppy disk
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CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM:
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                                       STREET: One Market,
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 99
                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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ZIP: 98104-7092
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                                USA
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Conservative 0;
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meTHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGIC
                                                                                                                                                ), Jaime A.

PLATELET-DERIVED GROWTH FACTOR RECEPTORS
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Pred. No.
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5.9.3e+02;
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

Floppy disk

MEDIUM TYPE: COMPUTER: II

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6291212
GENERAL INFORMATION:
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FILING DATE: 10-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/151,414
FILING DATE: 02-FEB-1988
ATTORNEY/AGENT INFORMATION:
NAME: DOW, KAIER B.
REGISTRATION NUMBER: 29,684
REGISTRATION NUMBER: 29,684
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                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: US 07/634,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
TITLE OF INVENTION: FUSIONS
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/326-2400
                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 07/309,322
FILING DATE: 10-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Rele
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1089 amino acids
TYPE: amino acid
TOPOLOGY: linear
FILING DATE: 22-JAN-1988
APPLICATION NUMBER: US 07/347,291
FILING DATE: 02-MAY-1989
                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.24
                                                                           APPLICATION NUMBER: US 0 FILING DATE: 27-DEC-1990
                                                                                                                                                         APPLICATION NUMBER: US/09/583,459A FILING DATE: 30-MAY-2000
                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Seed and Berry STREET: 6300 Columbia Center
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                         Seattle
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100.0%; Prr
                                                           US 07/146,877
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Pred. No.
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US-09-583-210-36
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APPLICANT: Sledzi
APPLICANT: Bell,
APPLICANT: Kindsv
                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEX: 3723836
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,510
FILING DATE: 27-DEC-1990
APPLICATION NUMBER: US 07/146,877
FILING DATE: 22-JAN-1988
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 30-MAY-200
CLASSIFICATION:
                                                                                                    REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                      APPLICATION NUMBER: US 07
FILING DATE: 02-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Maki J.D., David J.
REGISTRATION NUMBER: 31,3
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MEDIUM TYPE: Floppy disk
                                                  TELEFAX: 200
TELEFAX: 3723836
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ADDRESSEE: Seed and Berry
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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LENGTH: 1089 amino aci
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REFERENCE/DOCKET NUMBER: 990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206 622-4900
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              ENGTH:
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98104-7092
amino acid
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                 1089 amino acids
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                                                                                    206-682-6031
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Bell, Lillian A.
Kindsvogel Ph.D., Wayne R.
KINDSVOGEL Ph.D., Wayne R.
VENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
VENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
VENTION: FUSIONS
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100.0%;
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FILING DATE: 27-DEC-1990
APPLICATION NUMBER: US 07/146,877
FILING DATE: 22-JAN-1988
APPLICATION NUMBER: US 07/347,291
FILING DATE: 02-MAY-1989
ATTONNEY/AGENT INFORMATION:
NAME: Maki J.D., David J.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
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                                                                                                                              TOPOLOGY: 11
                                                                                                                                                                        SEQUENCE CHARACTERISTICS LENGTH: 1089 amino ac
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REFERENCE/DOCKET NUMBER: 99
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
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650 HLGPH 654
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CLASSIFICATION:
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nes 5; Conserv
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les 5; Conserv
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FILING DATE: 30-MAY-2000
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6300 Columbia Center
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Kindsvogel Ph.D., Wayne R.
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No. 9.3e+02;
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RESULT 184

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US-08-461-917-2
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TELEX: 372-836
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acid
TYPE: amino acid
TOPOLOGY: linear
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Sequence 36, App...
                                                                                                                                                                                                                  Sequence 2, Application US/08461917
Patent No. 6372438
GENERAL INFORMATION:
APPLICANT: WILLIAMS, Lewis T.
APPLICANT: ESCOBEDO, Jaime A.
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 9900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-4900
TELEFAX: 206-682-6031
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                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market, Steuart Street Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                    STREET: One much CITY: San Francisco STATE: California
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                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                        650 HLGPH
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nes 5; Conserv
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COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                COUNTRY:
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98104-7092
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6300 Columbia Center,
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100.0%; F1
 PC-DOS/MS-DOS
                                                                                                                                                                                                3, Lewis T.
), Jaime A.
PLATELET-DERIVED GROWTH FACTOR RECEPTORS
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                         ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: 1241

TELECOMMUNICATION INFORMATION:

TELECHONE: (415) 326-2400
INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415/326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/309,322
APPLICATION TOFEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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APPLICATION NUMBER: US 07/151,414
ETLING DATE: 02-FEB-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-FEB-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1089 amino acids
                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                              APPLICATION NUMBER: POFILING DATE: 19920128 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 94105
                                                                                                                                                                                                                                                                                                                                                   STREET: Steuart Street Tower, 20th Floor \setminus One Market STREET: Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100 nes 5; Conservative
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%LECOMMUNICATION INFORMATION:
TELEPHONE: 415/326-2400
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                                                                                                                                                                                                                                                                                                                                   San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application PC/TUS9200730
                                                                                                                                                                                                                                                                                                                     California
                 (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escobedo, Jaime A.
Williams, Lewis T.
VENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wolt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Giese, Neill A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fretto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tomlinson, James
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               326-2422
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100.0%; Pr
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                                                            Matches
                                                                                        Query Match
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APPLICANT: Williams, Lewis T.
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Matches 5; Conserv
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                                                                                                                                                                                                                    TELEFAX: (415) 326-24 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-FEB-1989
ATTORNEY/AGENT INFORMATION:
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LENGTH: 1089 amino acids
                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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650 HLGPH 654
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                                                                                                                                                                                                                                                                                NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PFILING DATE: 19920131 CLASSIFICATION: 435
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                                                                           Local
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SOFTWARE: PatentIn Release #1.24
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                             2 HLGPH 6
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                                                            Similarity 5; Conserv
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VENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
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Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   (415) 326-2400
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                                                                         Score 5; Pred. No.
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5. 9.3e+02;
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RESULT 188 US-08-574-959A-7

Sequence 7, Application US/08574959A

INFORMATION:

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GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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nes 5; Conserv
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REFERENCE/DOCKET NUMBER: DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
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                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDE
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                   PRIOR
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02109-1875
                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                           CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                 ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, Suite 510
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APPLICATION NUMBER: 08/574,959
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)%; Pred. No. 9.7
0; Mismatches
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5. 9.7e+02;
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                                                                                             Version #1.25
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                                                                ; MOLECULE TYPE: US-08-323-474-8
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Query Match
Best Local S
Matches 5
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Matches
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                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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SEQUENCE CHARACTERISTICS:
                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1138 amino acids
TYPE: amino acid
                                                                                                                                                                                                                           NAME: Seese, Kathryn A. 172
REGISTION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 266
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 26-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Cases Variation:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: NOVEL TYROSINE KINASE
                                                                                                                                                                                    TELEFAX: (20)
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                                                                                                                                                                                                TELEPHONE: (200) 233-0644
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res 5; Conserv
                                                                                                TOPOLOGY:
                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GPHRS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Any
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
 Similarity
5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617)227-74
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: DFN-008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 University
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33.3%; Score 5; DB ilarity 100.0%; Pred. No. 9. Conservative 0; Mismatches
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                                                                                                  linear
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100.0%; Pr/
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b; Pred. No. 9.7
0; Mismatches
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D. 9.7e+02;
                  DB 1; Le . 9.7e+02;
                                Length 1138;
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RESULT 192
US-08-220-240A-5
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Matches
                                                                Patent No. 5955291
GENERAL INFORMATION:
                                                                                                 Sequence
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Kempler, Ph.D., Gail Name: Kempler, Ph.D., Gail Name REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
                                APPLICANT:
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
    APPLICANT:
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CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: USSN 08/406,247 EILING DATE: 17-MAR-1995 APPLICATION NUMBER: USSN 08/144,992 EILING DATE: 28-OCT-1993 APPLICATION NUMBER: USSN 07/736,559 EILING DATE: 26-JUL-1991
                                                                                                                                                                                                            11 ESRAA 15
                                                                                                                                                                                                                                           Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                               Application US/08220240A
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Partanen, Ju.
                                                                                                                                                                                                                                                                                                                                                                                   1138 amino acids
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                Alitalo, Kari
Matikainen, Marja-Terttu
Partanen, Juha
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                                                                                                                                                                                                                                           Conservative
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PCT-US93-03076-2
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                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9303076 GENERAL INFORMATION:
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             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              APPLICANT: Whitehead Institute for TITLE OF INVENTION: GAP-Associated TITLE OF INVENTION: Transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/167,453
FILING DATE: 15-DEC-1993
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APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                              CITY:
STATE:
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                                                                                ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07 FILING DATE: 09-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illinoi
                                                                                             COUNTRY:
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                                                                                                                                                            ADDRESSEE:
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                                                                                                                            Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                               3: Hamilton, Brook, Smith & Reynolds, P.C
2 Militia Drive
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233 South Wacker Drive/6300 Sears Tower
                                                                                                 \mathbf{s}_{\mathbf{0}}
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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 PatentIn
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SYSTEM: PC-DOS/MS-DOS
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ANTIBODIES RECOGNIZING TIE RECEPTOR
TYROSINE KINASE AND USES THEREOF
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Pred. No.
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Version
                                                                                                                                                                                                                             Biomedical Research Protein p190 and
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Lei
o. 9.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1138;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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CURRENT APPLICATION DATA:

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US-08-479-722B-2
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TELEFAX: (713) 934-70:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1513 amino acids
                                NAME: FUSSEY, Shelley P.M.
RECISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: 4100.000500/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 934-7000
                                                                                                                                                                                                                                 APPLICATION NUMBER: US POFILING DATE: 21-FEB-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/479,722B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: LATENT TGF( BINDING PROTEIN (LTBP) TITLE OF INVENTION: GENES, COMPOSITIONS AND METHODS NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                        APPLICATION NUMBER: US 08/199,780 FILING DATE: 18-FEB-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               FILING DATE: 30-SEP-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Texa
COUNTRY: US
ZIP: 77040
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/O FILING DATE: 07-JUN-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            watch 33.3%; Score 5; DB Local Similarity 100.0%; Pred. No. 1.: 165 5; Conservative 0; Mismatches
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI92-03A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PILING DATE: 19930331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 PHRST 9
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7676 Hillmont, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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934-7011
934-7011
934-7011
                                                                                                                                                                                                                  US 08/316,650
                                                                                                                                                                                                                                                                     US PCT/US95/02251
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No. 1.2e+03;
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259 GPHRS 263

RESULT 196 US-09-091-219-24

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PCT-US95-02251-18
                                                                                      MOLECULE TYPE:
PCT-US95-02251-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application PC/TUS9502251 GENERAL INFORMATION:
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                               Matches
                                                          Query Match
                                                                                                                                                                         TELEFAX: (713) 789-26'
TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1833 amino aci
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/316,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Un:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 GPHRS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid TOPOLOGY: linear
                            Local Similarity
nes 5; Conserv
                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                           NAME: Parker, David L. REGISTRATION NUMBER: 32,165
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/199,780 FILING DATE: 18-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 30-SE
                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/02251 FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GPHRS 8
                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 5; Conserv
 4 GPHRS 8
                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Texas
                                                                                                                                              1833 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States of America
                                                                                                                                                                                                       (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                               Conservative
                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version
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                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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100.0%; Pred. NO.
100.0%; Pred. NO.
100.0%; Pred. NO.
                                         33.3%; Score 5;
100.0%; Pred. N
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                             Mismatches
                                            No.
                                           DB 5; Le
o. 1.5e+03;
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                                                          Length 1833;
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                             Gaps
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; ORGANISM: Foot-and-mouth disease virus
US-09-091-219-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Pater
SEQ ID NO 24
LENGTH: 2318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JENERAL INFORMATION:
APPLICANT: STUDDERT, Michael J.
APPLICANT: CRABB, Brendan S.
APPLICANT: FENG, Li
TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS
FILE REFERENCE: 040268/0151
CURRENT APPLICATION NUMBER: US/09/091,219
CURRENT FILING DATE: 1998-10-05
COURRENT FILING DATE: 1998-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/09091219 Patent No. 6171592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: PCT/AU96/00815
EARLIER FILING DATE: 1996-12-18
EARLIER APPLICATION NUMBER: AU PN7201
EARLIER FILING DATE: 1995-12-18
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: RIDER, James E.

TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
                                                                         NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1095 RSTPE 1099
                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                    APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New Yor
                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                     66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08602999A
                                                                                                                                                                                                                                                                                                                                                                                                                         E: Pennie & Edmonds
1155 Avenue of the Americas
                                     : (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DER, Channing J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUILLIAM, Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THORN, Judith M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPARKS, Andrew B.
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lo. 1.8e+03;
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US-08-278-865-97
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US-08-602-999A-97
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Sequence 97, Application US/08278865
Patent No. 6303574
GENERAL INFORMATION:
APPLICANT: KAY, BRIAN K.
APPLICANT: SPARKS, ANDREW B.
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6210919
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 162, Application US/08496841C Patent No. 6210919
                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 162: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC comparison

COMPUTER: IBM PC comparison

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/496,841C

FILING DATE: 28-Jun-1995

CLASSIFICATION: CUDKnown>

ATTORNEY/AGENT INFORMATION:

NAME: Paul F. Fehlner, Ph.D.

PFGTSTRATION NUMBER: 35.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity les 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 RSTP 10
                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 162:
                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
                                                                                                                                                             | STPE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ST. GEORGE-HYSLOP,
ROMMENS, JOHANNA M
                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 805 Third Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
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100.0%; Pr
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100.0%; Pr
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0; Mismatches
                                                                                                                                                                                                       Score 4; DB 4; Pred. No. 2e+0; Mismatches
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o. 2e+05;
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KAY, BRIAN K. SPARKS, ANDREW B.

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US-09-500-124-97
                                                                                                                                                                                                                                                                                                                                                                     -09-500 - Approx 8equence 97, Approx 80, 6432920
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                                                                                                                                                                                                                                                                                                                                                                SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
                                                             STREET: 1100 ...
STREET: New York
STATE: New York
STATE: New York
STATE: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PA PC COMPATIBLE
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,865
FILING DATE:
CLASSIFICATION: 514
CLASSIFICATION: 514
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                APPLICANT: RIDER, JaTITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: STC SH3 BINDING PEPTIDES AND METHODS OF INVENTION: ISOLATING AND USING SAME
                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity hes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
                                                           COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-007-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 RSTP 10
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                                                                                                                                                                                                                                                                                                                                                                                               Application US/09500124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 amino acids
                                                                                                                                                                                 RIDER, James E.
VENTION: SH3 BINDING PEPTIDES AND METHODS
VENTION: ISOLATING AND USING SAME
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QUILLIAM, LAWRENCE A.
DER, CHANNING J.
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Search completed: March 10, 2003, 14:31:17 Job time : 38 secs
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                           7 RSTP 10
                                                                                                                          4; Conservative
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US-09-895-035-12
US-09-785-474-2
US-09-785-474-28
US-09-785-474-32
US-09-785-474-32
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US-09-844-761-38777
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US-09-815-26-6773
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US-09-916-753-154

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US-09-916-106

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US-09-917-918-242-13042

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US-10-123-946-210

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US-10-140-471-210

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   0 US-09-923-444A-2
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US-10-174-590-458
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Sequence 37, Appl
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Sequence 1027, Ap
Sequence 1037, Ap
Sequence 1154, App
Sequence 154, App
Sequence 17, Appl
Sequence 154, App
Sequence 10, App
Sequence 210, App
Sequence 458, App
Sequence 458
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US-09-823-153-8

(US-09-823-153-8)

Sequence 8, Application US/09823153

Patent No. US2002025540A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

APPLICANT: Roberts, Susan

APPLICANT: Hendrick, Joseph

APPLICANT: Smith, David

APPLICANT: Vinitsky, Alexander

TITLE OF INVENTION: ISOLATION OF FUNCTIONALL

TITLE OF INVENTION: METHODS FOR DETECTION OF

FILE REFERENCE: D0004

CURRENT APPLICATION NUMBER: US/09/823,153

CURRENT FILING DATE: 2001-07-02

NUMBER OF SEQ ID NOS: 11

SOFTMARE: Patentin version 3.0

SEQ ID NO 8

LENGTH: 354

TYPE: PAT

ORGANISM: Artificial Sequence

FEATURE:

NAMEKKEY: misc_feature

OTHER INFORMATION: Description of Artificia
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                                   Query Match
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Matches 15
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                                   l Similarity
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ACTIVITY AND INHIBITORS THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09785474
Patent No. US20010012626A1
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH
WASCO, WILMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/895,035
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09,116,640
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 14
SOFTMARE: PERL Program
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09895035
Patent No. US20020082211A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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APPLICANT: Murry, Lynn E.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PRESENILIN VARIANT
FILE REFERENCE: PC-0047 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KDY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020082211A1 g1244638
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APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609.4180002
                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NOMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION - <Unknown>
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: STEENE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Genetic Alterations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Pred. No. 1.9e-08;
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1 SHLGPHRSTPESRAA 15

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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ
US-09-785-474-4
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US-09-785-474-4
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Matches
                    Query Match
Best Local
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                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/706,344

FILING DATE: 30-AUG-1996

APPLICATION NUMBER: 60/003,054

FILING DATE: 31-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REGISTRATION NUMBER: 40,679
                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SHLGPHRSTPESRAA 15
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Genetic Alterations Related To Familial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
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ZIP: 20005-3934
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                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                   TELEFAX: 202-371-2540
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Conservative
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                100.0%;
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Score 15; DB 10;
Pred. No. 1.9e-08;
; Mismatches 0;
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Pred. No. 1.
                                                                                       ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                       0609.4180002
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1.9e-08;
mes 0;
                               Length 467;
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Indels
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Gaps
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0,
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SEQUENCE DESCRIPTION: SEQ ID NO: 28: US-09-785-474-28
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US-09-785-474-30
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US-09-785-474-28
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                                                                                                                                                          Sequence 30, Application US/09785474 Patent No. US20010012626A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 06.09.418
REFERENCE/DOCKET NUMBER: 0609.418
TELEPHONE: 20-371-2500
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                             346
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                      CORRESPONDENCE ADDRESS: ADDRESSEE: STERNE,
                                              Alzheimer's NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                  TITLE OF INVENTION: Genetic Alterations Related To Familial
                                                                                                                      APPLICANT: TANZI, RUDOLPH WASCO, WILMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GO
STREET: 1100 NEW YORK AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Genetic Alterations Related To Familial Alzheimer's Disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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    EE: STERNE, KESSLER, GO
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                                                                                                                                                                                                                                                                                                                                                                         0,
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Pred. No. 1.9e-08;
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                Disease
      GOLDSTEIN & FOX P.L.L.C
E, SUITE 600
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 467;
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US-09-785-474-32
US-09-785-474-32
Sequence 32, Application US/09785474
PAtent No. US20010012626A1
PATENT TANZI, RUDOLPH
APPLICANT: TANZI, RUDOLPH
MASCO, WILMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear;

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-785-474-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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Best Local Similarity
Matches 15; Conserv
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NAME: KIM, JUDITH U.
REGISTRATION UMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609.4180002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 30:
                                                      COUNTRY: USA
ZIP: 2005-3934

ZIP: 2005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Verentin Application Data:
Application Number: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: CUDKnown>
PRIOR APPLICATION: CUDKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 SHLGPHRSTPESRAA 360
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIAL Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/785,474
FILING DATE: 20-Feb-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
OFFICE OF THE PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KES
STREET: 1100 NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Genetic Alterations Related To Familial Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                    APPLICATION NUMBER: 08/706,344 FILING DATE: 30-AUG-1996
                                                                                                                                                                                                                                                                                             STATE: DC
                                                                                                                                                                                                                                                                                                               CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 467 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/706,344
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: 60/003,054
FILING DATE: 31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
NUMBER: 60/003,054
                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's
                                                                                                                                                                                                                                                                                                                                 KESSLER, GOLDSTEIN & FOX P.L.L.C
DRK AVENUE, SUITE 600
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Pred. No. 1.9e-08
); Mismatches 0
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Length 467; Indels

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Gaps

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-754-949-4
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                                                                                             GENERAL INFORMATION:
APPLICANT: Monteiro, et al.
TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presenilin
FILE REFERENCE: 4115-161
CURRENT APPLICATION NUMBER: US/09/878,454A
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 2000-06-11
PRIOR FILING DATE: 2000-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09754949
Patent No. US20020015939A1
GENERAL INFORMATION:
APPLICANT: MCCARTHY, JUSTIN
APPLICANT: CORDELL, BARBARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                      SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CORDELL, BARBARA
TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS OF
TITLE OF INVENTION: NEURONAL DEGENERATION
FILE REFERENCE: SCIOS.012A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 16 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/754,949
CURRENT FILING DATE: 2001-01-04
                                                                       NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
ORGANISM: Homo sapiens
                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                 346 SHLGPHRSTPESRAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 SHLGPHRSTPESRAA 360
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                   467
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Pred. No.
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. 1.9e-08;
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020082211A1 g1709856
US-09-895-035-14
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                                                                     ; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-071-900-1
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US-10-071-900-1
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PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PERL Program
SEQ ID NO 14
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/09895035 Patent No. US20020082211A1 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                         APPLICANT: Rommens, Johanna
APPLICANT: Eraser, Paul E.
APPLICANT: Eraser, Paul E.
TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: 1034/1F910-US1
CURRENT APPLICATION NUMBER: US/10/071,900
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/227,725
PRIOR PRIOR APPLICATION NUMBER: US/09/227,725
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 4
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Patterson, Chandra
APPLICANT: Murry, Lynn E.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: HUMAN PRESENILIN VARIANT
FILE REFERENCE: PC-0047 CIP
CURRENT APPLICATION NUMBER: US/09/895,035
CURRENT FILING DATE: 2001-06-29
CURRENT FILING DATE: 2001-06-29
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APPLICANT: Rommens, Johanna
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 1.9e-08;
; Mismatches 0;
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Pred. No. 1.9e-08;
; Mismatches 0;
                 Score 15; DB 12; Pred. No. 1.9e-08;
 Mismatches
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1 SHLGPHRSTPESRAA 15

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; NAME/KEY: misc_feature
; OTHER INFORMATION: Desc
US-09-823-153-5
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APPLICANT: Vinitsky, Alexander
TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACT
TITLE OF INVENTION: METHODS FOR DETECTION OF ACT
FILE REFERENCE: D0004
CURRENT APPLICATION NUMBER: US/09/823,153
CURRENT FILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 15
TYPE: PRT
TYPE: PRT
TYPE: PRT
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                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/823,153
CURRENT FILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 16
TYPE: PRT
                                  Query Match
Best Local
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APPLICANT: Bristol-Myers Squibb Company
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Best Local Similarity
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APPLICANT: Smith, David
APPLICANT: Smith, David
APPLICANT: Vinitsky, Joseph
APPLICANT: Vinitsky, Alexander
TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX
TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
FILE REFERENCE: D0004
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Roberts, Susan
APPLICANT: Pak, Roger
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                                                                                                                                 FEATURE:
                                                                                                                                                ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description of Artificial Sequence:
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                                  Similarity
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Smith, David
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                   Conservative
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                                                                                              Description of Artificial Sequence:
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                                 86.7%; Score 13; 100.0%; Pred. No.
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Pred. No.
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. 1.1e-07;
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1.1e-07;
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US-10-012-034A-16
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LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                Matches
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Best Local Similarity
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APPLICANT: Ben-Sasson, Shmuel
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                                                                                                                                       NAME/KEY: AMIDATION LOCATION: (0)...(19)
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                                                                Similarity 6; Conserv
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TITLE OF INVENTION: SHORT PEPTIDES FROM THE A-REGION OF TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MO TITLE OF INVENTION: ACTIVITY FILE REFERENCE: 1242.2003-000 CURRENT APPLICATION NUMBER: US/09/734,520 CURRENT APPLICATION NUMBER: US/09/734,520 CURRENT FILING DATE: 2000-12-11 NUMBER OF SEQ ID NOS: 122 SOFTWARE: FASTSEQ FOR Windows Version 4.0 SEQ ID NO 16 LENGTH: 19 TYPE: PRT ORGANISM: Unknown FEATURE: OTHER INFORMATION: PDGFR-b
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US-09-734-520-16
JS-09-734-520-16
Sequence 16, Application US/09734520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/10012034A Patent No. US20020137141A1 GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ben-Sasson, Shmuel
TITLE OF INVENTION: SHORT PEPTIDES FROM THE A-REGION OF
TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: BEN-SASSON-5A
CURRENT APPLICATION NUMBER: US/10/012,034A
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 09/734,520
PRIOR FILING DATE: 2000-12-11
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 133
SOFTWARE: FastSEQ for Windows Version
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                    Score 6; I
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                    DB 12;
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US-09-864-761-38777
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US-09-864-761-38777
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PRIOR FILING DATE: 2000-08-03
PRIOR PPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence
SEQ ID NO 38777
LENGTH: 55
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 09/774,203 PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: Aeomica-X-1
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                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
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                                                                                         INFORMATION:
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Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank, David R.
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EXPRESSED IN ADULY
EXPRESSED IN HELA
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100.0%;
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                                                                                  IN BRAIN, SIGNAL = 8.
IN HEART, SIGNAL = 4
HIT: P75320, EVALUE
                                                                                                                                                   IN PLACENTA, SIGNAL = 12
IN LUNG, SIGNAL = 6.8
IN BONE MARROW, SIGNAL =
IN FETAL LIVER, SIGNAL =
                                                                                                                                                                                                                                             IN ADULT LIVER, SIGNAL - 6.5
IN HELA, SIGNAL - 9.8
  Score 6;
Pred. No.
    DB 10;
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RESULT 18
US-09-738-626-6773
US-09-738-626-6773, Application US/09738626
; Publication No. US20020197605A1
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US-09-815-242-13506
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APPLICANT: NAKAGAWA, SATOSHI
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-03-21
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                              APPLICANT:
                                                           APPLICANT:
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                             APPLICANT:
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                                                                                                                                                                                                                                                                                     171 PESRAA 176
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/2
FILING DATE: 2001-02-16
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                                                      HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                               MIZOGUCHI,
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                                                                                                                                    ANDO, SEIKO
                             IKEDA, MASATO
OZAKI, AKIO
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                                                                                                                                               HIROSHI
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Pred. No.
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Query Match
Best Local Similarity
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US-09-147-052-4
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                                                                                                                                                                 Sequence 14, Application US/09866510 Patent No. US20020111304A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 4
LENGTH: 10
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6773
TLENGTH: 739
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APPLICANT: KAZLAUSKAS, ANDRIUS
APPLICANT: IKUNO, YASUSHI
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
FILE REFERENCE: ERM-104.01
CURRENT APPLICATION NUMBER: US/09/866,510
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/250,747
PRIOR APPLICATION NUMBER: 60/289,103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SAITOH, Shuji
APPLICANT: TSUZAKI, YOShinari
APPLICANT: YANAGIDA, NO. US20010014335Aloru
TITLE OF INVENTION: NOVEL FUSED PROTEIN, GENE THEREFOR, RECOMBINANT VECTOR,
TITLE OF INVENTION: RECOMBINANT VIRUS, AND ITS USE
FILE REFERENCE: 981167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 08-103548 PRIOR FILING DATE: 1996-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-0
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CURRENT FILING DATE: 1999-04-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                174 TPESRA 179
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Pred. No.
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Pred. No.
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59;
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                                                                                ; SEQUENCE DESCRIPTION: US-09-955-363-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 21
US-09-955-363-2
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NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                TELEX: 3723836
INFORMATION FOR SEQ ID NO: 2:
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APPLICATION NUMBER: US 07/634,510

FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 07/347,291

FILING DATE: 02-MAY-1989

ATTORNEY/AGENT INFORMATION:

NAME: MAKİ J.D., DAVİD J.

REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity nes 6; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1106 amino acids
                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 990008.446C3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center
                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/955,363
FILING DATE: 18-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                 TELEPHONE: 206-622-49
TELEFAX: 206-682-6031
TELEX: 3723836
                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: WA
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Kindsvogel Ph.D.,
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          40.0%; 5
100.0%; Pr
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100.0%;
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                                                                                                SEQ
             Score 6; DB 9; Pred. No. 85; 0; Mismatches
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656 SHLGPH

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SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 18
LENGTH: 1106
TYPE: PRT
ORGANISM: Homo sapiens
US-09-866-510-18
RESULT 24
US-09-866-510-20
JS-09-866-510-20
Sequence 20, Application US/09866510
Patent NO. US20020111304A1
GENERAL INFORMATION:
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Patent No. US20020111304A1
GENERAL INFORMATION:
APPLICANT: KAZLAUSKAS, ANDRIUS
APPLICANT: IKUNO, YASUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.08;
Matches 6; Conservative
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                               Query Match
Best Local :
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SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/866,510 CURRENT FILING DATE: 2001-05-25 PRIOR APPLICATION NUMBER: 60/250,747 PRIOR FILING DATE: 2000-12-01 PRIOR APPLICATION NUMBER: 60/289,103 PRIOR APPLICATION NUMBER: 60/289,103 PRIOR FILING DATE: 2001-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/289,103
PRIOR FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 33
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
FILE REFERENCE: ERM-104.01
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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APPLICANT: IKUNO, YASUSHI
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
FILE REFERENCE: ERM-104.01
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TYPE: PRT
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                                                                                                                                       656 SHLGPH 661
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nes 6; Conserv
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Pred. No. 85;
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Mismatches
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; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-22
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Best Local Similarity
6; Conserva
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US-09-866-510-22
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US-09-734-520-75
                                                                                                                                                           Sequence 75, Application US/09734520 Patent No. US20020115173A1
                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: IKUNO, YASUSHI
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
FILE REFERENCE: ERM-104.01
CURRENT APPLICATION NUMBER: US/09/866,510
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/250,747
PRIOR APPLICATION NUMBER: 60/250,747
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 60/289,103
PRIOR APPLICATION NUMBER: 60/289,103
PRIOR APPLICATION SUMBER: 60/289,103
PRIOR APPLICATION NUMBER: 60/289,103
PRIOR FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 33
APPLICANT: Ben-Sasson, Shmuel TITLE OF INVENTION: SHORT PEPTIDES FROM THE A-REGION OF TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE FILLE OF INVENTION: ACTIVITY FILE REFERENCE: 1242.2003-000 CURRENT EPPLICATION NUMBER: US/09/734,520 CURRENT FILING DATE: 2000-12-11
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CURRENT ELIZATION NUMBER: US/09/866,510
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/250,747
PRIOR FILING DATE: 2000-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: IKUNO, YASUSHI
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100.0%; Pr
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Windows Version 4.0

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; OTHER INFORMATION: PDGFR-b; NAME/KEY: MYRISTATE; LOCATION: (1)...(0); NAME/KEY: AMIDATION; LOCATION: (0)...(12); US-09-734-520-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: MYRISTATE
; LOCATION: (1)...(0)
; NAME/KEY: AMIDATION
; LOCATION: (0)...(12)
US-09-734-520-76
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                                 GENERAL INFORMATION:

APPLICANT: Ben-Sasson, Shmuel
TITLE OF INVENTION: SHORT PEPTIDES FROM THE A-REGION OF
TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: BEN-SASSON=5A
CURRENT APPLICATION NUMBER: US/10/012,034A
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 09/734,520
PRIOR FILING DATE: 2001-12-11
                                                                                                                                                                                                                      Sequence 75, Application US/10012034A Patent No. US20020137141A1
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 76
LENCTH: 12
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: PDGFR-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Pred. No. 17;
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RESULT 30
US-09-734-520-15
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Best Local Similarity
---hes 5; Conserve
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; NAME/KEY: AMIDATION
; LOCATION: (0)...(12)
US-10-012-034A-75
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                                                                                                 GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel
TITLE OF INVENTION: SHORT PEPFIDES FROM THE A-REGION OF
TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE
TITLE OF INVENTION: ACTIVITY
TITLE OF INVENTION: ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 76
                                                                                                                                 Sequence 15, Application US/09734520 Patent No. US20020115173A1
                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 76, Application US/10012034A Patent No. US20020137141A1
TITLE OF INVENTION: SHORT PEPTIDES FROM THE A-REGION OF TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE TITLE OF INVENTION: ACTIVITY FILE REFERENCE: 1242.2003-000 CURRENT APPLICATION NUMBER: US/09/734,520 CURRENT FILING DATE: 2000-12-11
                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/012,034A CURRENT FILING DATE: 2001-12-11 PRIOR APPLICATION NUMBER: 09/734,520 PRIOR FILING DATE: 2000-12-11 NUMBER OF SEQ ID NOS: 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: BEN-SASSON=5A
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NAME/KEY: MYRISTATE
LOCATION: (1)...(0)
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OTHER INFORMATION: PDGFR-b
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ORGANISM: Artificial Sequence
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17;
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RESULT 31
US-10-012-034A-15
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; OTHER INFORMATION: PDGFR-a
US-09-734-520-15
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APPLICANT: Ben-Sasson, Shmuel
TITLE OF INVENTION: SHORT PEPFIDES FROM THE A-REGION OF
TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: BEN-SASSON-5A
CURRENT APPLICATION NUMBER: US/10/012,034A
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 09/734,520
PRIOR FILING DATE: 2000-12-11
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Best Local S
Matches 5
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SOFTWARE: FBSTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 19
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SOFTWARE: FastSEQ for
SEQ ID NO 15
LENGTH: 19
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL!
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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ORGANISM: Unknown
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6 HLGPH 10
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Pred. No.
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PUDLICATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P1
CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
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US-09-774-639-274
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Best Local (
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NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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OTHER INFORMATION: EXPRESSED IN PLACENTA,
OTHER INFORMATION: EXPRESSED IN ADULT LIVE
OTHER INFORMATION: EXPRESSED IN FETAL LIVE
OTHER INFORMATION: EXPRESSED IN BRAIN, SIG
OTHER INFORMATION: EXPRESSED IN BRAIN, SIG
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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FILING DATE: 2000-09-21
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100.0%; Pr
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s; Pred. No. 42;
0; Mismatches
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LUNG, SIGNAL = 0.75
FETAL LIVER, SIGNAL = 0.68
BRAIN, SIGNAL = 1.2
BONE MARROW, SIGNAL = 0.73
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D. 42;
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Best Local Similarity
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Best Local Similarity
~~+~hes 5; Conserv
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-274
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Publication No. US20030003555A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P1
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                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                  PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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CURRENT FILING DATE: 2001-07-09
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PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 371
                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
                                                                 APPLICATION NUMBER: US 60/236,359
FILING DATE: 2001-0 APPLICATION NUMBER:
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Chen, Wensheng
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Hanzel, David K.
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                  2001-01-30
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Pred. No
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                                                                            ; OTHER INFORMATION: US-09-764-847-695
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US-09-764-847-695
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                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 695
LENGTH: 61
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 695, Application Patent No. US20020132767A1 GENERAL INFORMATION:
Query Match 33.3%; Score 5; DB Best Local Similarity 100.0%; Pred. No. 71 Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/764,847 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: I
OTHER INFORMATION: I
OTHER INFORMATION: I
OTHER INFORMATION: I
                                                                                                                                                                                                                                                                    Prior application data removed - NUMBER OF SEQ ID NOS: 2003
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                                                                                                               NAME/KEY: SITE LOCATION: (59)
                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                      FEATURE:
                                                                                                                                                                      ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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EXPRESSED IN ADULT LIVER, SIGNAL = 0.66

EXPRESSED IN FETAL LIVER, SIGNAL = 0.72

EXPRESSED IN BRAIN, SIGNAL = 0.67

EXPRESSED IN BONE MARROW, SIGNAL = 0.76

EXPRESSED IN PLACENTA, SIGNAL = 0.64

EXPRESSED IN PLACENTA, SIGNAL = 0.64

EXPRESSED IN PLACENTA, SIGNAL = 0.64

EXPRESSED IN PLACENTA, SIGNAL = 0.64
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100.0%; Pr
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                     DB 10;
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                                   Length 61;
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SHLGP 5

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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 33764
LENGTH: 91
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Sequence 33764, Application
Patent No. US20020048763A1
                                                                                                                     OTHER INFORMATION: I OTHER INFORMATION: I OTHER INFORMATION: OTHER INFORMATION: INFORMATION:
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CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
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PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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                                                                            INFORMATION:
INFORMATION:
                                                     INFORMATION:
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Hanzel, David K
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                                                EXPRESSED
EXPRESSED
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                                                                                                                MAP TO AL035610.2

EXPRESSED IN BT474, SIGNAL = 5.2

EXPRESSED IN FETAL LIVER, SIGNAL = 7.2

EXPRESSED IN PLACENTA, SIGNAL = 7.9

EXPRESSED IN PLACENTA, SIGNAL = 5.9
  EXPRESSED EXPRESSED
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                                                                       IN BONE MARROW, SIGNAL - IN HBL100, SIGNAL - 5.4
LUNG, SIGNAL - 6.8
ADULT LIVER, SIGNAL -
BRAIN, SIGNAL - 9.3
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; OTHER INFORMATION:
US-09-864-761-33764
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US-09-738-626-5971
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APPLICANT: EGGELING, LOTHAR
APPLICANT: NAMPOOTHIRI, MADHAVAN
TITLE OF INVENTION: NUCLEOPTIDE SEQUENCES WHI
FILE REFERENCE: 21123/280306/MAS
CURRENT APPLICATION NUMBER: US/09/852,137
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: DE 100 23 400.3
PRIOR FILING DATE: 2000-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JF 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 5971
                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                       Sequence 2, Application US/09852137 Patent No. US20020055154A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5971, Application US/09738626 Publication No. US20020197605A1
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                                                                                                                                     APPLICANT: MOCKEL, BETTINA
APPLICANT: WEISSENBORN, ANKE
APPLICANT: PFEFFERLE, WALTER
APPLICANT: SAHM, HERMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125 CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18 PRIOR APPLICATION NUMBER: JP 99/377484 PRIOR FILING DATE: 1999-12-16
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OCHIAI, KEIKO
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                                                                                                                                                                                                                                                                                                                                                                33.3%; bred. No.
100.0%; Pred. No.
17e 0; Mismatches
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HIT: AA746130.1, EVALUE 1.00e-50
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Pred. No.
                                                                                         SEQUENCES WHICH CODE FOR THE ACP GENE
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o. 1.1e+02;
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b. le+02;
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; LENGTH: 97
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-852-137-2
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 99/632,366
PRIOR PELICATION NUMBER: US 99/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
                     SOFTWARE: Annomax Sequence Listing SEQ ID NO 41798 LENGTH: 98 TYPE: PRT
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Sequence 41798, Application US/09864761
Patent No. US20020048763A1
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 97
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                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
                                                                                                             PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION UNMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR FILING DATE: 2001-01-30
  ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILE REFERENCE: Aeomica-X-1
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
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sapiens
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Pred. No.
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                                                                                            Engine vers. 1.1
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Query Match
Best Local Similarity
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US-09-902-941-1671
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US-09-736-457-1671
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1671
LENGTH: 109
                                                                                                                                                                                          Sequence 1671, Application US/09902941 Patent No. US20020172952A1
                                                                                                                                                                                GENERAL INFORMATION:
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Matches 5; Conserv
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APPLICANT:
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APPLICANT:
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OTHER INFORMATION: E
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OTHER INFORMATION: E
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APPLICANT: Wang, Tongtong
APPLICANT: Watnabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                               APPLICANT:
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                         Carter, Darrick
Fanger, Gary R.
Vedvick, Thomas S.
Bangur, Chaitanya S.
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Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
                                                                                                 Watanabe, Yoshihiro
Johnson, Jeffrey C.
Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fan, Liqun
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Retter, Marc
                                                                                        Marnerakis, Margarita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mannion, Jane
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EXPRESSED IN BRAIN, SIGNAL = 1.4
EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
EXPRESSED IN HEART, SIGNAL = 1.8
EST_HUMAN HIT: D54392.1, EVALUE 4.60e+00
SWISSPROT HIT: Q98910, EVALUE 1.10e+00
Andria
COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chaitanya
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100.0%; Pr
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100.0%; Pi
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%; Pred. No. 1.2
0; Mismatches
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 AND METHODS FOR THE THERAPY
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APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR APPLICATION NUMBER: 000-03-08
PRIOR FILING DATE: 1900-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1175
                                                                                                                                                                                                                                  US-09-925-300-1175
; Sequence 1175, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-626-1671
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US-09-849-626-1671
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US-09-902-941-1671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bangur, Chaitanya
APPLICANT: Fanger, Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Switzer, Anne
APPLICANT: MCNeill, Patricia
APPLICANT: Clapper, Jonathan
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CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1671
LENGTH: 109
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SOFTWARE: FRSTSEQ for Windows Version 3.0
SEQ ID NO 1671
LENGTH: 109
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Best Local :
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C16
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
FILE REFERENCE: 2101
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McNeill, Patricia
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Pred. No. 1.2e+02;
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b. 1.2e+02;
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; TYPE: PRT
; ORGANISM: HOMO S
US-10-004-551-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6171, Application US/09738626 Publication No. US20020197605A1
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Best Local
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Best Local 9
                                                                    FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SHIMKETS, RICHARD A
APPLICANT: FERNANDES, ELMA
APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYUUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
EILE REFERENCE: 15966-559
CURRENT APPLICATION NUMBER: US/10/004,551
CURRENT FILING DATE: 2001-12-05
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NAME/KEY: SITE
LOCATION: (50)
                                  PRIOR APPLICATION NUMBER: JP 00/159162 PRIOR FILING DATE: 2000-04-07
                                                                                                                                                            APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAKAGAWA, SATOSHI
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nes 5; Conserv
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APPLICATION NUMBER: JP 00/280988 FILING DATE: 2000-08-03
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5; Conserv
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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ilarity 100.0%;
Conservative (
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100.0%; Pred. No.
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5. 1.2e+02;
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1.3e+02;
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; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
; SEQ ID NO 86
; LENGTH: 126
; TYPE: PRT
ORGANIZM: Physcomitrella patens
US-09-734-569-86
                                                                                                                                                                                                                        RESULT 48
US-09-764-868-781
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Best Local Similarity 100.
"Thomas 5; Conservative
                                                                                                                                                                        Sequence 781, Application US/09764868 Patent No. US20020168711A1 GENERAL INFORMATION:
 Prior application data removed - refer to PALM NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 781
TENGTH: 129
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Sequence 86, Application US/09734569
Patent No. US20020064816A1
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Best Local :
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SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 6171
LENGTH: 126
                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PT332
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved TITLE OF INVENTION: in the synthesis of carbohydrates FILE REFERENCE: BASF-NAE-1332-99-US CURRENT FILING DATE: 05/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16
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Duwenig, Elke
Schmidt, Ralf-Michael
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Bischoff, Friedrich
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Ehrhardt, Thomas
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b; Pred. No. 1.3
0; Mismatches
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Pred. No.
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o. 1.3e+02;
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RESULT 50

US-09-764-864-1425

; Sequence 1425, Application

; Patent No. US20020132753A1

; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: JP 9/377484
PRIOR FILLING DATE: 2000-12-18
PRIOR FILLING DATE: 199-12-16
PRIOR APPLICATION NUMBER: JP 9/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILLING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-08-03
PRIOR FILLING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6788
LENGTH: 130
TYPE: DET
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LOCATION: (112)
OTHER INFORMATION:
US-09-764-868-781
                                                                                                                    ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6788
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                                                          Matches
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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NAME/KEY: SITE
LOCATION: (105)
OTHER INFORMATION: 1
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17
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                           7 RSTPE 11
RSTPE
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OCHIAI, KEIKO
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TATEISHI, NAOKO
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                                                        33.3%; Score 5; DB
100.0%; Pred. No. 1.
Live 0; Mismatches
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Pred. No.
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                                                          .4e+02;
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APPLICANT: Rosen et al.

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US-09-764-868-1017
                                                                                                                                             US-09-764-868-1017
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. ;
SEQ ID NO 1017
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1017, Application US/09764868 Patent No. US20020168711A1 GENERAL INFORMATION:
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                                                                     Matches
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TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                  Prior application data removed - refer to NUMBER OF SEQ ID NOS: 1510
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                                                                                                                                               NAME/KEY: SITE
LOCATION: (134)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (140)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (142)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (114)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (126)
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                            FEATURE:
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LOCATION: (127)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
 62
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                                                                Local Similarity es 5; Conserv
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 STPES 66
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                                 STPES 12
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Pred. No. 1.5e+02;
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Pred. No.
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LENGTH: 161

TYPE: PRT
ORGANISM: Eulemur fulvus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1).. (485)
OTHER INFORMATION: Taxon
US-09-747-155-243
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US-09-747-155-243
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; LENGTH: 149
; TYPE: PRT
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                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.0 SEQ ID NO 243
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 243, Application US/09747155 Patent No. US20020151692A1
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                                                            Query Match
Best Local (
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APPLICANT: Glorgi, Dominique
TITLE Glorgi, No. US20020151692Alel Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 19904-008 (C009B6834US)
CURRENT APPLICATION NUMBER: US/09/747,155
CURRENT FILING DATE: 2000-12-21
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 00/159162 PRIOR FILING DATE: 2000-04-07
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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11 ESRAA 15
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                                            Similarity 5; Conserv
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OCHIAI, KEIKO
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SENOH, AKIHIRO
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                                                                                                                        Taxon -
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o. 1.7e+02;
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; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 798; LENGTH: 164; TYPE: PRT; ORGANISM: Homo sapiens US-09-902-941-798
Query Match
Best Local Similarity
""+ches 5; Conserve
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US-09-902-941-798
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 798
LENCTH: 164
TYPE: PRT
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                                                                                                                                                                                                                                                                  APPLICANT: VedVick, Thomas S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: MCNabb, Andoria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478617
CURRENT APPLICATION NUMBER: US/09/902,941
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NUMBER OF SEQ ID NOS: 2002
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APPLICANT: Wang, Ajun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
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Fanger, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marnerakis, Margarita
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Johnson, Jeffrey C.
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Vedvick, Tom
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Bangur, Chaitanya
Lodes, Michael A.
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Retter, Marc
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                     Conservative
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                                    33.3%; Score 5; 1
100.0%; Pred. No.
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o. 1.7e+02;
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o. 1.7e+02;
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                                             FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,356
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 201-01-30
PRIOR FILING DATE: 201-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 201-01-30
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US-09-849-626-798
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Matches
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APPLICANT: Wanger, Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Switzer, Anne
APPLICANT: McNeill, Patricia
APPLICANT: MCNeill, Patricia
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C16
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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             PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
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Hanzel, David K.
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o. US20020197669A1
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100.0%; Pred. No. 1.
tive 0; Mismatches
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o. 1.7e+02;
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APPLICATION NUMBER: PCT/US01/00663 APPLICATION NUMBER: PCT/US01/00668

2001-01-30

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AGNIO, MAIC

AGNIO, Jane

APPLICANT: Fan, Liqun

ATTILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.478C15

CURRENT APPLICATION NUMBER: US/09/736,457

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 1864

SOFTWARE: FASTSEQ for Windows Ver-

SEQ ID 01678

LENGTH: 177

TYPE: PRT

ORGANT.
                                          Query Match
Best Local Similarity
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                                                                                                                       ; ORGANISM: Homo sapiens US-09-736-457-1678
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL -
OTHER INFORMATION: EST_HUMAN HIT: AI146468.1, I
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ORGANISM: Homo sapiens
FEATURE:
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122 LGPHR 126
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                            3 LGPHR 7
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EVALUE 4.00e-03
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; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 1678; LENGTH: 177
; TYPE: PRT; ORGANISM: Homo sapiens
US-09-849-626-1678
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Matches 5
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LENGTH: 177
TYPE: ~~~
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APPLICANT: Henderson, Robert A.
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Best Local Similarity
Matches 5; Conserv
                                     Query Match
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APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C17
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
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                                                                                                                                                                                                         APPLICANT: Wang, Aljun
APPLICANT: Wang, Tongtong
APPLICANT: Switzer, Anne
APPLICANT: Switzer, Anne
APPLICANT: McNeill, Patricia
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TILE REFERENCE: 210121.478C16
CURRENT EPPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
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APPLICANT: Fanger, Gary
APPLICANT: Wang, Aijun
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5; Conservative
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Johnson, Jeffrey C.
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 Conservative
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100.0%; Pred. No. 1.8e+02;
Live 0; Mismatches 0;
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 Mismatches
                   DB 9; Le
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RESULT 62

US-09-811-284-176

; Sequence 176, Application US/09811284

; Patent No. US20020058306A1
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; OTHER INFORMATION: Incyte ID No. US20030013099A1 2238363CD1
US-10-093-766-52
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Sequence 52, Application US/10093766; Publication No. US20030013099A1; GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL Program
SEQ ID NO 52
LENGTH: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Vogeli, Gabriel
SOFTWARE: Pa
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CURRENT FILING DATE: 2001-03-16
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APPLICANT: Jones, David A.
APPLICANT: Karpf, Adam R.
TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
FILE REFERENCE: PA-0047 US
                                         PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/189,918 PRIOR FILING DATE: 2000-03-16
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                                                                                APPLICATION NUMBER: 60/192,935
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                                                                                                                                                                                  FILING DATE:
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APPLICATION NUMBER: 60/192,830
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                                                                                                    FILING DATE:
                                                                                                                       APPLICATION NUMBER: 60/192,155
                                                                                                                                         FILING DATE: 2000-03-27
                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/192,933
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                      PatentIn
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                      version 3.0
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Pred. No. 1.9e+02;
0; Mismatches 0;
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APPLICANT: Spaderna, Steven K.

APPLICANT: Leite, Marlo W.

TITLE OF INVENTION: AORTIC Carboxypeptidase-Like Proteins and TITLE OF INVENTION: Encoding Same
FILE REFERENCE: 15966-581 CIP
CURRENT APPLICATION NUMBER: US/09/996,015
CURRENT APPLICATION NUMBER: US/09/996,015
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/841,741
PRIOR APPLICATION NUMBER: 60/159,613
PRIOR APPLICATION NUMBER: 60/159,613
PRIOR APPLICATION NUMBER: 60/175,534
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: 60/175,534
PRIOR FILING DATE: 2000-01-11
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US-09-996-015-43
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 43
LENGTH: 192
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                     Sequence 44, Application US/09996015 Publication No. US20030032166A1
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PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: 60/175,534
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/224,086
                                                                                                                                                                                                                                                                            APPLICANT: Quinn, Kerry E. APPLICANT: Pena, Carol A. E.
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Leite, Marlo W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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100.0%;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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o. 1.9e+(
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TITLE OF INVENTION: AORTIC Carboxypeptidase-Like Proteins and Nucleic Acids
TITLE OF INVENTION: Encoding Same
FILE REFERENCE: 15966-581 CIP
CURRENT APPLICATION NUMBER: US/09/996,015
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/641,741
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 60/159,613
PRIOR APPLICATION NUMBER: 60/159,613
PRIOR APPLICATION NUMBER: 60/175,534
PRIOR APPLICATION NUMBER: 60/175,534
PRIOR APPLICATION NUMBER: 60/175,534
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/224,086
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
""" 5; Conserve
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Best Local Similarity
Thehes 5; Conserve
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US-09-996-015-8
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-015-47
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-015-44
                                                                                                                                                               Sequence 8, Application US/09996015 Publication No. US20030032166A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Sequence 47, Application US/09996015
Publication No. US20030032166A1
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SEQ ID NO 44
               APPLICANT: Quinn, Kerry E.
APPLICANT: Pena, Carol A. E.
APPLICANT: Li, Li
APPLICANT: Spaderna, Steven K.
APPLICANT: Leite, Marlo W.
TITLE OF INVENTION: Acortic Carboxypeptidase-Like
FILE REFERENCE: 15966-581 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Quinn, Kerry E.
APPLICANT: Pena, Carol A. E.
APPLICANT: Li, Li
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URRENT APPLICATION NUMBER: US/09/996,015
                                                                                                                                                                                                                                                                                                    140 LGPHR 144
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Leite, Marlo W.
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100.0%; Pred. No.
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Pred. No.
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5. 2e+02;
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0. 2e+02;
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                                                      Proteins and Nucleic Acids
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-015-8
                                                                                                                             ; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5128
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5128
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US-09-738-626-5128
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
RIOMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 60/159,613
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: 60/175,534
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/224,086
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5128, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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Best Local :
                                                                Matches
                                                                             Query Match
Best Local Similarity
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114 STPES 118
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mes 5; Conserv
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                              8 STPES 12
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAYASHI, MIKIRO
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                                                                Conservative
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                                                                               33.3%; Score 5; 1
100.0%; Pred. No.
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5. 2e+02;
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                                                                Gaps
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RESULT 68 US-09-925-301-898 : Sequence 898, Application US/09925301 : Patent No. US20020052308A1

GENERAL INFORMATION:

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; ORGANISM: Staphylococcus aureus US-09-815-242-5905
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                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                 NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 5905
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 898
LENGTH: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A PROCESS: NC/09/815.242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE LOCATION: (205)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
      Local Similarity
les 5; Conserv
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                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trawick, John D.
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            Conservative
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    33.3%; Score 5; 1
100.0%; Pred. No.
Live 0; Mismatci
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          Mismatches
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; DB 10; LLC.,
No. 2.4e+02;
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                                             Length 248;
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CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 60/220,273
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/221,650
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/221,233
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/220,912
PRIOR APPLICATION NUMBER: 60/220,912
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/218,875
PRIOR APPLICATION NUMBER: 60/218,875
PRIOR APPLICATION NUMBER: 60/218,870
PRIOR APPLICATION NUMBER: 60/218,870
PRIOR APPLICATION NUMBER: 60/218,870
PRIOR APPLICATION NUMBER: 60/218,870
PRIOR APPLICATION NUMBER: 60/218,870
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PRIOR APPLICATION NUMBER: 60/218,870
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PRIOR APPLICATION NUMBER: 60/218,870
PRIOR FILING DATE: 2000-07-18
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US-09-764-853-658
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 658
LENGTH: 269
TYPE: PRT
                                              Query Match
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Best Local :
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                                                                                                                                                                                                     SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 40, Application US/09908193 Publication No. US20020192748A1
Best Local Similarity
Matches 5; Conserv
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
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APPLICANT: PADIGARU, MURALIDHARA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
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                                                                                                                                                    LENGTH: 27
TYPE: PRT
                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/218,901
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                         33.3%; Score 5; |
100.0%; Pred. No.
ore 5; DB 9; Le red. No. 2.6e+02; Mismatches 0;
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o. 2.6e+0
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                                                 Length 271;
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79 HRSTP 83

HRSTP 10

RESULT 72 US-09-738-626-4071

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PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILLING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILLING DATE: 1999-03-12
NUMBER: OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1344
LENGTH: 310
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: YOKOI, HABUHIKO
APPLICANT: YOKOI, HABUHIKO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKIAIO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT EILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1990-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
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Sequence 1344, Application US/09925300; Patent NO. US20020151681A1; GENERAL INFORMATION:
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LENGTH: 280
TYPE: PRT
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                     Query Match
Best Local Similarity
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APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PALO1
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
CURRENT FILING.
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SOFTWARE: PatentIn ver.
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)S: 7059
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33.3%;
100.0%;
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100.0%; F
tive 0;
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Score 5; DB 10;
Pred. No. 3e+02;
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o. 2.7e+02;
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RESULT 75
US-09-791-932-63
; Sequence 63, Application US/09791932
; Publication No. US20030003451A1
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NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1009
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Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
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PRIOR APPLICATION NUMBER: 60/:
PRIOR APPLICATION NUMBER: 60/:
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CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/184,305
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TYPE: PRT
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                                 PRETLING DATE: 50/21.

PREPLICATION NUMBER: 60/21

OR APPLICATION NUMBER: 60/21

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OR APPLICATION NUMBER: 60/21
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APPLICATION NUMBER:
              APPLICATION NUMBER: FILING DATE: 2000
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FILING DATE: 2000-03-1
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Wood, Linda S.
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Parodi, Luis A.
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100.0%; Pr/
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              2000-03-03
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RESULT 77
US-09-902-941-1863
Sequence 1863, Application US/09902941
Patent No. US20020172952A1
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1863
LENGTH: 314
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SEQ ID NO 63
LENGTH: 313
                                                              GENERAL INFORMATION:
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APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478015
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PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2000-04-03
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APPLICANT: Wang, Aijun
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PRIOR APPLICATION NUMBER:
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                                                                                                                                                                      259 LGPHR 263
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nes 5; Conserv
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nes 5; Conserv
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Vedvick, Tom
Carter, Darrick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lodes, Michael
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                                                                                                                                                                                                                               Conservative
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r, Chaitanya
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100.0%; Pred. No.
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o. 3e+02;
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APPLICANT: Carter, Darrick

APPLICANT: Fanger, Gary R.

APPLICANT: Hedvick, Thomas S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: McNabb, Andria

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.478C17

CURRENT APPLICATION NUMBER: US/09/902,941

CURRENT FILING DATE: 2001-07-10

NUMBER OF SEG ID NOS: 2002

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1863
                                                                                                                                                                                          RESULT 79
US-09-975-719-23
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Best Local Similarity
""" bes 5; Conserve
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                                                                                                                              Sequence 23, Application US/09975719 Publication No. US20030022349A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1863
LENGTH: 314
TYPE: PRT
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Best Local
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APPLICANT: Bangur, Chaitanya
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                                                                                                                                                                                                                                                                                                                                                                          Matches
                    TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID TITLE OF INVENTION: SEQUENCES AND USES THEREOF FILE REFERENCE: 00786/361003
                                                                                   APPLICANT: Ausubel, Frederick M. APPLICANT: Rahme, Laurence G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
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APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fanger, Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
CURRENT APPLICATION NUMBER: US/09/975,719
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
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100.0%; F1
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tive 0; Mismatches
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b; Pred. No. 3e+
0; Mismatches
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o. 3e+02;
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; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (314)
; OTHER INFORMATION: Any Amino Acid
US-09-908-193-39
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 318
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-975-719-23
RESULT 81
US-09-738-626-4350
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CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 60/220, 273
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/221, 650
PRIOR APPLICATION NUMBER: 60/221, 233
PRIOR APPLICATION NUMBER: 60/221, 233
PRIOR APPLICATION NUMBER: 60/221, 233
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/218,875
PRIOR APPLICATION NUMBER: 60/218,875
PRIOR APPLICATION NUMBER: 60/218,870
PRIOR APPLICATION NUMBER: 60/218,870
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
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SOFTWARE: PatentIn Ver. 3
SEQ ID NO 39
LENGTH: 327
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APPLICANT: SHIMKETS, RICHARD A.
APPLICANT: ZEHUGEN, BRYAN
APPLICANT: MALYANKAR, URIEL M.
APPLICANT: MALYANKAR, URIEL M.
APPLICANT: PADIGARU, MURALIDHARA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 21402-062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 09/199,637
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: US 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/218,901 PRIOR FILING DATE: 2000-07-18
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus musculus
                                                                                   136 HRSTP 140
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13 HRSTP 17
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Pred. No.
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o. 3.1e+02;
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR ETLING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 4350
LENGTH: 329
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US-09-886-055-211
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 211, Application US/09886055 Patent No. US20020132273A1 GENERAL INFORMATION:
                                                                                                                                                                                                           SEQ ID NO 211
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                                                                   Matches
                                                                                                 Query Match
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APPLICANT:
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                                                                                                                                                                                                                                                                                          APPLICANT: STRYER, LUBERT
APPLICANT: ZOZULYA, SERGEY
APPLICANT: ZOZULYA, SERGEY
TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
FILE REFERENCE: 078003-0277150
CURRENT EPPLICATION NUMBER: US/09/886,055
CURRENT FILING DATE: 2001-06-22
                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/213,812
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 522
SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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                                                                                                                                                                      LENGTH: 330
TYPE: PRT
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288 ESRAA 292
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                                  11 ESRAA 15
                                                               Local Similarity es 5; Conserv
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TATEISHI, NAOKO
SENOH, AKIHIRO
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OCHIAI, KEIKO
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ANDO, SEIKO
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100.0%; Pred. No.
17e 0; Mismatches
                                                                                   33.3%; Score 5;
100.0%; Pred. No.
                                                                   0;
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o. 3.2e+02;
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RESULT 83 US-09-908-193-37

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; TYPE: PRT; ORGANISM: Homo sapiens US-09-908-193-37
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                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/221,650
PRIOR FILLING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/221,233
PRIOR FILLING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/220,912
PRIOR FILLING DATE: 2000-07-26
PRIOR FILLING DATE: 2000-07-18
PRIOR FILLING DATE: 2000-07-18
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Best Local Similarity 100.
Thes 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/908,193
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 60/220,273
PRIOR FILING DATE: 2000-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PADIGARU, MURALIDHARA TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY FILE REFERENCE: 21402-062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication No
                                                                PRIOR APPLICATION NUMBER: 60/218,870 PRIOR FILING DATE: 2000-07-18 PRIOR APPLICATION NUMBER: 60/218,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MALYANKAR, URIEL M.
APPLICANT: PADIGARU, MURALIDHARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: RASTELLI, LUCA
APPLICANT: SHIMKETS, RIC
APPLICANT: ZERHUSEN, BRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/908,193
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 60/220,273
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/221,650
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
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PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/220,912
PRIOR FILING DATE: 2000-07-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
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                              PRIOR FILING DATE: 2000-07-18
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SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Ver. 2.1
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ZERHUSEN, BRYAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALYANKAR, URIEL M.
PADIGARU, MURALIDHARA
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100.0%; Pred. No.
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o. 3.2e+02;
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                                                                                                                                                                                                                                     RESULT 86
US-10-114-170-263
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                     Sequence 263, Application v, ...
Publication No. US20030023075A1

GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.

APPLICANT: Blattner, Valerie
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Query Match
Best Local Similarity
Thes 5; Conserve
                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/291,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR FILING DATE: 2000-05-23
PRIOR PRIOR PRICING DATE: 2000-05-26
PRIOR PRICING DATE: 2000-05-26
PRIOR PRICING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PRICING DATE: 2000-12-3
PRIOR PRICING DATE: 2000-12-3
PRIOR PRICING DATE: 2000-12-3
PRIOR PRICING DATE: 2000-12-3
PRIOR PRICING DATE: 2000-12-3
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PRICING DATE: 2000-12-3
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PRICING DATE: 2001-02-16
PRIOR PRICING DATE: 2001-02-16
                                                                                                                                                 US-09-815-242-12043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Mus musculus US-09-908-193-38
                                                                                                                                                                                               SOFTWARE: Fascs:
SOFTWARE: Fascs:
SEQ ID NO 12043
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Best Local S
Matches 5
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LENGTH: 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITER.011A
                                                                                                                                                                                    LENGTH: 33
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haselbeck, APPLICANT: Ohlsen, Ka
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                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
269 ESRAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 HRSTP 148
                                    11 ESRAA 15
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les 5; Conserv
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Yamamoto, Robert T.
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Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trawick, John D.
                                                                          Conservative
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100.0%; Pr
                                                                                            33.3%; Score 5; I
100.0%; Pred. No.
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Burland, Nicole T.

DB 10; L 5. 3.3e+02;

Length 350

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             US-09-908-805B-25
                                                                                                                                                                                                    APPLICANT: ALEXANDE
APPLICANT: VINEY, E
APPLICANT: VINEY, E
APPLICANT: WILLSON,
APPLICANT: RICHARDS
APPLICANT: STARR, E
APPLICANT: NICHOLSO
                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09908805B Patent No. US20020147307A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEPAX: (608) 251-5000
TELEPAX: (608) 251-5000
INFORMATION FOR SEQ ID NO: 263:
SEQUENCE CHARACTERISTICS:
                             CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 08/962,560
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 81
                                                                                                                              APPLICANT: METCALF, Donald APPLICANT: NICOLA, NICOS A TITLE OF INVENTION: THERAPEUFILE REFERENCE: 10976Z
SOFTWARE: PE
                                                                                           CURRENT APPLICATION NUMBER: US/09/908,8058
CURRENT FILING DATE: 2001-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 ESRAA 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Welch, Rod
TITLE OF INVENTION: No. US20030023075Alel Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                   PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 53701-2113
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STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                           RICHARDSON, Rachael T
                                                                                                                                                                                                                                                             WILLSON, Tracey A
                                                                                                                                                                                                                                                                              VINEY, Elizabeth M
                                                                                                                                                                                                        NICHOLSON,
                                                                                                                                                                                                                                                                                                    ALEXANDER, Warren S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 348 amino acids
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                   Ver.
                                                                                                                                                                                                                                                                                                                 Douglas J
                                                                                                                                                                                                                          Robyn
                                                                                                                                                THERAPEUTIC AND DIAGNOSTIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.3%;
                                                                                                                                                                                                      Sandra E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 5; DB 9; Pred. No. 3.3 0; Mismatches
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5. 3.3e+02;
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US-10-108-714-4
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                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     Sequence 3763, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10108714 Patent No. US20020128445A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/108,714

CURRENT FILING DATE: 2002-03-28

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/267,423

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/239,431

PRIOR FILING DATE: EARLIER FILING DATE: 1994-05-05

NUMBER OF SEQ ID NOS: 10
             CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                       APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gil, Daniel W.
APPLICANT: Woodward, David F.
TITLE OF INVENTION: No. US20020128445Alel Human Prostaglandin EP Receptor FILE REFERENCE: 17023 DIV CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Regan, John w. APPLICANT: Gil, Daniel W.
                                                                                                                                                                                     APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                              APPLICANT:
                                                                                                                                                  APPLICANT:
                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
PRIOR APPLICATION NUMBER: JP 00/159162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: UNSURE LOCATION: (167)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 HRSTP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 PESRA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 PESRA 14
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les 5; Conserv
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5; Conserv
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TATEISHI, NAOKO
                                                                                                                                                                                                                    HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                               ANDO, SEIKO
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                                                                                                                                                               SENOH, AKIHIRO
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100.0%;
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DB 12; I

Length 358; Indels

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; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-870-759-73
                                                                                                                                                                                                                                                                                                                                   US-09-165-522-16

US-09-165-522-16

Sequence 16, Application US/09165522

Publication No. US20030023990A1

GENERAL INFORMATION:
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Best Local Similarity
Thes 5; Conserve
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-870-759-73
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Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
FILE REFERENCE: 870759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 3763
LENGTH: 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 STPES 196
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 5; Conserv
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                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                             Yang, Di
TITLE OF INVENTION: JNK3 MODULATORS AND METHODS OF
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                         CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Flavell, Richard
Rakic, Pasko
                                                                                                                                                                                                                                            Kuan, Chia-Yi
                                                                                                                                                                                                                                                                Whitmarsh, Alan
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US-09-939-833-6
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                                                                                                                                                       SEQ ID NO 6
LENGTH: 386
TYPE: PRT
                                                              Matches
                                                                              Best
                                                                                           Query Match
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/939,833
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US/09/390,326
PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ver
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND TITLE OF INVENTION: METHODS OF USE FILE REFERENCE: 0125-0016US
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MCTIGUE, MICHELE A.
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75 HLGPH 79
                                                             Local Similarity es 5; Conserv
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ses 5; Conserv
                              2 HLGPH 6
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,522
FILING DATE: 02-Oct-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           VILLAFRANCA, J. ERNEST APPELT, KRZYSZTOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/060,995 FILING DATE: 03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                     PARAST, CAMRAN V.
TEMPCYZK-RUSSEL, ANNA
GEHRING, MICHAEL R.
MROCZKOWSKI, BARBARA
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SHOWALTER, RICHARD
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Pred. No.
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                                                              Mismatches
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o. 3.6e+02;
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5. 3.6e+02;
                                                                                          Length 386;
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US-09-939-754-6

Sequence 6, Application US/09939754 Patent No. US20020051965A1 GENERAL INFORMATION:

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CHAEL R.

KAN, CHEN-CHEN

VILLAFRANCA, J. ERNEST

APPLICANT: APPELT, KRIVSZTOF

TITLE OF INVENTION: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND
FILE REFERENCE: 0125-0016US

CURRENT APPLICATION NUMBER: US/09/939,832

CURRENT APPLICATION NUMBER: 09/390,326

PRIOR APPLICATION NUMBER: 09/390,326

PRIOR FILING DATE: 1999-09-07

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver

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Best Local Similarity
""+rhes 5; Conserv
                                               ; TYPE: PRT
; ORGANISM: E.
US-09-939-832-6
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; TYPE: PRT
; ORGANISM: E. coli
US-09-939-754-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09939832 Patent No. US20020127538A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
 Query Match
Best Local Similarity
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PRIOR APPLICATION NUMBER: 09/390,326
PRIOR EILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS- 17
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MCTIGUE, MICHELE A.
APPLICANT: WICKERSHAM, JOHN A.
APPLICANT: PINKO, CHRIS
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APPLICANT:
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APPLICANT: APPELT, KRZYSZTOF
TITLE OF INVENTION: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND
TITLE OF INVENTION: METHODS OF USE
TILE REFERENCE: 0125-0016US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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GEHRING, MICHAEL R.
MROCZKOWSKI, BARBARA
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PINKO, CHRIS
SHOWALTER, RICHARD
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 33.3%;
100.0%;
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Pred. No.
Score 5; L
Pred. No.
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o. 3.6e+02;
 DB 10; L
b. 3.6e+02;
              Length 386;
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US-09-729-674-172
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                                                                                                                                                                                                                                                                                                                                         RESULT 96
US-09-742-954-14
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PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: PATENTIN VEI. 2.0
SEQ ID NO 172
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                SOFTWARE:
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09742954 Patent No. US20010005749A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Matches 5; Conserva
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                        APPLICANT: Hitz, William D.

APPLICANT: Kinney, Anthony J.

TITLE OF INVENTION: Aromatic Amino Acid Catabolism Enzymes
FILE REFERENCE: BB-1197
CURRENT APPLICATION NUMBER: US/09/742,954
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/094,783
PRIOR EILING DATE: JULY 31, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
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APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
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                                                           NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
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TYPE: PRT
ORGANISM: Glycine max
                                 ENGTH:
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د.
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McCoy, John M.
LaVallie, Edward R.
                                                                                                                                                                                                                   Morgante, Michele
Rafalski, J. Antoni
                                                                                                                                                                                                                                              Falco, S. Carl
                                                                                                                                                                                                                                                                Cahoon, Rebecca E.
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                                                                                                                                                                                                                                                                            Cahoon, Edgar B.
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Treacy, Maurice
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Evans, Cheryl
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...rliCANT: Secrist, Mary
...rliCANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C9
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FASTSEQ for Windows Variable Compounds
SEQ ID NO 34
LENGTO: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/286,488
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 34
LENGTH: 431
TYPE: PRT
ORGANISM: Babesia microti
US-09-286-488-34
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                       Query Match
Best Local Similarity
Watches 5; Conserve
                                                                                                                    ; ORGANISM: Babesia microti
US-09-737-178-34
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US-09-737-178-34
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C3
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
                                                                                                                                                       TYPE: PRT
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nes 5; Conserv
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nes 5; Conserv
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     STPES 12
                                          Conservative
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                                    33.3%; Score 5; DB 10; 100.0%; Pred. No. 4e+02; tive 0; Mismatches
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100.0%; Pred. No.
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Pred. No.
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o. 4e+02;
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lo. 3.9e+02;
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                                        Indels
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Best Local Similarity
Whiches 5; Conserve
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US-09-815-242-5207
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                                                                                     PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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US-10-108-605-37
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                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLERIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCOD
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                      PRIOR FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 60/269,308
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                                      PRIOR FILING DATE: 2001-02-16
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TYPE: PRT
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Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto, Robert T.
Xu, H. Howard
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for Windows Version 4.0
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100.0%; Pred. No. 4e-
tive 0; Mismatches
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APPLICANT: OZAKI, KIO
APPLICANT: OZAKI, KIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATCHTIN VET. 3.0
SEQ ID NO 4037
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Best Local Similarity
""+"ches 5; Conservi
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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4037
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US-09-738-626-4037
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TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5207
                                                                                                                                                                                                                                        US-09-815-242-10237
                                                                                                                                                                                Sequence 10237, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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LENGTH: 439
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Best Local :
                                                     APPLICANT:
APPLICANT:
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                                                                                                       APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith Ward APPLICANT: Wall, Daniel
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, MIKIRO
APPLICANT: HAYASHI, MIKIRO
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                      PPLICANT:
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                       Zyskind, Judith W. Wall, Daniel
                                    Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
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                                                                                        Trawick, John D.
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100.0%; Pred. No. 4.
Live 0; Mismatches
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TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10237
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                                                           NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13956
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Best Local (
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
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PRIOR APPLICATION NUMBER: 6
PRIOR FILING DATE: 2000-05-
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                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/253,625
PRIOR TILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                         TYPE: PI
ORGANISM: Salmonella typhi
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mes 5; Conserv
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FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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Zyskind, Judith W.
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100.0%; Pred. No.
tive 0; Mismatch
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; LOCATION: (1)...(471)
; OTHER INFORMATION: Xaa = Any Amino
US-09-815-242-13956
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
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; Publication No. US200
; GENERAL INFORMATION:
; APPLICANT: McCarthy
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PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/34
PRIOR APPLICATION NUMBER: 09/36
PRIOR APPLICATION NUMBER: 09/36
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/36
PRIOR APPLICATION NUMBER: 09/39
PRIOR FILING DATE: 1999-09-20
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PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09//
PRIOR FILING DATE: 1999-02-26
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PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1999-05-14
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nes 5; Conserv
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FTI ING DATE: 1999-09-30
                                     APPLICATION NUMBER: 09/6
FILING DATE: 2000-06-29
                                                                       APPLICATION NUMBER: 09/0 FILING DATE: 2000-06-29
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FILING DATE: 2000-06-19
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FILING DATE: 2000-02-25
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APPLICATION NUMBER: 09/
FILING DATE: 1999-06-18
       APPLICATION NUMBER: 09/1
FILING DATE: 2000-09-20
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FILING DATE: 2000-05-14
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FILING DATE: 1999-12-29
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VENTION: SECRETED PROTEINS AND USES THEREOF
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Pred. No. 4.3e+02
0; Mismatches 0
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RESULT 106
US-09-739-254-154
; Sequence 154, Application US/09739254
; Patent No. US20010021700A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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; ORGANISM: Haemophilus influenzae US-09-815-242-10999
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US-09-815-242-10999
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10999
LENGTH: 480
TYPE: PRT
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APPLICANT:
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITER 011A
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60 RSTPE
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Local Similarity 100.0%; Pred. No.
mes 5; Conservative 0; Mismatch
                    7 RSTPE 11
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Xu, H. Howard
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Trawick, John D.
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64
                                                                              Conservative
                                                                                              33.3%; Score 5; DB 10; L
100.0%; Pred. No. 4.4e+02;
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                                                                              Mismatches
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o. 4.4e+02;
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NITLE OF INVENTION: 49 Human Secreted Proteins

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; NAME/KEY: SITE ; LOCATION: (205)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-739-254-154
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                                                                                                      ; NAME/KEY: SITE
; LOCATION: (205)
; OTHER INFORMATION:
US-09-904-615-154
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                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 154, Application Patent No. US20020026040A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 154
LENGTH: 483
                                                                                                                                                                                                                                                                                           SOFTWARE: Pa
SEQ ID NO 154
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Best Local
                                     Matches
                                                      Query Match
Best Local
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TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PE032P1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (194)
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EARLIER FILING DATE: 2000-02-23
EARLIER APPLICATION NUMBER: PCT/US99/19330
EARLIER FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 60/097,917
EARLIER APPLICATION NUMBER: 60/098,634
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                                                                                                                                                                    NAME/KEY: SITE LOCATION: (194) OTHER INFORMATION:
                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                           LENGTH: 483
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                                   Local Similarity
les 5; Conserv
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ilarity 100.0%;
Conservative
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                                 Score 5; DB 10; Le
Pred. No. 4.4e+02;
0; Mismatches 0;
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Pred. No. 4.4e+02;
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PRIOR APPLICATION NUMBER: US 60/257,431
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 106
LENGTH: 491
TYPE: PRT
ORGANISM: Artificial Sequence
Qy
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US-10-029-180-106
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Best Local Similarity
Watches 5; Conserv
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                                                                                                   ; OTHER INFORMATION: US-10-029-180-106
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Best Local
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                                                                                                                                                                                                                                                                            APPLICANT: Trueheart, Josh
APPLICANT: Zhang, Lixin
TITLE OF INVENTION: NO. US20020182708A1el Regulators of Fungal Gene Expression
FILE REFERENCE: MIC-004
CURRENT APPLICATION NUMBER: US/10/029,180
CURRENT FILING DATE: 2001-12-22
CURRENT FILING DATE: 2001-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Leboulle, Gerard
TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACERIZATION OF
TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
TITLE OF INVENTION: GLANDS
FILE REFERENCE: VANM229.001CP1
CURRENT APPLICATION NUMBER: US/09/910,430
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: PCT/BE00/00061
PRIOR APPLICATION NUMBER: CO.0013426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: GB 9913425.6 PRIOR FILING DATE: 1999-06-09 NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Godfroi, Edmond
APPLICANT: Bollen, Alex
APPLICANT: Leboulle, Gera
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   TPESR 13
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                                   Similarity 5; Conserv
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Milna, G. Todd
Sherman, Amir
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                                    Conservative
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                                                                                                                   fungal gene
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100.0%; Pr
                                   33.3%; Score 5; DB
100.0%; Pred. No. 4.
tive 0; Mismatches
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                             DB 9; Lc., 4.5e+02; 0;
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TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-997-900-2
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APPLICANT:
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APPLICANT: Hu, Weiming
TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
TITLE OF INVENTION: in Plants
TITLE OF INVENTION: in Plants
FILE REFERENCE: 043753/241148 (5849-20A)
CURRENT APPLICATION NUMBER: US/09/997,900
CURRENT FILING DATE: 2001-11-30
CURRENT FILING DATE: 2001-11-30
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                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/106,239
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 09/426,568
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 11
                                                                                    PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                            PRIOR FILING DATE: 2000-11-27
                                                                                                                                                PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
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APPLICANT: Costello, Colleen
APPLICANT: Sun, Ming
APPLICANT: Hu, Weiming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 PESRA 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 PESRA 14
                                       APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto, Robert T.
Xu, H. Howard
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Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trawick, John D.
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for Windows Version 4.0
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Pred. No
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o. 4.5e+02;
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TITLE OF INVENTION: Plant Cellulose Synthases
FILE REFERENCE: BB1170 US CIP
CURRENT APPLICATION NUMBER: US/09/900,237
CURRENT FILING DATE: 2001-07-06
PRIOR PPLICATION NUMBER: 60/092,844
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-13
PRIOR APPLICATION NUMBER: PCT/US99/15871
PRIOR APPLICATION NUMBER: 09/720383
PRIOR APPLICATION NUMBER: 09/720383
PRIOR FILING DATE: 1999-07-13
PRIOR APPLICATION NUMBER: 09/720383
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 20
LENGTH: 506
TYPE: PRT
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Best Local Similarity
Thes 5; Conserv
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US-09-900-237-20
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Best Local Similarity
5; Conserve
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US-09-900-237-20
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                                                                                     CURRENT APPLICATION NUMBER: US/09/996,015
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/641,741
PRIOR FILING DATE: 2000-08-18
                                                                                                                                                             TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids TITLE OF INVENTION: Encoding Same FILE REFERENCE: 15966-581 CIP
               PRIOR APPLICATION NUMBER: 60/159,613
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: 60/175,534
PRIOR FILING DATE: 2000-01-11
                                                                                                                                                                                                                                                                                                                                                               09-996-015-45
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                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     169 STPES 173
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APPLICATION
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                                                                                                                                                                                                                 Li, Li
Spaderna, Steven K.
Leite, Marlo W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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PRIOR FILING DATE: 2000-08-09
RUMBER OF SEQ ID NOS: 47
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 45
LENGTH: 510
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-015-45
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"""+"hes 5; Conserv
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CÜRRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/0449911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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OR APPLICATION NUMBER: 60/059115
OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059117
OR APPLICATION NUMBER: 60/05912
OR APPLICATION NUMBER: 60/05912
OR APPLICATION NUMBER: 60/05918
OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059263
OR FILING DATE: 1997-09-18
OR APPLICATION NUMBER: 60/059352
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/059352
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/05988
OR APPLICATION NUMBER: 60/05988
OR FILING DATE: 1997-09-20
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/05285
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062285
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/06287
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/06287
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumas,Daniel
Watanabe,Colin K
Wood,William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stewart, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/10028072
5. US20030004311A1
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Pred. No. 4
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OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/066511
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/066770
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/069212
OR FILING DATE: 1997-12-11
OR APPLICATION NUMBER: 60/069218
OR APPLICATION NUMBER: 60/069218
OR APPLICATION NUMBER: 60/069218
OR APPLICATION NUMBER: 60/069218
OR APPLICATION NUMBER: 60/069218
OR APPLICATION NUMBER: 60/069334
OR FILING DATE: 1997-12-11
OR APPLICATION NUMBER: 60/069694
OR FILING DATE: 1997-12-16
OR APPLICATION NUMBER: 60/072320
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DR APPLICATION NUMBER: 60/064809

DR FILING DATE: 1997-11-07

DR APPLICATION NUMBER: 60/065186

DR FILING DATE: 1997-11-12

DR APPLICATION NUMBER: 60/065846

DR FILING DATE: 1997-11-17

DR APPLICATION NUMBER: 60/066364

DR FILING DATE: 1997-11-21

DR FILING DATE: 1997-11-21
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OR FILING DATE: 1997-10-27
OR APPLICATION NUMBER: 60/063550
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063561
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063704
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063733
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063735
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063735
OR APPLICATION NUMBER: 60/063736
OR APPLICATION NUMBER: 60/063738
OR APPLICATION NUMBER: 60/063738
OR FILING DATE: 1997-10-29
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OR APPLICATION NUMBER: 60/062816

OR FILING DATE: 1997-10-24

OR APPLICATION NUMBER: 60/063045

OR FILING DATE: 1997-10-24

OR APPLICATION NUMBER: 60/063082

OR FILING DATE: 1997-10-31
                                                                                                                                                                   OR APPLICATION NUMBER: 60/077791
OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
OR APPLICATION NUMBER: 60/079663
OR APPLICATION NUMBER: 60/079663
                    R FILING DATE: 1998-02-2;
R APPLICATION NUMBER: 60,
R FILING DATE: 1998-03-2;
R FILING DATE: 1998-03-3;
R APPLICATION NUMBER: 60,
R APPLICATION NUMBER: 60,
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-02-09
APPLICATION NUMBER: 60/074092
FILING DATE: 1998-02-09
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APPLICATION NUMBER: 60/073612
FILING DATE: 1998-02-04
APPLICATION NUMBER: 60/074086
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FILING DATE: 1997-L0-24
APPLICATION NUMBER: 60/063327
FILING DATE: 1997-10-27
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APPLICATION NUMBER: 60/064248
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                         : 1998-03-31
NUMBER: 60/
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60/081229

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PRIOR
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OR APPLICATION NUMBER: 60/089532

OR FILING DATE: 1998-06-17

OR APPLICATION NUMBER: 60/089599

OR FILING DATE: 1998-06-17

OR APPLICATION NUMBER: 60/089907

OR APPLICATION NUMBER: 60/089907

OR APPLICATION NUMBER: 60/089947

OR FILING DATE: 1998-06-19

OR FILING DATE: 1998-06-19
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OR APPLICATION NUMBER: 60/01
OR APPLICATION NUMBER: 60/01
OR APPLICATION NUMBER: 60/01
OR APPLICATION NUMBER: 60/01
OR FILING DATE: 1998-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/01
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/01
R APPLICATION NUMBER: 60/01
R FILING DATE: 1998-06-10
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R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-05-12
R APPLICATION NUMBER: 60/08
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-05-13
R FILING DATE: 1998-05-13
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085579
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085697
                                    APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
                                                                                                                           APPLICATION NUMBER: 60/
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-23
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FILING DATE: 1998-05-22
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APPLICATION NUMBER: 60/
FILING DATE: 1998-05-07
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FILING DATE: 1998-04-28
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APPLICATION NUMBER: 60/082999
FILING DATE: 1998-04-24
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081818
FILING DATE: 1998-04-15
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/
                  APPLICATION NUMBER: 60/091519
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FILING DATE: 1998-06-10
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1998-07-02
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RESULT 116
US-10-123-904-210
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US-10-121-049-210
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LENGTH: 519
TYPE: PRT
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Best Local S
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/121,049

CURRENT FILING DATE: 2002-04-12

PRIOT APPLICATION FILENCE PRIOT APPLICATION OF SECOND OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF SECOND NUMBER OF S
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69 GPHRS 73
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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                                                   Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                                Gao, Wei-Qiang
Gerritsen, Mary E.
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Filvaroff, Ellen
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                                                                                                                                      Goddard, Audrey
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Stewart, Timothy A.
                            Smith, Victoria
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o. US20030022328A1
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b. US20030022239A1
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; Pred. No. 4.7e+02;
0; Mismatches 0;
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RESULT 118
US-10-175-746-210
; Sequence 210, Application US/10175746
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SEQ ID NO 210
LENGTH: 519
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-470-210
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 210
LENGTH: 519
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
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                                                                                                                                            Local Similarity
les 5; Conserv
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nes 5; Conserv
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                                                                                  GPHRS 73
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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Pred. No.
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o. 4.7e+02;
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RESULT 119
US-10-176-918-210
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US-10-175-746-210
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 210
LENGTH: 519
TYPE: PRT
Prior Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 210
LENGTH: 519
TYPE: PRT
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                                                                          APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C382
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93330R1C353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
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Watanabe, Colin K
Wood, William
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Watanabe, Colin K
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Filvaroff, Ellen
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Filvaroff, Ellen
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                                                               See File Wrapper or Palm
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US-10-176-921-210
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US-10-176-921-210
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US-10-176-918-210
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 210
LENGTH: 519
TYPE: PRT
                                                                                                                                                                 Sequence 210, Application US/10137865
Publication No. US20030032155A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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Best Local
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CURRENT FILING DATE: 2002-06-20
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C288
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| 69 GPHRS 73
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les 5; Conserv
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nes 5; Conserv
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                                                            Gerritsen, Mary E. Goddard, Audrey
                                                                                                     Desnoyers, Luc
Filvaroff, Ellen
                              Godowski, Paul J. Gurney, Austin L.
                                                                                           Gao, Wei-Qiang
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Watanabe, Colin K
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Godowski, Paul J.
Gurney, Austin L.
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                Sherwood, Steven
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                                                                                                                                                                                                                                                                                                                                                33.3%; Score 5; DB 9; Le ilarity 100.0%; Pred. No. 4.7e+02; Conservative 0; Mismatches 0;
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Pred. No.
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o. 4.7e+02;
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RESULT 123
US-10-142-431-210
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; SEQ ID NO 210
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-474-210
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                                                                         Query Match
Best Local S
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CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or Fi
NUMBER OF SEQ ID NOS: 550
LENGTH: 519
TYPE: PRT
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2002-05-06
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                                                           Local Similarity hes 5; Conserv
69 GPHRS 73
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69 GPHRS 73
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                  4 GPHRS 8
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
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Wood,William
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o. US20030032156A1
                                                              Conservative
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100.0%; Pred. No.
                                                                                                                                                                                                                See Palm or File Wrapper
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Pred. No. 4.7e+02;
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Sequence 210, Application US/10142431 Publication No. US20030036179A1

APPLICANT: Baker, Kevin P.

Beresini, Maureen

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US-10-142-431-210
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C211
CURRENT APPLICATION NUMBER: US/10/143.114
CURRENT FILING DATE: 2002-05-09
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 210
LENGTH: 519
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CURRENT FILING DATE: 2002-05-10
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 210
LENGTH: 519
TYPE: PRT
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                Stewart, Timothy A.
                                                                                                                                                                                                                   Smith, Victoria
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                                                                                                                                                                                     Tumas,Daniel
                                                                                                                                                                                                                                                                                                                                                                      Beresini, Maureen
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; Prior Application removed -
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 210
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-002-210
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US-10-143-114-210
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                                                                                                                                                                     Sequence 133, Application US/10001843 Patent No. US20020132255A1
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APPLICANT:
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APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to
FILE REFERENCE: DEX-0267
CURRENT APPLICATION NUMBER: US/10/001,843
CURRENT FILING DATE: 2001-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
                                                        APPLICANT:
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69 GPHRS 73
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Cafferkey, Robert
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                                                                     Sun, Yongming
Liu, Chenghua
                                                                                                                          Salceda, Susana
Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhanq, Zemin
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Wood, William
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Godowski, Paul J.
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith, Victoria
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-015-6
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Best Local Similarity
"atches 5; Conserve
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                                                                                                                                                                       Sequence 78, Application US/09782980
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PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 218
SOFTWARE: Patentin version 3.1
SEQ ID NO 133
LENGTH: 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/175,534
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/224,086
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/96,015 CURRENT FILING DATE: 2001-11-28 PRIOR APPLICATION NUMBER: 09/641,741 PRIOR FILING DATE: 2000-08-18 PRIOR APPLICATION NUMBER: 60/159,613 PRIOR FILING DATE: 1999-10-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Quinn, Kerry E.
APPLICANT: Pena, Carol A.
APPLICANT: Li, Li
APPLICANT: Spaderna, Steve
APPLICANT: Leite, Marlo W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids TITLE OF INVENTION: Encoding Same FILE REFERENCE: 15966-581 CIP
                                     APPLICANT:
                                                   APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
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INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG,
                 Pan,
                                  White, David
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APPLICANT: OZAKI, AKIO

APPLICANT: OZAKI, AKIO

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738,626

CURRENT FILLING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR FILING DATE: 2000-04-07
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US-09-738-626-5305
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 09/276,400
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: 60/117,580
PRIOR APPLICATION NUMBER: 09/014,195
PRIOR APPLICATION NUMBER: 09/014,195
PRIOR FILING DATE: 1998-01-27
PRIOR FILING DATE: 1998-01-27
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Best Local Similarity
Matches 5; Conserv
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APPLICANT:
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
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CURRENT FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: PCT/US00/02125
PRIOR FILING DATE: 2000-01-27
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PRIOR FILING DATE: 1998-05-29
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PRIOR FILING DATE: 1998-01-27
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FILING DATE: 1999-04-21
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TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
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OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIZOGUCHI, HIROSHI
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Pred. No.
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Patent NO. USAULTINE
GENERAL INFORMATION:
SERVICIONIS 1801 APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001220
CURRENT APPLICATION NUMBER: US/10/118,328
CURRENT APPLICATION DATE: 2002-04-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-738-626-6059; Application US/09738626; Publication NS-0020020197605A1
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                                                                                                                                                                                                               RESULT 131
US-10-118-328-4
                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Corynebacterium glutamicum US-09-738-626-5305
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 6059
LENGTH: 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 5305
LENGTH: 608
TYPE: PRT
                                                                                                                                                                              Sequence 4, Application US/10118328 Patent No. US20020169289A1
                                                                                                                                                                                                                                                                                                                                              Matches
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APPLICANT:
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PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 70 SOFTWARE: Patentin ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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                                                                                                                                                                                                                                                                              163 STPES 167
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mes 5; Conserv
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TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCHIAI, KEIKO
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                                                                                                                                                                                                                                                                                                                                              Conservative
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100.0%;
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Pred. No.
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5.6e+02;
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Best Local S
Matches 5
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                                                                                                                                 Matches
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LENGTH: 709
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/282,460 PRIOR FILING DATE: 2001-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
721 STPES
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nes 5; Conserv
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                                                              8 STPES 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/923,444A
FILING DATE: 08-Aug-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 43,9
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/062,815
FILING DATE: 199-12-20
ATTORNEY/AGENT INFORMATION:
NAME: Michele M. Wales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NEUROTRANSMITTER TRANSPORTER NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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                                                                                                                             Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 727 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Human Genome Scie
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (301)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MD
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725
                                                                                                                                 Conservative
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100.0%; Pr
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                                                                                                                             Score 5; DB 1
s; Pred. No. 6.3
0; Mismatches
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5. 6.2e+02;
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RESULT 133

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Hodge, Martin R.

FILE OF INVENTION: NO. US20020142428A1el Kinases and Uses Thereof

FILE REFERENCE: 35800/234862

CURRENT APPLICATION NUMBER: US/09/862,027

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: US 09/345,473

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 82

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 42

LENGTH: 733

TYPE: PRT

ORGANISM: Homo Sapiens

US-09-862-027-42
                               RESULT 135
US-10-176-758-458
US-10-176-758-458
; Sequence 458, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
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Best Local Similarity
Watches 5; Conserve
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US-10-174-590-458
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
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APPLICANT: | APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
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                                                                                                                                                       140 LGPHR 144
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nes 5; Conserv
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 Baker, Kevin P.
Chen, Jian
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Smith, Victoria
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Pred. No. 6.4e+02;
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CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILLING DATE: 2002-06-19
Prior Application removed - See File Wrapper
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
ELENGTH: 734
TYPE: PAT
ORGANISM: Homo Sapien
US-10-175-737-458
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US-10-175-737-458
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
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140 LGPHR 144 ·
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Godowski, Paul J.
Gurney, Austin L.
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Godowski, Paul J.
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RESULT 137 US-10-173-706-458 ; Sequence 458, Application US/10173706 ; Publication No. US20030022293A1

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                                      Query Match
Best Local Similarity
"heres 5; Conservi
                                                                                                           ; TYPE: PRT; ORGANISM: Homo Sapien US-10-175-738-458
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US-10-175-738-458
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
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CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
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140 LGPHR 144
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Godowski, Paul J.
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RESULT 139

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140 LGPHR 144

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; SEQ ID NO 458
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-458
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
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APPLICANT:
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CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                              TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C70
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93430R1C60
CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
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Godowski, Paul J.
Gurney, Austin L.
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Godowski, Paul
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b. US20030022295A1
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100.0%; Pred. No.
tive 0; Mismatc
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                       DB y;
No. 6.4e+02;
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3 LGPHR 7

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; Prior Application removed -
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 458
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-913-458
Query Match
Best Local Similarity
Thes 5; Conserve
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
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Best Local
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/176,913
CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                      APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C66
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TYPE: PRT
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Godowski, Paul J.
Gurney, Austin L.
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Desnoyers, Luc
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                Conservative
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                              33.3%; Score 5; 100.0%; Pred. No.

    See file Wrapper or Palm

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                                ; ORGANISM: HOMO US-10-180-557-458
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Best Local Similarity
The 5; Conserve
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US-10-180-552-458
                                                                          Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
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LENGTH: 734
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APPLICANT:
                                                                                                                                      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C147
CURRENT APPLICATION NUMBER: US/10/180,557
CURRENT FILING DATE: 2002-06-25
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CURRENT APPLICATION NUMBER: US/10/180,552
CURRENT FILING DATE: 2002-06-25
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS. ENCODING THE SAME
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NUMBER OF SEQ ID NOS: 612
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ORGANISM: Homo Sapien
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Godowski, Paul J.
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b. US20030022301A1
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                                               Sapien
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 33.3%;
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Score 5;
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 DB 9;
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RESULT 145
US-10-173-700-458
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US-10-174-572-458
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
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                          Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
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                                                                                      FILE REFERENCE: P3430R1C40
CURRENT APPLICATION NUMBER: US/10/174,572
CURRENT FILING DATE: 2002-06-18
                                                                                                                              APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT FILING DATE: 2002-06-17
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ORGANISM: Homo Sapien
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nes 5; Conserv
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Godowski, Paul J.
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Watanabe, Colin K.
Wood, William I.
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; Mismatches 0;
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o. 6.4e+02;
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Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 SEG ID NO 458 LENGTH: 734 TYPE: PRT ORGANISM: Homo Sapien US-10-174-579-458
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US-10-174-579-458
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Prior Application removed – See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
                                        CURRENT APPLICATION NUMBER: US/10/174,582
CURRENT FILING DATE: 2002-06-18
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APPLICANT:
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                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C36
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CURRENT FILING DATE: 2002-06-18
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                             Smith, Victoria Watanabe, Colin K. Wood, William I.
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RESULT 150
US-10-175-739-458
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Best Local Similarity
Watches 5; Conserv:
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LENGTH: 734
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APPLICANT:
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                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C46
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NUMBER OF SEQ ID NOS: 612
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Local Similarity 100.0%;
nes 5; Conservative (
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APPLICATION NUMBER: US/10/175,739 FILING DATE: 2002-06-19
                                                                                                                                                                                                                         Baker, Kevin P.
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Godowski, Paul J.
                                                                        Zhang, Zemin
                                                                                     Watanabe, Colin K. Wood, William I.
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Smith, Victoria
                                                                                                                                                 Gurney, Austin L.
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; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 458
; LENGTH: 734
; TYPE: PRT
; ORCANISM: Homo Sapien
US-10-175-740-458
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US-10-175-743-458
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US-10-175-740-458
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
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TYPE: PRT
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Best Local
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Best Local Similarity
Matches 5; Conser
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 TITLE OF INVENTION:
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                                                                                                      Godowski, Paul J. Gurney, Austin L.
                                           Smith, Victoria Watanabe, Colin K. Wood, William I.
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Godowski, Paul
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SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
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R FILING DATE: 1997-11-22 R APPLICATION NUMBER: 60, R FILING DATE: 1997-11-24 R APPLICATION NUMBER: 60, R FILING DATE: 1997-12-11 R APPLICATION NUMBER: 60, R FILING DATE: 1997-12-12 R APPLICATION NUMBER: 60, R FILING DATE: 1997-12-12 R APPLICATION NUMBER: 60, R FILING DATE: 1997-12-13 R APPLICATION NUMBER: 60, R APPLICATION NUMBER: 60, R APPLICATION NUMBER: 60, R FILING DATE: 1998-03-11 R APPLICATION NUMBER: 60, R FILING DATE: 1998-03-21 R APPLICATION NUMBER: 60, R FILING DATE: 1998-03-22 R APPLICATION NUMBER: 60, R FILING DATE: 1998-03-22 R APPLICATION NUMBER: 60, R FILING DATE: 1998-03-23 R APPLICATION NUMBER: 60, R APPLICATION NUMBER: 60, R APPLICATION NUMBER: 60, R APPLICATION NUMBER: 60, R APPLICATION NUMBER: 60, R APPLICATION NUMBER: 60, R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-03 R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-04 R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-04 R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-06 R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-06 R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-06 R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-06 R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-06 R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-06 R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-06 R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-06 R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-06 R APPLICATION NUMBER: 60, R FILING DATE: 1998-04-06 R APPLICATION NUMBER: 60, R APPLICATION NUMB	REFERENCE: P3 RYPILING DATE: R PPLICATION R FILING DATE: R PPLICATION R FILING DATE: R APPLICATION R PILING DATE: R APPLICATION
	PRIOR APPLICATION NUMBER: 60/081195 PRIOR FILING DATE: 1998-04-09 PRIOR FILING DATE: 1998-04-09 PRIOR FILING DATE: 1998-04-15 PRIOR APPLICATION NUMBER: 60/082568 PRIOR FILING DATE: 1998-04-21 PRIOR APPLICATION NUMBER: 60/082569 PRIOR FILING DATE: 1998-04-21 PRIOR APPLICATION NUMBER: 60/082704 PRIOR FILING DATE: 1998-04-22 PRIOR APPLICATION NUMBER: 60/082797 PRIOR APPLICATION NUMBER: 60/083727 PRIOR APPLICATION NUMBER: 60/083495 PRIOR APPLICATION NUMBER: 60/083495 PRIOR APPLICATION NUMBER: 60/083495 PRIOR PILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/083496 PRIOR APPLICATION NUMBER: 60/083496 PRIOR APPLICATION NUMBER: 60/083496 PRIOR APPLICATION NUMBER: 60/083496 PRIOR APPLICATION NUMBER: 60/083496 PRIOR APPLICATION NUMBER: 60/08359 PRIOR APPLICATION NUMBER: 60/084366 PRIOR APPLICATION NUMBER: 60/084366 PRIOR APPLICATION NUMBER: 60/084639 PRIOR APPLICATION NUMBER: 60/084639 PRIOR APPLICATION NUMBER: 60/084643 PRIOR APPLICATION NUMBER: 60/084643 PRIOR APPLICATION NUMBER: 60/084643 PRIOR APPLICATION NUMBER: 60/084643 PRIOR APPLICATION NUMBER: 60/084643 PRIOR APPLICATION NUMBER: 60/084643 PRIOR APPLICATION NUMBER: 60/084643 PRIOR APPLICATION NUMBER: 60/084643 PRIOR APPLICATION NUMBER: 60/084643 PRIOR APPLICATION NUMBER: 60/084643 PRIOR APPLICATION NUMBER: 60/084643 PRIOR APPLICATION NUMBER: 60/085573 PRIOR APPLICATION NUMBER: 60/085573 PRIOR APPLICATION NUMBER: 60/085579 PRIOR APPLICATION NUMBER: 60/085579 PRIOR APPLICATION NUMBER: 60/085579 PRIOR APPLICATION NUMBER: 60/085579 PRIOR APPLICATION NUMBER: 60/085579 PRIOR APPLICATION NUMBER: 60/085579 PRIOR APPLICATION NUMBER: 60/085579 PRIOR APPLICATION NUMBER: 60/085579

APPLICATION NUMBER: 60/088722 FILING DATE: 1998-06-10

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-09

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APPLICATION NUMBER:

1998-06-05 1998-06-04

60/088326

APPLICATION NUMBER: 60/088738

1998-06-10

60/088740

FILING DATE:

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US-10-176-488-458
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Prior Application removed
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
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Best Local Similarity
                                                                 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C119
CURRENT APPLICATION NUMBER: US/10/176,488
CURRENT FILING DATE: 2002-06-21
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088861
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-10
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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100.0%; Pred. No.
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                                                 See File Wrapper
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CURRENT APPLICATION NUMBER: US/10/176,492
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
SEQ ID NO 458
LENCTH: 734
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-492-458
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; ORGANISM: Homo
US-10-176-488-458
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US-10-176-492-458
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Best Local S
Matches 5
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Publication No. US20030027273A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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APPLICANT:
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APPLICANT:
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              APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C92
CURRENT APPLICATION NUMBER: US/10/176,747
CURRENT FILING DATE: 2002-06-20
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APPLICANT:
APPLICANT:
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les 5; Conserv
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Goddard, Audrey
Godowski, Paul J
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Gurney, Austin L.
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Smith, Victoria
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5. US20030027272A1
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100.0%; Pr
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See File Wrapper or Palm
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s; Pred. No. 6.4
0; Mismatches
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RESULT 157
US-10-176-985-458
: Sequence 458, Application US/10176985
: Publication No. US20030027277A1
; GENERAL INFORMATION:
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Best Local Similarity
Thehes 5; Conserv
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; ORGANISM: Homo Sapien
US-10-176-750-458
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SEQ ID NO 458
LENGTH: 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C99
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Goddard, Audrey
                                                                                                              Godowski, Paul J. Gurney, Austin L.
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                                                    Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                         Zhang, Zemin
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0; Mismatches
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Pred. No.
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; SEQ ID NO 458
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-985-458
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US-10-176-987-458
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US-10-176-991-458
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CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
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GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-06-21
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            APPLICANT:
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            Smith, Victoria Watanabe, Colin Wood, William I.
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; Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 ; SEQ ID NO 458 ; ENGTH: 734 ; TYPE: PRT : ORGANISM: Homo Sapien US-10-176-992-458
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US-10-176-993-458
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US-10-176-992-458
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CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
ENGTH: 734
                                                           APPLICANT:
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APPLICANT:
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CURRENT FILING DATE: 2002-06-21
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                             Godowski, Paul J.
Gurney, Austin L.
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Godowski, Paul J.
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; Prior Application removed - St; NUMBER OF SEQ ID NOS: 612; SEQ ID NO 458; LENGTH: 734; LENGTH: 734; TYPE: PRT; ORGANISM: Homo Sapien
US-10-184-658-458
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; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo S
US-10-176-993-458
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                                                                          GENERAL INFORMATION:
                                                                                     Sequence 2, Application US/09996015
Publication No. US20030032166A1
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APPLICANT:
                                         APPLICANT: Quinn, Kerry E. APPLICANT: Pena, Carol A. E.
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RIC228
CURRENT APPLICATION NUMBER: US/10/184,658
CURRENT FILING DATE: 2002-06-28
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CURRENT APPLICATION NUMBER: US/10/176,993
CURRENT FILING DATE: 2002-06-20
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Godowski, Paul J.
Gurney, Austin L.
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D. US20030027281A1
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Spaderna, Steven K. Leite, Marlo W.

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PRIOR APPLICATION NUMBER: 09/641,741
PRIOR APPLICATION NUMBER: 60/159,613
PRIOR APPLICATION NUMBER: 60/159,613
PRIOR APPLICATION NUMBER: 60/175,534
PRIOR APPLICATION NUMBER: 60/275,534
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/224,086
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 47
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 734
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-015-2
                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/173,695; CURRENT FILING DATE: 2002-06-17; Prior Application removed - See File Wrapper; NUMBER OF SEQ ID NOS: 612; SEQ ID NO 458; SEQ ID NO 458; LENGTH: 734; TYPE: PRT; ORGANISM: Homo Sapien
US-10-173-695-458
RESULT 165
US-10-173-697-458
; Sequence 458, Application US/10173697
; Publication No. US20030032102A1
; GENERAL INFORMATION:
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US-10-173-695-458
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CURRENT FILING DATE: 2001-11-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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140 LGPHR 144
                                                                                                                        140 LGPHR 144
                                                                                                                                              3 LGPHR 7
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K.
Wood, William I.
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Pred. No. 6.4e+02;
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Pred. No.
                                                                                                                                                                                             Mismatches
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Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
ORGANISM: HOMO Sapien
US-10-173-705-458
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US-10-173-705-458
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Best Local Similarity 100.
Watches 5; Conservative
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SEQ ID NO 458
LENGTH: 734
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                                                            Matches
                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                 APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C18
CURRENT APPLICATION NUMBER: US/10/173,705
CURRENT FILING DATE: 2002-06-17
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2002-06-17
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140 LGPHR 144
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                                                                         Local
                             3 LGPHR 7
                                                         1 Similarity 100
5; Conservative
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K.
Wood, William I.
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Godowski, Paul
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o. US20030032103A1
                                                            33.3%; Score 5; DB
100.0%; Pred. No. 6.
tive 0; Mismatches
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                                                       DB 9; L., vo. 6.4e+02; 0;
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RESULT 167 US-10-174-576-458

Sequence 458, Application US/10174576 Publication No. US20030032104A1

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                                            Query Match
Best Local Similarity
"~+~hes 5; Conserve
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US-10-174-585-458
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CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
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Matches 5; Conserv
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C37
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                              3 LGPHR 7
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LGPHR 144
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Goddard, Audrey
Godowski, Paul J.
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                                                              Conservative
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                                                                         33.3%; Score 5; 1
100.0%; Pred. No.
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                                                            Mismatches
                                                                         DB 9; Le
o. 6.4e+02;
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US-10-175-747-458
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Best Local Similarity
Watches 5; Conserv
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                                                      PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PRIOR APPLICATION NUMBER: 60/063120
PRIOR APPLICATION NUMBER: 60/063120
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
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US-10-174-586-458
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CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul d
APPLICANT: Gurney, Austin I
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                                                                                                                                                                                                                                                        APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9430R1C44
CURRENT APPLICATION NUMBER: US/10/175,747
CURRENT FILING DATE: 2002-06-19
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                  PRIOR APPLICATION NUMBER: 60/063121 PRIOR FILING DATE: 1997-10-24
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Gurney, Austin L.
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Godowski, Paul
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Goddard, Audrey
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NUMBER: 60/063486
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o. 6.4e+02;
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FILING DATE: 1998-06-10

APPLICATION NUMBER:

60/088826

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; SEQ ID NO 458
; LENCTH: 734
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-481-458
                RESULT 172
US-10-176-485-458
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US-10-176-481-458
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Sequence 458, Application US/10176485
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C98
CURRENT APPLICATION NUMBER: US/10/176,481
CURRENT FILING DATE: 2002-06-21
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NUMBER OF SEQ ID NOS: 612
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OR FILING DATE: 1998-06-16

OR APPLICATION NUMBER: 60/089538

OR FILING DATE: 1998-06-17

OR APPLICATION NUMBER: 60/089598

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Godowski, Paul J.
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-487-458
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US-10-176-487-458
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NUMBER OF SEQ ID NOS: 612
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TYPE: PRT
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Publication No. US20030032110A1
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CURRENT FILING DATE: 2002-06-20
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/10/176,485
CURRENT FILING DATE: 2002-06-20
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140 LGPHR 144
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CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
ORGANISM: Homo Saplen
US-10-176-493-458
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US-10-176-756-458
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US-10-176-756-458
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SEQ ID NO 458
LENGTH: 734
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/176,756
CURRENT FILING DATE: 2002-06-21
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3 LGPHR 7
                                              Local Similarity es 5; Conserv
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Godowski, Paul J.
Gurney, Austin L.
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RESULT 177
US-10-176-919-458
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US-10-176-911-458
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US-10-176-911-458
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                                                                      ; ORGANISM: HOMO US-10-176-919-458
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NUMBER OF SEQ ID NOS: 612
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APPLICANT: WOOD, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C63
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CURRENT FILING DATE: 2002-06-20
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     h 33.3%; Score 5; DB Similarity 100.0%; Pred. No. 6. 5; Conservative 0; Mismatches
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; ORGANISM: Homo Sapien US-10-176-978-458
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US-10-176-978-458
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
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                                                                                                                     CURRENT APPLICATION NUMBER: US/10/176,978
CURRENT FILING DATE: 2002-06-21
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CURRENT FILING DATE: 2002-06-21
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Godowski, Paul J.
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RESULT 181
US-10-180-543-458
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Prior Application removed -
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
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NUMBER OF SEQ ID NOS: 612
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                                                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C161
CURRENT APPLICATION NUMBER: US/10/180,543
CURRENT FILING DATE: 2002-06-25
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APPLICANT: Chen,Jian
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Gurney, Austin L.
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Godowski, Paul
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Prior Application removed - See
NUMBER OF SEQ ID NOS: 612
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Best Local Similarity
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US-10-180-546-458
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US-10-180-543-458
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APPLICANT: WOOD, WILLIAM I.

APPLICANT: Zhang.Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TILE REFERENCE: P3430R1C156
CURRENT APPLICATION NUMBER: US/10/180,546
CURRENT FILING DATE: 2002-06-25
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
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CURRENT FILING DATE: 2002-06-25
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Goddard, Audrey
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K.
Wood, William I.
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US-10-180-549-458
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US-10-180-547-458
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
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Matches
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LENGTH: 734
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GENERAL INFORMATION:
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       CURRENT APPLICATION NUMBER: US/10/180,549
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                      APPLICANT: zhang, zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RIC151
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CURRENT FILING DATE: 2002-06-25
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C157
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                Smith, Victoria
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US-10-180-555-458
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US-10-180-549-458
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LENGTH: 734
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LENGTH: 734
                APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93430R1C163
CURRENT APPLICATION NUMBER: US/10/180,555
CURRENT FILING DATE: 2002-06-25
CURRENT FILING DATE: 2002-06-25
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APPLICANT:
    TITLE
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Prior application removed
NUMBER OF SEQ ID NOS: 612
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    INVENTION:
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                                                                                    Godowski, Paul J.
Gurney, Austin L.
                            Watanabe, Colin K. Wood, William I.
                                                                          Pan, James
                                                                                                                Goddard, Audrey
                                                                                                                               Desnoyers, Luc
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Goddard, Audrey
                Zhang, Zemin
                                                         Smith, Victoria
                                                                                                                                               Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood, William I.
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SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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b. 6.4e+02;
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RESULT 189
US-10-183-010-458
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Best Local Similarity
"-+-hes 5; Conserv
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                                                                                                                                  Sequence 458, Application US/10183010 Publication No. US20030032126A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
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LENGTH: 734
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                                                         APPLICANT:
                                                                                                    APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 19430R1C177
FILE REFERENCE: 19430R1C177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/180,559
CURRENT FILING DATE: 2002-06-25
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                                            APPLICANT:
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APPLICANT:
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                              APPLICANT:
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                                                         Goddard, Audrey
Godowski, Paul
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                                         Gurney, Austin L.
                                                                                       Desnoyers, Luc
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Godowski, Paul
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              Smith, Victoria
                            Pan, James
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Pred. No.
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CURRENT APPLICATION NUMBER: US/10/183,010
CURRENT FILING DATE: 2002-06-26
Prior Application removed - See File Wrapper
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
ORGANISM: Homo Sapien
US-10-183-010-458
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US-10-183-012-458
; Sequence 458, Applica
; Publication No. US200
; GENERAL INFORMATION:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C164
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/183,012
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
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hes 5; Conserv
                                OR APPLICATION NUMBER: 60/01
BR FILING DATE: 1997-10-28
BR APPLICATION NUMBER: 60/01
BR FILING DATE: 1997-10-29
BR APPLICATION NUMBER: 60/01
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FILING DATE: 1997-10-28
                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/063486 FILING DATE: 1997-10-21
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FILING DATE: 1997-10-24
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FILING DATE: 1997-10-31 APPLICATION NUMBER: 60/
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Godowski, Paul
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b. US20030032127A1
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100.0%;
                                    60/063870
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    See File Wrapper or Palm

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OR APPLICATION NUMBER: 60/080194

OR FILING DATE: 1998-03-31

OR APPLICATION NUMBER: 60/080327

OR FILING DATE: 1998-04-01

OR FILING DATE: 1998-04-01

OR FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21
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FILING DATE: 1997-12-
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APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084639
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-09
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APPLICATION NUMBER: 60/
FILING DATE: 1998-04-08
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FILING DATE: 1998-03-
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APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077649
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             APPLICATION NUMBER: 60/084640
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DR APPLICATION NUMBER: 60/088028
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088029
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088033
DR FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/088740 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088811 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824
                                                    APPLICATION NUMBER: 60/089090 FILING DATE: 1998-06-12
                                                                                                                                APPLICATION NUMBER: 60/088863 FILING DATE: 1998-06-11
                                                                                                                                                                                      APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088861
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FILING DATE: 1998-06-05
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APPLICATION NUMBER:
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FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/087208
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FILING DATE: 1998-05-18
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Best Local S
Matches 5
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Prior Application removed - See
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
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                                                                   APPLICANT:
APPLICANT:
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Best Local :
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                                        APPLICANT:
                                                                                                                                                     APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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CURRENT APPLICATION NUMBER: US/10/184,614
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              TITLE
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
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| 140 LGPHR 144
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             T: Zhang, Zemin INVENTION: SEC
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5; Conserv
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5; Conserv
                                                                                         Gurney, Austin L.
                                        Smith, Victoria Watanabe, Colin Wood, William I.
                                                                                                            Goddard, Audrey
Godowski, Paul
                                                                                                                                         Desnoyers, Luc
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Gurney, Austin L.
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Godowski, Paul
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              SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING
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100.0%; Pr
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No. 6.4e+02;
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; FILE REFERENCE: p3430R1C210
; CURRENT APPLICATION NUMBER: US/10/
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See F1
NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 458
; LENCTH: 734
; TYPE: PRT
                                                                                                 US-10-184-637-458
Sequence 458, Application US/10184637
Publication No. US20030032131A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Desnoyers, Luc
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Best Local Similarity
Watches 5; Conserve
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US-10-184-635-458
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US-10-184-635-458
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Best Local (
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TYPE: PRT
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Godowski, Paul J.
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Watanabe, Colin K. Wood, William I.
                             Smith, Victoria
                                             Pan, James
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0; Mismatches
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; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: 93430R1C206
; CURRENT APPLICATION NUMBER: US/10/184,637
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEG ID NOS: 612
; SEQ ID NO 458
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-637-458
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US-10-184-646-458
                                                                                                               Sequence 458, Applic Publication No. US20 GENERAL INFORMATION:
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LENGTH: 734
TYPE: PRT
ORGANISM: Homo Sapien
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Matches 5; Conserv
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                                                                                  APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/184,646
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C221
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Gurney, Austin L. Pan, James
                                                  Desnoyers, Luc
Goddard, Audrey
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RESULT 198
US-10-187-594-458
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                                                                Sequence 458, Application US/10187594 Publication No. US20030032135A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-06-27
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENCTH: 734
TYPE: PRT
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CURRENT FILTMG DATE: 2002-06-28
Prior Application removed - See File Wrap:
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
EILE REFERENCE: P3430RIC187
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APPLICANT:
                               APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C212
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Watanabe, Colin K.
Wood, William I.
Desnoyers, Luc
Goddard, Audrey
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Gurney, Austin L.
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LENGTH: 734
TYPE: PRT
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 458
LENGTH: 734
TYPE: PRT
Sequence 458, Application US/10187745
Publication No. US20030032137A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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CURRENT APPLICATION NUMBER: US/10/187,594
CURRENT FILING DATE: 2002-07-01
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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CURRENT FILING DATE: 2002-07-02
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APPLICANT: Chen, Jian

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APPLICANT: Gurney, Austin L.
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presenilin I-463 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999 C;Accession: S63683 R;Sahara, N; Yahagi, Y; Takagi, H; Kondo, T; Okochi, M; Usami, M; Shirasawa, FEBS Lett. 381, 7-11, 1996 δÃ A;Cross-references: EMBL:U40379; NID:g1244637; PIDN:AAB05894.1; PID:g1244638 C;Superfamily: presentlin A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-463 <SNAP A; Title: Identification and characterization of presentiin I-467, I-463 and I-374. A; Reference number: S63683; MUID:96193901; PMID:8641442 A; Accession: S63683 Matches Query Match 342 SHLGPHRSTPESRAA 356 Local Similarity 1 SHLGPHRSTPESRAA 15 Conservative 100.0%; 0; Score 15; Pred. No. Mismatches DB 2; 1 2.7e-09; 0; Length 463; Indels 0; Gaps 0

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F:224-236/Domain: t
F:224-264/Domain: t
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F:408-428/Domain: t
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A;Cross-references: GDB:135682; OMIM:104311
A;Map position: 14424.3-14q24.3
C;Superfamily: presenilin
C;Keywords: alternative splicing; Alzheimer's
                                                                                                       H75253

hypothetical protein - Deinococcus radiodurans (strain R1)
c;Species: Deinococcus radiodurans
c;Species: Deinococcus radiodurans
c;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_cl
c;Accession: H75253
R;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-467 <RES>
A;Cross-references: GB:L42177; NID:g904129; PIDN:AAC42094.1; PID:g904130
C;Superfamily: presentlin
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C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 29-Sep-1999
C;Accession: I78388
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F;164-185/Domain:
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A; Residues: 24-32; 254-256, 290-292; 316-317, 376-379 <VIW>
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       nite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, J.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, Smith, H.O.; Venter, J.C.; Fraser, C.M. ence 286, 1571-1577, 1999
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A.Title: The complete sequence of the 1,683-kb pSymB megaplasmid

A.Reference number: A95842; MUID:21396508; PMID:11481431

A.Accession: E95911

A.Accession: A95842; MUID:21396508; PMID:11481431
A;Cross-references: GB:AL591985; PIDN:CAC48957.1; PID:
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F:, Finan, T.M.; Long, S.R.; Puhler, A.; F
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable transcription regulator, LacI family protein [imported] - Sinorhizobium
C:Species: Sinorhizobium meliloti
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A; Residues: 1-343 < KUR>
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C;Accession: E95911
                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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PIDN:CAC48957.1; PID:g15140442;

GSPDB:GN00167

Vorholter, F.J.;

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Abola, P.; Ampe, F.; Barloy-Hubl S.; Federspiel, N.A.; Fisher, R

D.H.; Kiss, S.; Wells, I

D.H.; Wong,

, C.

Lelau ; Yeh,

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A; Nolecule type: DNA
A; Residues: 1-347 <WHI>
A; Cross-references: GB: AE002089;
A; Cross-references: Strain R1
                                                                                                                                      A; Gene: CC3359
C; Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase
                                                                                                                                                                    C; Genetics:
A; Gene: CC2359
                                                                                                                                                                                                                                                                                      A; Reference number: A87249; A; Accession: F87541
                                                                                                                                                                                                                                                                                                      R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzysey, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein CC2359 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change C;Accession: F87541
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F87541
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                                                                                                                                                                                                              A;Cross-references: GB:AE005673; NID:g13423888; PIDN:AAK24330.1;
                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-327 <S
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139 TPESRAA 145
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nilarity 100.0%;
Conservative 0
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                                                                                          DB 2;
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                                                                                                            Length 327
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presentilin 1 protein isoform 463 - lesser mouse lemur
C:Species: Microcebus murinus (lesser mouse lemur)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 13-Sep-1998
C;Accession: JC5081
C;Accession: JC5081
R;Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Petter, A.; Bons, N.; Bellis, A:Title: Molecular cloning, sequencing, and brain expression of the presentlin 1 gene in A:Reference number: JC5080; MUID:97079199; pMID:8920931
A;Contents: brain
A;Contents: brain
A;Contents: brain
A;Contents: brain
A;Contents: brain
A;Contents: uccleic acid sequence not shown
A;Accession: JC5081
A;Status: nucleic acid sequence not shown
A;Accession: JC5081
A;Contents: brain
C;Comment: This protein is an intermembrane protein with seven transmembrane domains. It
C;Genetics:
A;Gene: ps1
C;Genetics:
A;Gene: ps1
C;Superfamily: presenilin
C;Keywords: transmembrane #status predicted <TMA>
F;129-150/Domain: transmembrane #status predicted <TMA>
F;129-150/Domain: transmembrane #status predicted <TMA>
F;119-100/Domain: transmembrane #status predicted <TMA>
F;217-234/Domain: transmembrane #status predicted <TMA>
F;240-257/Domain: transmembrane #status predicted <TMA
F;250-257/Domain: transmembrane #status predicted <TMA
F;250-257/Domain: transme
                                                                                                                                                                                                             R; Calenda, A.; Mestre-Frances, N.; Czech, C.; Pradier, L.; Petter, A.; Bons, Biochem. Biophys. Res. Commun. 228, 430-439, 1396
A; Title: Molecular cloning, sequencing, and brain expression of the presentil A; Reference number: JC5080; MUID:97079199; PMID:8920931
A; Accession: JC5080
      A; Experimental source: brain C; Comment: This protein is an intergral membrane protein with seven transmembrane C; Genetics:
                                                                                        A;Cross-references: EMBL:Z71333; NID:g1707591; PIDN:CAA95930.1; PID:g1707592
                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-467 < CAL>
                                                                                                                                                                                                                                                                                                                                                                          presenilin 1 protein isoform 467 - lesser mouse lemur
C;Spectes: Microcebus murinus (lesser mouse lemur)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 20-Jun-2000
C;Accession: JC5080
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A; Molecule type: nucleic acid
A; Residues: 1-87 <GES>
A; Note: sequence extracted fro
                                                                                     from other geographical regions.
A;Reference number: A45714; MUID:93124536; PMID:8419636
A;Contents: HTLV_IMEL5
A;Accession: F45714
                                                                                                                                                                      R;Gessain, A.; Boeri, E.; Yanagihara, R.; Gallo, R.C.; Franchini, J. Virol. 67, 1015-1023, 1993
A;Title: Complete nucleotide sequence of a highly divergent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Reywords: transmembrane protein
F:82-100/Domain: transmembrane #status predicted <
F:133-154/Domain: transmembrane #status predicted
F:164-185/Domain: transmembrane #status predicted
F:195-213/Domain: transmembrane #status predicted
                                                               A; Status: preliminary; not compared
                                                                                                                                                                                                                                              C; Accession: F45714
                                                                                                                                                                                                                                                                probable regulatory protein p13 II, alternative splice form - human T-cell lymphotrop
C;Species: human T-cell lymphotropic virus type 1, HTLV-1
C;Date: 22-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 23-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfami.
C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methionine-tRNA ligase (EC 6.1.1.10) mets - Mycoplasma pneumoniae (strain ATCC 29342) 
N;Alternate names: hypothetical protein B01_orf512; methionyl-tRNA synthetase mets 
C;Species: Mycoplasma pneumoniae 
A;Variety: ATCC 29342 
C;Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 03-Jun-2002 
C;Accession: S73457
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A; Residues: 1-512 <HIM>
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A; Map position:
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extracted from NCBI backbone (NCBIP:122473)
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Score 6;

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A;Cross-references: GB:AE006469; PIDN:AAK64878.1; PID:g14523295; GSPDB:GN00165 A;Experimental source: strain 1021, megaplasmid pSymA R;Gallbert, F.; Finan, T. M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barld Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisl L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K. A;Title: The composite genome of the legume symbiont sinorhizobium meliloti. A; Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein SMa0412 [imported] - Sinorhizobium meliloti (strain 1021) magaplasm c; Species: Sinorhizobium meliloti
C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C; Accession: D95289
R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, Ralman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A; Reference number: A95262; MUID:21396509; PMID:11481432
A; Accession: D95289
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A; Residues: 1-87 <TSU>
A; Cross-references: GB:M37301; NID:g541634;
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Mol. Biol. Med. 5,
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A;Genome: plasm:
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nes 6; Conser
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5, 29-42, 1988
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A; Map position: 1
C; Superfamily: molybdenum
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A; Molecule type: DNA
A; Residues: 1-168 <WHI>
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A; Introns: 37/3; 79/3
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A; Contents: HTLV-IMEL5
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-K
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-K
C;Accession: E75257
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson,
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback,
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
Science 286, 1571-1577, 1999
R;Gessain, A.; Boeri, E.; Yanagihara, R.; Gallo, R.C.; Franchini, G. J. Virol. 67, 1015-1023, 1993
A;Title: Complete nucleotide sequence of a highly divergent human T-cell leukemia from other geographical regions.
A;Reference number: A45714; MUID:93124536; PMID:8419636
                                                                                                                               probable regulatory function protein p30 II, alternative splice form - human C;Species: human T-cell lymphotropic virus type 1, HTLV-1 C;Date: 22-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 23-May-1997 C;Accession: E45714
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A;Experimental source: strain Rl
C;Genetics:
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100.0%; Pred. No. 13
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:AE000513; NID:g6460395; PIDN:AAF12111.1; PID:g646
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11;
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T.; Zalewski,
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A; Molecule type: DNA
A; Residues: 1-257 < KUR>
A; Cross-references: GB: AL591985; PIDN: CAC49796.1; PID: g15141283; GSPDB: GN00167
A; Cross-references: GB: AL591985; PIDN: CAC49796.1; PID: g15141283; GSPDB: GN00167
A; Experimental source: strain 1021, megaplasmid pSymB
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlı
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisl
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
Science 293, 668-672, 2001
                                                                                       A; Contents: annotation C; Genetics:
                                                                                                                                         A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; I hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; A;Title: The composite genome of the legume symbiont Sinorhizoblum meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A95842; A; Accession: D96016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: D96016
R; Finan, T.M.; Weid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable exodeoxyribonuclease III (EC 3.1.11.2) [imported] - Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001
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A;Note: sequence extracted from NCBI back
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Koralnik, I.J.; Gessain, A.; Klotman, M.E.; Lo Monico, A.; Berneman, Z.N.; Franchini, Proc. Natl. Acad. Sci. U.S.A. 89, 8813-8817, 1992
A;Title: Protein isoforms encoded by the px region of human T-cell leukemia/lymphotropic A;Reference number: A46181; MUID:92409607; PMID:1528897
A;Accession: C46181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pX-tax-orf II (alternatively spliced) - human T-cell lymphotropic virus type C;Species: human T-cell lymphotropic virus type 1, HTLV-1 C;Date: 22-Sep-193 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000 C;Accession: C46181; D46181
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                                                                A; Gene: xthA4; SMb20689
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nes 6; Conser
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           exodeoxyribonuclease
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Conservative 0; Misma
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DNA replication and repair RecF protein xF0003 [imported] - xylella fastidiosa C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 *sequence_revision 20-Aug-2000 *text_change 17-Nov-2000
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Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Status. F87498
A;Status. F87498
A;Status. F87498
                                                                                                                                                                                                                                                                                  R:Murphy, L.; Harris, D.; Thomson, N.R.; Parkhill, submitted to the EMBL Data Library, August 1999 A; Reference number: Z21619 A; Accession: T37031
                                                                                                                                                                                                                                                                                                                                                  C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
C;Accession: T37031
                                                                                                                                                                                                        A;Cross-references: EMBL:AL109989; PIDN:CAB53424.1; GSPDB:GN00070; SCOEDB:SCJ12.12c A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-262 <STO>
A;Cross-references: GB:AE005673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Nierman, W.C.; Feldblyum, B.; Laub, M.T.; DeBoy, R.T.
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C;Accession: F87498
RESULT 20
                                                                                                                                                                         A; Gene:
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A; Residues: 1-301 <MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein SCJ12.12c -
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 6; DB;
; Pred. No. 19
0; Mismatches
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Pred.
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Pred. No.
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                                                                                                              Mismatches
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                                                                                                                 4 6;
No.
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21;
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5. 19;
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                                                                                                                                                                                                                                                                                                                                    J.; Barrell,
                                                                                                                                           Length 301
                                                                                                                                                                                                                                                                                                                                                               #text_change 03-Dec-1999
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A;Cross=references: GB:AE003855; GB:AE003849; NID:g9104760; PIDN:AAF82816.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. BerNeto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madeira, A.M.B. N.; Madeira, H.M.F.; Marsino, C.L.; Marques, M.V.; Martins, F. A., Authors: Martina, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Migaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.R.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A.R. Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Carulli, J.P.; Hartl, D.L. denetics 132, 193-204, 1992
A;Title: Variable rates of evolution among Drosophila opsin genes. A;Reference number: $40691; MUID:93012921; PMID:1398053
A;Accession: $40693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 opsin rh3 - fruit fly (Drosophila pseudoobscura)
C;Species: Drosophila pseudoobscura
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
C;Accession: $40603; $65548; $244607
R;Carulli, J.P.; Hartl, D.L.
                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: the authors translated the codon GCA for residue R;Carulli, J.P. submitted to the EMBL Data Library, November 1992 A;Reference number: S65546 A;Accession: S65548
                                                                                                                                                                                                                A;Gene: FlyBase:Dpse/Rh3
A;Cross·references: FlyBase:FBgn0012709
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-123,'L',125-241,'Q',243-254,'R',256-382 <CAW>
A; Cross-references: EMBL:X65879; NID:g9081; PIDN:CAA46710.1;
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A; Residues: 1-382 <CAR>
A; Cross-references: EMBI
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Pred. No.
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Pred. No.
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iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, P. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Larding, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mavy, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlye T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; The complete genome sequence of the Gram-positive bacterium Bacillus subtilla, Reference number: A69580; MUID:98044033; PMID:9384377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein DKFZp434H0717.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gali
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A; Cross-references: EMBL: AL122102
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A; Accession: T34535
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R; Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann,
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A;Experimental source: strain 168
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A; Residues: 1-401 <KUN>
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28
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100.0%; Pr
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RESULT 24 D87297 conserved

hypothetical protein CC0389 [imported] - Caulobacter crescentus

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RESULT 26
H98112
histidine-tRNA ligase (EC 6.1.1.21) [imported] - Streptococcus pneumoniae (strain histidine-tRNA ligase (EC 6.1.1.21) [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002
C;Accession: H98112
R;HOskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, F., R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, Y., P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-429 <KUP>
A;Cross-references: GB:AE005672; PIDN:AAK76180.1; PID:g14973634; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP2121
C;Superfamily: histidine-tRNA ligase; histidine-tRNA ligase homology
A;Reference number: A97872;
A;Accession: H98112
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D. Inson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001

A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus A; Reference number: A95000; MUID:21357209; PMID:11463916

A; Accession: C95248
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A;Reference number: A87249; MUID:21173698; PMID:11259647
A.Accession: D87297
A.Accession: D87297
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: D87297
R;Nierman, M.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft
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C;Genetics:
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A; Residues: 1-408 <STO>
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llarity 100.0%;
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White, O.; Salzberg,
Holt, I.E.
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S.L.; Lewis,
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M.R.;
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Radune, D.; Holtzapple,
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A;Reference number: S31927
A;Accession: S31927
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-475 <KIR>
A;Cross-references: EMBL:X70991; NID:g38459; PID:g38460
                                                                                                                                                                                                                                  drop9 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision
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Blochem. Blophys. Res. Commun. 231, 392-396, 1997
A:Title: Cloning of Xenopus presenilin-alpha and -beta cDNAs and A:Reference number: JC5390; MUID:97223465; PMID:9070286
A;Accession: JC5390
A;Accession: JC5390
A;Status: nucleic acid sequence not shown
A;Residues: 1-433 <TSU>
A;Residues: 1-433 <TSU>
A;Cross-references: DDBJ:DB4427; NID:g1944353; PIDN:BAA19570.1;
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                                                                                                                                                               submitted to the EMBL Data Library, February 1993 A; Reference number: S31927
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F;374-394/Domain:
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 04-Jun-1997 #sequence_revision 18-Jul-1997
C;Accession: JC5390
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A;Residues: 1-429 <KUR>
A;Residues: 1-429 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAL00733.1; PID:g15459628; GSPDB:GN00174
C;Genetics:
A;Gene: hisS
C;Superfamily: histidine-tRNA ligase; histidine-tRNA ligase homology
C;Keywords: ligase
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A;Residues: 1-640 ~KUR>
A;Cross-references: GB:BA000019; PIDN:BAB72668.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all0711
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A:Note: Nostoc sp. Strain PCC 7120 is a synonym of A
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #
C:Accession: AE1895
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein - Rhodobacter capsulatus
C;Specias: Rhodobacter capsulatus
C;Specias: Rhodobacter capsulatus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03510
R;Vicek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsula; Reference number: Z14955; MUID:97404404; PMID:9256491
A;Accession: T03510
                                                                                                                             preprotein translocase secA - Mycoplasma genitalium c;SpecLes: Mycoplasma genitalium c;SpecLes: Mycoplasma genitalium C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 17-Nov-2000 C;Accession: I64207
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A:Map position: 1
                 C.A.; Venter, J.C. Science 270, 397-403, 1995
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium A;Reference number: A64200; MUID:96026346; PMID:7569993
                                                                                        R; Fraser, C.M.; Gocayne, J.D.; M.; Fuhrmann, J.; Nguyen, D.; U
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE1895
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A; Residues: 1-617 < VLC>
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NA Res. 8, 205-213, 2001
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Pred. No.
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                                                                                          ; Adams, M.D.;
T.R.; Saudek,
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42;
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                                                                                        Clayton, R.A.; Fleischmann, R.D. D.M.; Phillips, C.A.; Merrick,
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30-Jun-2002
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RNA-directed RNA polymerase (EC 2.7.7.48) - Cymbidium ringspot virus X,Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase N;Contains: 33K protein C. Species: Cymbidium ringspot virus C. Species: Cymbidium ringspot virus C. Date: 31-Mar-1990 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000 C;Accession: S05456; JS0268 R. Grieco, F.; Burgyan, J.; Russo, M. R. Grieco, F.; Burgyan, J.; Russo, M. R. Grieco, F.; Burgyan, J.; Russo, M. R. Fittle: The nucleotide sequence of Cymbidium ringspot virus RNA. A, Reference number: JS0268; MUID:8936663; PMID:2771646 A, Accession: S05456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Hearne, P.Q.; Knorr, D.A.; Hillman, B.I.; virology 177, 141-151, 1990
A:Title: The complete genome structure and A:Reference number: A35315; MUID:90281577; A:Accession: A35315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: readthrough of the terminator UAG occurs between codons AAA for 296-Lys and C;Superfamily: carnation mottle virus RNA-directed RNA polymerase; barley yellow dwe C;Keywords: nucleotidyltransferase; RNA biosynthesis; RNA replication F;1-296/Product: 33K protein #status predicted <P33> F;527-694/Domain: barley yellow dwarf virus RNA-directed RNA polymerase homology <BY
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A;Experimental source: strain G-37
C;Comment: The "nucleotide-binding motif B" and "DEAD motif" featur
is adjacent to the identified motif and a third conserved motif is
A; Cross-references:
A; Accession: JS0268
                                              A; Molecule type: genomic A; Residues: 1-818 <GRI>
                                                                     A;Status: preliminary; translation A;Molecule type: genomic RNA
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A; Residues: 1-817 <HEA>
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C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
C;Accession: A35315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Contains: 33K protein
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                      EMBL: X15511;
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                      NID:g59020; PIDN:CAB38439.1;
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5. 52;
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                      PID: 94469160
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Glycoprotein B precursor - Marek's disease virus (strain RBIB)
C:Species: Marek's disease virus
C:Species: Marek's disease virus
C:Species: Marek's disease virus
C:Species: Marek's disease virus
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jun-2000
C:Accession: A32402; B32402
C:Accession: A32402; B32402
A;Title: Nucleotide sequence and characterization of the Marek's disease virus homologue
A;Reference number: A32402; MUID:89293086; PMID:2544666
A;Accession: A32402
A;Mclecule type: DNA
A;Residues: 1-865 <ROS>
A;Cross -references: GB:D13713; EMBL:D00506; NID:g221836; PIDN:BAA02866.1; PID:g221837
A;Accession: B32402
A;Mclecule type: protein
A;Residues: 250-271:304-330 <ROS2>
A;Mclecule type: protein
A;Residues: 250-271:304-330 <ROS2>
C;Superfamily: herpesvirus glycoprotein B
C;Keywords: glycoprotein; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-865/Product: glycoprotein B #status predicted <TN1>
F;732-752/Domain: transmembrane #status predicted <TN2>
F;37,184,332,364,406,425,631/Binding site: carbohydrate (Asn) (covalent) #status predicted <TN2>
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R;Rubino, L.; Burgyan, J.; Russo, M.
submitted to the EMBL Data Library, March 1995
A;Description: Molecular cloning and complete nucleotide sequence of carnation A;Reference number: S52717
A;Molecular type: genomic RNA
A;Residues: 1-851 <RUB>
A;Cross references: EMBL:X85215; NID:g755716; PIDN:CAA59478.1; PID:g755718
C;Superfamily: carnation mottle virus RNA-directed RNA polymerase; Darley yello C;Reywords: nucleotidyltransferase; RNA biosynthesis; RNA replication F;561-728/Domain: barley yellow dwarf virus RNA-directed RNA polymerase homolog
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A; Residues: 1-296,298-483,717,485-818 <GR2>
A; Cross-references: GB:X15511
A; Note: readthrough of the terminator TAG occurs between codons AAA for 296-Lys and C; Superfamily: carnation mottle virus RNA-directed RNA polymerase; barley yellow dwa C; Keywords: nucleotidyltransferase; RNA biosynthesis; RNA replication E;1-296/Product: 33K protein #status predicted <TYP>
F;528-695/Domain: barley yellow dwarf virus RNA-directed RNA polymerase homology <BY
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8-695/Domain: barley yellow dwarf virus RNA-directed RNA polymerase
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5. 52;
             DB 1;
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RESULT 38
T30815
platelet-derived growth factor receptor beta - Japanese C;Speciles: Fugu rubripes (Japanese pufferfish) C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text C;Accession: T30815 R;How, G.F.; Venkatesh, B.; Brenner, S.
                                                                                                                                                                                                                                                                                                                                                                                   Rianonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_san A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_san A;Note: published errata appeared in Science 283, 35, 1999; Sciencession: 888794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable major core protein 113L W;Alternate names: MC113L C;Species: MO11uscum contagiosum C;Date: 05-Nov-1999 #sequence_rev C;Accession: T30715
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                                                                                                                                                                                                                                                                         C;Genetic:
A;Gene: K07F5.12a
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A;Molecule type: DNA
A;Residues: 1-981 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein K07F5.12a [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #t
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C; Superfamily:
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A;Accession: T30715
A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-889 <SEN>
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100.0%;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a human tumorigenic poxvirus: MUID:96325459; PMID:8670425
                                                                                                                                                                                                                                                                                                                    PIDN:CAA94287.1; PID:g4008375; GSPDB:GN00022; CESP:K07
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Pred. No.
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61;
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                                #text_change 02-Jun-2000
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platelet-derived growth factor receptor beta precursor - mouse
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 10-Sep-1999
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 10-Sep-1999
C;Accession: A25742
R;Yarden, Y; Escobedo, J.A.; Kuang, W.J.; Yang-Feng, T.L.; Daniel, T.O.; Tremble, P.M.;
Nature 323, 226-232, 1986
A;Title: Structure of the receptor for platelet-derived growth factor helps define a fam
A;Reference number: A25742; MUID:87014762; PMID:3020426
A;Accession: A25742
A;Molecule type: mRNA
A;Residues: 1-1098 <YAR>
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
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A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-references: EMBL:X04367; NID:953618; PIDN:CAA27882.1; PID:953619
A;Cross-r
platelet-derived growth factor receptor beta precursor - human N.Contains: protein-tyrosine kinase (EC 2.7.1.112) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 11-Jun-1999 C.Accession: A28206; A31195; A38268; A31925; B31925; C31925 R.Gronwald, R.G.K.; Grant, F.J.; Haldeman, B.A.; Hart, C.E.; O'Hara, P.J.; F.Proc. Natl. Acad. Sci. U.S.A. 85, 3435-3439, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;597-964/Domain: protein kinase homology <KIN>
F;605-613/Region: protein kinase ATP-binding motif
F;404,88,102,214,291,306,353,370,444,467,478/Binding site: carbohydrate (Asn) (covalent)
F;53-99,148-189,334-290,435-507/Disulfide bonds: #status predicted
F;633/Active site: Lys #status predicted
F;653/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict.
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A:Title: Conserved linkage betwen the pufferfish (Fugu rubripes) and human geta; Reference number: 220882; MUID:97129405; PMID:8973913
A:Recession: T30815
A:Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-1048 <HOW>
A:Cross-references: EMBL:U63926; NID:g1752706; PID:g1752707; PIDN:AAC60062.1
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobuli
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                                     P.J.; Hagen,
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      RESULT 41
T01367
hypothetical
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A; Noticula: Inc. Compared with Conceptual Clausiation
A; Molecula type: DNA
A; Residues: 1047-1106 <RO3>
C; Comment: The extracellular domain is predicted to include five immunoglobulin-like
C; Generitos:
C; Generitos:
C; Generitos: GDB:PDGFRB
A; Cross references: GDB:120710; OMIM:173410
A; Map position: Sq13-5q32
C; Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homolog
C; Superfamily: macrophage colony-stimulating factor 1 receptor; heterodim
C; Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodim
C; Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodim
C; Superfamily: macrophage colony-stimulating factor 1 receptor; heterodim
C; Superfamily: macrophage colony-stimulating factor 1 receptor; heterodim
C; Superfamily: macrophage colony-stimulating factor 1 receptor; heterodim
C; Superfamily: macrophage colony-stimulating factor 2 receptor; heterodim
C; Superfamily: macrophage colony-status predicted <ENT>
F; 1-102/Domain: simunoglobulin homology <IMM2>
F; 1-102/Domain: immunoglobulin homology <IMM2>
F; 1-102/Domain: immunoglobulin homology <IMM3>
F; 1-102/Domain: immunoglobulin homology <IMM4>
F; 1-102/Domain: immunoglobulin homology <IMM4>
F; 1-106/Domain: intracellular *status predicted <IMT>
F; 506-610/Domain: intracellular *status predicted <IMT>
F; 506-610/Domain: protein kinase ATP-binding motif
F; 45,89,103,215,230,292,307,354,371,468,479/Binding site: carbohydrate (Asn) (covalen)
F; 54-100,149-190,235-291,436-508/Disulfide bonds: *status predicted
F; 634/Active site: Lys *status predicted
F; 634/Active site: phosphate (Tyr) (covalent) (by autophosphorylation) *status predicted
F; 64-104, F; 64-105, F; 64-105, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F; 64-106, F
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A;Reference number: A90908; MUID:8S
A;Accession: A31925
A;Status: not compared with concept
A;Molecule type: DNA
A;Residues: 676-727 <ROB>
A;Accession: B31925
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A; Molecule type: mRNA
A; Residues: 1-240, 'D', 242-1106 < CLA>
A; Residues: 1-240, 'D', 242-1106 < CLA>
A; Cross references: GB:M21616; NID:9189729; PIDN:AAA36427.1; PID:9189730
A; Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A; Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A; Reference number: A38268; MUID:91062389; PMID:2247464
A; Accession: A38268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: not compared with A;Molecule type: DNA A;Residues: 901-932 <RO2> A;Accession: C31925
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A; Residues: 828-884 <PAR>
R; Reberts, W.M.; Look, A.T.;
Cell 55, 655-661, 1988
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A;Cross-references: GB:J03278; NID:g189731; PIDN:AAA60049.1;
A;Cross-references: GB:J03278; NID:g189731; PIDN:AAA60049.1;
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Best Local :
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Biol. 8, 3476-3486, 1988
                                                                                                                                         Similarity
6; Conser
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661
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100.0%; Pr
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MUID:89028677; PMID:2846185
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                                                                                                                                                                              Score 6;
                                                                                                                                         Mismatches
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L.; Ek, B.;
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protein At2g34680 [imported] - Arabidopsis thaliana

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A; Cross-references: EMBL:x66028
C; Superfamily: CHD-1 protein; cl
C; Keywords: DNA binding
F: 293-336/Domain: chromobox homc
F; 387-427/Domain: chromobox homc
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A; Residues: 1-1680 <ROU>
A; Residues: 1-1680 <ROU>
A; Cross-references: EMBL.AC003096; NID:g3132469; PID:g3132477
A; Experimental source: Cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talleuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ven Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Accession: F84759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Delmas, V.; Stokes, D.G.; Perry, R.P. 1993
Proc. Natl. Acad. Sci. U.S.A. 90, 2414-2418, 1993
A;Title: A mammalian DNA-binding protein that contains a chromodomain A;Reference number: A47392; MUID:93211972; PMID:8460153
A;Accession: A47392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: KYBP protein for the model of Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A47392; S21568 R;Delmas, V.; Stokes, D.G.; Perry, R.P.
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A;Accession: T01367
                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 772-1711 <DE2>
                                                                                                                                                                                                                                                      R;Delmas, V.; Perry, R.P. submitted to the EMBL Data Library, May 1992 A;Description: KYBP, a mammalian protein that A;Reference number: S21568 A;Accession: S21568
                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: S194 plasmacytoma cells A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:128272, NCBIP:128273) R;Delmas, V.; Perry, R.P.
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A; Map position: 2
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
C;Accession: T01367; F84759
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1711 <DEL>
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A; Residues: 1-1680 <STO>
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  Query Match
Best Local Similarity
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                                                                           chromobox homology <CB1>
chromobox homology <CB2>
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  40.0%;
100.0%;
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                                                                                                                                                      chromobox homology
                                                                                                                                                                                                                                                                                                       protein that contains the SNF2/SWI2 helicase
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Score 6; I
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome II BAC T29F13 genomic sequence
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o. 99;
  DB 1;
. 1e+02;
                         Length 1711;
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Traser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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R;Skadsen, R.W.; Herbst, J.M. submitted to the EMBL Data Li A;Reference number: Z15316 A;Accession: T04371

Library,

July

#text_change 08-Oct-1999

C; Accession:

T04371

A;Status: preliminary;

translated

from GB/EMBL/DDBJ

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RESULT 44
S58277
                                                            RESULT 45
T04371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Su, X.Z.; Heatwole, V.M.; Werthelmer, S.P.; Guinet, F.; Herrfeldt, J.A.; Peterson, Cell 82, 89-100, 1995
A;Title: The large diverse gene family var encodes proteins involved in cytoadherenc A;Reference number: 220487; MUID:95330813; PMID:7606788
A;Accession: T28626
thaumatin-like protein - barley (fragment)
C;Species: Hordeum vulgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999
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                                                                                                                                                                   Qγ
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A; Residues: 1-18 <SMR>
                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, January 1995
A;Description: Conservation of a methylation imprint and a putative imprinting box
A;Reference number: S58277
A;Accession: S58277
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C;Accession: S58277
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A; Introns: 2197/3
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A; Residues: 1-2664 <SUX>
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C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                              C; Keywords: growth factor receptor
                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: X83702; NID: g929644; PIDN: CAA58675.1;
                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Smrzka,
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nes 6; Conser
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100.0%;
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b; Pred. No. 1.5
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                           I.; Fischer, G.F.; Barlow, D.P
                                                                                                                                                                                                        0,
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A; Residues: 1-26 <SKA>
A; Cross-references: EMBI
A; Experimental source: c; Genetics:
A; Gene: perm2
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C; Genetics:
A; Gene: HPX-2
C; Superfamily:
C; Keywords: DN
                                                                                                                                                                                                                                                                 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia phiserence number: A86491; MUID:20330349; PMID:10871362
A;Accession: F86491
                                                                                                                                                                                                                                                                                                                             hypothetical protein CPj0006 [imported] - Chlamydophila pneumoniae (strain C;Speckes: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: F86491
R;Shirai, M; Hirakawa, H; Kimoto, M; Tabuchi, M; Kishi, F; Ouchi, K;
                                                                                                                                                             A;Cross-references: GB:BA000008; NID:g8978379;
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 144, 213-219, 1994

A; Title: Identification of homeobox genes expressed in human A; Reference number: 137554; MUID:94314219; PMID:7518789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 15-Oct-1999
C;Accession: 137554
R;Moretti, P; Simmons, P.; Thomas, P.; Haylock, D.; Rathjen, P.; Vadas, M.
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RESULT
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A; Residues: 1-51 <STO>
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A; Residues: 1-39 < RES>
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A; Status: preliminary; translated
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                                                                                                                     Query Match
Best Local !
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Best Local
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A binding; }
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100.0%; Pr
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homeobox; nucleus; transcription regu
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Pred. No.
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32;
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RESULT 49
G72355
                                                                             R;Asoh, S.; Matsuzawa, H.; Ishino, F.; Strominger, J.L.; Matsuhash Eur. J. Biochem. 160, 231-238, 1986
A;Title: Nucleotide sequence of the pbpA gene and characteristics A;Reference number: A91176; MUID:87030266; PMID:3533535
A;Accession: A24995
                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Thermotoga maritima
C; Date: 11-Jun-1999 #sequence_
C; Accession: G72355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein - Chlamydophila pneumoniae (strain CWL029)
c;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
c;Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 05-May-2000
C;Accession: C72131
                                                                                                                                                                 C;Species: Escherichia coli
C;Date: 30-Jun-1988 #sequence_revision
C;Accession: A24995; C64798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;TILLE: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: G72355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Nelson, K.E.; Clayton, R.A.; Garrett, M.M.; Stewart, A.M.;
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A;Cross-references: GB:X04516; GB:D00001; GB:N00001; NID:g42313; PIDN:CAA28199.1; R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, .A.; Rose, D.J.; Mau, B.; Shao, Y.
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A; Residues: 1-51 <ARN>
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                                                 A; Molecule type: DNA
A; Residues: 1-69 <ASO>
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A; Residues: 1-56 <ARN>
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Pred. No.
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63;
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58;
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ps, C.A.; Richardson,
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Science 277, 1453-1462, 1997

A.Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503

A.Accession: C64798

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-69 <BLAT>
A;Cross-references: GB:AE000168; GB:U00096; NID:91786849; PIDN:AAC;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: ybeB

A;Map position: 15 min
C;Superfamily: Escherichia coli ybeB protein
                                                                                                                                                                                                                                                                                                                                                        hypothetical protein ybeB [imported] - Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escherichia coli (strain 0157:H7, sul c;Speciles: Escheri
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G85563
      A;Gene: ybeB
C;Superfamily:
                                                                        A;Cross-references: GB:AE005174; NID:g12513538; PIDN:AAG54971.1; GSPDB:GN00145; UWGP:207
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-69 <STO>
                                                                                                                                                                                                                                 A; Status: preliminary
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C; Superfamily:
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c;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C;Accession: C90713
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
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A;Molecule type: DNA
A;Residues: 1-69 <HAY>
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DNA Res. 8, 11-22, 2001
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Yasunaga, T.; Kuhara, S.;
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MUID:21074935; PMID:11206551
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Shiba, T.; Hattori, I
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Shinagawa,
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hypothetical protein BMEI1474 [imported] - Brucella melitensis (strain 16M) c;Specias: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AD3436
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, 7R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, 7R;DelVecchio, V.G.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghar, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
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C;Species: Caenorhabditis elegans
C;Date: 12-Mar-1993 #sequence_revision
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                                                                                      A; Introns:
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A; Residues: 1-82 <KER>
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                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-76 < KAW>
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R; Kawarabayasi, Y.;
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Human S182 gene, Human early onset Homo sapiens PS-1

Human

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                                                                                                                                                                                                                                                                   Early onset Alzheimer's expressed sequence tag;
                                                                                                                                                                                                                                                                                                             Early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        express them or containing antisense sequences, antibodies selective for these mutant forms of the proteins and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for drug screening. The antibodies can also be used e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New presentlin genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders, etc.
                                                                                                                                        Misc-difference
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EST; activated T cell.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A set of polypeptides (AAW11786-91) have sequences deduced from the 3 reading frames, of both strands, of a human activated T-cell cDNA clone (AAT59473) that corresponds to an expressed sequence tag (EST) of the early onset Alzheimer's disease (EOAD) gene. EOAD gene products (see also AAW11768-85 and AAW11792-97) can be expressed in host cells and used to screen for agonists or antagonists useful in EOAD therapy, or to raise antibodies useful in the diagnosis of EOAD or predisposition to EOAD.

(N.B. in-frame stop codons in the 6 reading frames of the cDNA clone are ignored in the translated polypeptide sequences given in
                                                                                                                                                                                                                                                                                                                                                              Chimeric - Bacteria.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease; gamma-secretase; beta-amyloid precursor protein; betaAFPS1; glutathione-S-transferase; GST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 69-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-100161/09
N-PSDB; AAT59473.
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  WPI; 2001-648575/74
                                                     Roberts SB,
                                                                                                   (BRIM ) BRISTOL WYERS SQUIBB CO
                                                                                                                                                     03-APR-2000;
                                                                                                                                                                                                           30-MAR-2001;
                                                                                                                                                                                                                                                              11-00°x-2001.
                                                                                                                                                                                                                                                                                                           ₩0200175435-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS1 loop -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE12901 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-XUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SHLGPHRSTPESRAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 100 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacterial glutathione-S-transferase fusion protein.
                                                  Hendrick JP, Vinitsky A,
                                                                                                                                                                                                           2001WO-US10453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                        2000US-194495P
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Pred. No. 1.5e-08;
Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       betaAPP;
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                                                  Lewis M,
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                                                     Smith DW,
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RESULT 4
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Matches 15
                                                  (HARD ) HARVARD COLLEGE.
                                                                                                                                      16-AUG-1995;
                                                                                                                                                                                    15-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to the field of plaque amyloid deposits that are the hallmarks of Alzheimer's disease. In particular, the invention relates to an isolated, functionally-active protein that has gamma-secretase activity. Gamma-secretase activity is necessary for amyloid production. The present invention also relates to methods for isolating integral-membrane proteins and protein complexes, including the gamma-secretase protein of the invention. The method is useful for monitoring the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the protein contains the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the protein contains the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the protein contains the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the cleavage of beta-amyloid precursor protein (betaAPP) by damma-secretase when the cleavage of beta-amyloid precursor protein (betaAPP) are the cleavage of beta-amyloid precursor protein (betaAPP) and the cleavage of beta-amyloid precursor protein (betaAPP) are the cleavage of beta-amyloid precursor protein (betaAPP) and the cleavage of beta-amyloid precursor protein (betaAPP) and the cleavage of beta-amyloid precursor protein (betaAPP) and the cleavage of beta-amyloid precursor protein (betaAPP) and the cleavage o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel gamma secretase capable of cleaving be amyloid peptide -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354
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Pred. No.
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2.8e-08;
hes 0;
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RESULT 5
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Matches 15
This sequence is the PS1/429 presentilin peptide (II) of the Invention. Cells transformed with the DNA are used to produce recombinant (II) and analogues, useful e.g. as immunogens for generating an immune response against PS1/429. (II) is a new product of the PS1 gene, mutations in which cause Alzheimer's disease (AD). The nucleic acids are
                                                                                                                                                                                                                                              18-JUL-1996;
06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                               apoptosis.
                                                                                     Claim
                                                                                                            DNA encoding presentlin peptide PS1/429 and its analogues - useful for diagnosis and treatment of Alzheimer's disease
                                                                                                                                                     WPI; 1998-042186/04.
N-PSDB; AAV17357.
                                                                                                                                                                                             Chisholm JC,
                                                                                                                                                                                                                                                                                         03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying genes which cause improper chromosome segregation, screening for inhibitors of chromosome missegregation and processe caused by genes encoding chromosome missegregation promoters was exemplified using Alzheimer's disease. The sequences given in AAT87401 to AAT87426 can be used in the above methods. The five mutations indicated in the Peatures Table cosegregate with early-onset familial Alzheimer's disease. It is predicted that these mutations result in increased levels of cells with trisomy 21 in carriers of the mutation compared with non-carriers.
                                                                                                                                                                                                                     (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                    11-DEC-1997
                                                                                                                                                                                                                                                                                                                                             WO9746678-A1
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             Presenilin peptide; | Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS1/429 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW41429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW41429 standard; Protein; 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying genes which cause chromosome missegregation - useful for identifying causes of and treatments for diseases, e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-165297/15.
N-PSDB; AAT87402.
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                             PS1/429; immunogen; immune response; PS1 gen mitochondrial pathology; neurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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Pred. No.
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3.2e-08;
hes 0;
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Best Local
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                                                                                                                                                                                                                                    31-JUL-1995;
28-APR-1995;
28-JUN-1995;
This sequence represents mutated versions of the human presenilin-1-2 protein (see AAW05734 for wild type sequence). AAW05734 represents a different wild type form of presenilin-1 that results from alternate
                                                                                                                                                                                        (HSCR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; mutein.
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                                                             Claim 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
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                                                                                                                                   WPI; 1996-497631/49.
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                                                                                      presenilin genes - useful for diagnosis, therapy and drug
sening of familial Alzheimer's disease, cerebral disorders, etc.
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15; Conserv
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V TORONTO GOVERNING COUNCIL.
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95US-0431048.
95US-0496841.
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253..254
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3.3e-08;
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28-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                     (HSCR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; mutein.
                                                                                                                                                                                   New presenilin genes - useful for screening of familial Alzheimer's
                                                                                                                                                                                                                                                                WPI; 1996-497631/49.
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AAW05736-W05760 represent mutated versions of the human presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a different wild type form of presenilin-1 that results from alternate splicing of the genomic DNA sequence. The presenilins are a family of

Claim

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178pp;

English.

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28-APR-1995;
28-JUN-1995;
            AAW05736-W05760 represent mutated versions of the human presentiin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a different wild type form of presentilin-1 that results from alternate splicing of the genomic DNA sequence. The presentlins are a family of highly conserved integral membrane proteins with a common structural motif, common alternate splicing patterns, and common mutational hot
                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                                                                                                                                              Fraser PE,
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95US-0431048.
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AAW05733 and AAW05734 represent the two different forms of wild type human presentiin-1 (PS-1). This form of presentlin-1 results from alternate splicing of the genomic DNA sequence. AAW05762 represents the coding sequence for wild type human PS-2. The presentlins are a family of highly conserved integral membrane proteins with a common structural methic, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemornhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding these sequences can be used for diagnosis of these diseases. These proteins, or vectors that express them or containing antisense sequences, antibodies selective for mutant forms of these proteins (such as AAW05738) and modulators of PS gene expression are
                                                                                                                                                                                                                     Claim
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28-APR-1995
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                                                                                                                                                                                                                                             screening
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  Matches
                                                                                                                   disease (FAD) patients, 6 late onset sporadic Alzheimer's disease (AD) patients and 4 neurologically normal subjects, indicated that mRNA transcripts of the presentlin 1 gene in samples from various brain regions occur in 2 forms, PS-1-long (containing a VRSQ motif) and PS-1-short (lacking the VRSQ motif, i.e. the protein denoted by the present sequence), and that the PS-1-long levels in hippocampus and frontal cortex samples are significantly lower in FAD patients than in AD and normal subjects.
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                                                                                                                                                                                                                                                                               transcript in a sample of genetic material, where the alternative splice site encodes AAW22944, or detecting AAW22944 in the protein encoded by the mRNA. Tests on 3 early onset familial Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosis of, or susceptibility to neurological disease - specifically Alzheimer's disease, by detecting aberrant splicing in
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                                                                                                                                                                                                                                                                                                                                       Identifying susceptibility to a neurological disease, comprise detecting an alternative splice site in a polyadenylated mRNA
                                                                                                                                                                                                                                                                                                                                                                                                           Example
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(UYSF-) UNIV SOUTH FLORIDA DEPT PSYCHIATRY.
(UNIW ) UNIV WASHINGTON.
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                       Similarity
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Pred. No. 3.6e-08;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mutants of the S182 gene associated with familial disease - and related protein and transgenic animals, models for screening and assessing potential drugs
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                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A 463-amino acid polypeptide (AAW11840) is the product of a full-length cDNA (AAT59536) of an early onset Alzheimer's disease (EOAD) splice variant gene. A 467-amino acid polypeptide (AAW11839) is the product of a full-length cDNA (AAT59535) of the EOAD gene. The 2 polypeptides can be produced in transformed host cells and used to raise antibodies, or to identify antagonist/inhibitor cpds. useful in the treatment of Alzheimer's disease, esp. EOAD.
                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   frameshift mutation; age-related disease; neurodegenerative disorder. Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; alcoholic liver disease; multiple scleros; multiple scleros; alcoholic liver disease; multiple scleros; multiple scleros; multiple scleros; multiple scleros; multiple scleros; multiple scleros; multiple scleros; multiple scleros; multiple scleros; multiple scleros; multiple scleros; multiple scleros; multiple scleros; multiple scleros; multiple scleros; multipl
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frameshift mutation; age-related disease; neurodegenerative disorder;
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N-PSDB; AAT59536.
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13-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SHLGPHRSTPESRAA 15
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                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                              mobility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                          group protein-C; neuroendocrine specific protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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95US-0001142.
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Pred.
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No.
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hes 0;
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RESULT 14
AAW23965
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease, Down's Syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis, alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA mather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated proteins Tau and Big Tau, ubiquitin B, apolipoprotein E microtubule associated protein 2 (MAP2), neurofilament-L, neurofilament-M, neurofilament-F, presenilin II, presenilin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A.
                                                                                                                            Presenilin-1; PS1 gene; human; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; epilepsy; mental retardation; diagnosis; therapy; transgenic animal.
                  Misc-difference
                                                 Misc-difference
                                                                                                Homo sapiens
                                                                                                                                                                                             Human presenilin-1.
                                                                                                                                                                                                                              20-JUL-1998
                                                                                                                                                                                                                                                            AAW23965;
                                                                                                                                                                                                                                                                                          AAW23965 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Figure 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYUT-) RIJKSUNIV UTRECHT.
(ROYA-) ROYAL NETHERLANDS ACAD
(UYRO-) UNIV ROTTERDAM ERASMUS.
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DB; AAX75761.
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                                                Location/Qualifiers
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                                  'note= "Phell7Ser mutation site
                                                                                                                                                                                                                                                                                          Protein; 463 AA.
                                                                                                                                                                                                                                                                                                                                                                        356
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 "Ile439Val mutation site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   el method for the diagnosis of a disea an RNA molecule that has a frameshift
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
3.6e-08;
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(Claim 1)"
                               (Claim 1)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   463;
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RESULT 15
AAW42375
ID AAW42
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AC AAW42
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DT 08-JU
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DE Human
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Matches
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05-JUL-1996;
12-JUL-1996;
08-NOV-1996;
                                                                                                                                                                                                                                                                                                                                        and epilepsy. Use of the nucleic acids and proteins comprising or derived from the presentlins is made in screening and dlagnosing FAD, identifying and developing therapeutics for treatment of FAD, and in producing cell lines and transgenic animals useful as models of FAD. Methods for identifying substances that bind to, or modulate the activity of a presenilin protein, and methods for identifying substances that affect the interaction of a presenilin interacting protein with a presenilin protein are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid sequence was deduced from an isolated cDNA clone (see AAV04667). Another hPS1 sequence (see AAW23964) results from alternative splicing of the hPS1 mRNA transcript. A murine PS1 homologue (see AAW23965) and a human presentlin-2 protein (see AAW23967) are also provided. Mutations in the PS-1 and PS-2 genes are linked to the development in humans of forms of familial Alzheimer's disease (FAD) and may be causative of other disorders, e.g. cognitive, intellectual, neurological or physiological disorders such as cerebral haemorrhage, schizophrenia, depression, mental retardation and epilepsy. Use of the nucleic acids and proteins comprising or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated mutant presentiin-1 genes - useful for developing products for use in detection, diagnosis and therapy of Alzheimer's disease and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide comprises human presentlin-1 (hPS1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 185-186; 238pp; English.
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              Human presenilin I gene product.
                                            08-JUN-1998 (first entry)
                                                                           AAW42375
                                                                                                       AAW42375 standard; Protein; 463 AA.
                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                         Local
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15; Conservative
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96US-0021673.
96US-0021700.
96US-0029895.
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                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                         Score 15;
Pred. No.
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                                                                                                                                                                                                                                          ; DB 19;
. 3.6e-08;
ches 0;
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ID AAY51393
AC AAY51
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XX Human
XX SPE-4
KW SPE-4
KW muscl
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(PS-I) gene product. A novel variant of PS-I encoded by a clone
consisted from a human cerebellar cDNA library contains a 4-amino
control insertion (VRSQ) between residues 26 and 27. This variant
control insertion (VRSQ) between residues 26 and 27. This variant
control insertion (VRSQ) between residues 26 and 27. This variant
control insertion alternative use of a 5' exon donor site in the exon
control in genes associated with Alzhelmer's disease and familial
control in genes associated with Alzhelmer's disease and familial
control in genes associated with Alzhelmer's disease and familial
control in genes associated with Alzhelmer's disease and familial
control in genes associated with Alzhelmer's disease and familial
control in genes associated with alzhelmer's disease (FAD). Methods are provided for
control in genes associated with alzhelmer's disease for a 4-amino acid motif (VRXQ).

control in genes associated with alzhelmer's disease for genes and in genes
control in genes associated for control in genes and familial
control in genes associated with alzhelmer's disease. The presence of these
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Best Local
                                             SPE-4; immunogen; diagnosis; nematode; Alzheimer's disease; brain; muscle; peripheral blood cell; neuroprotectant; nootropic; S182; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding presenelin I - useful for diagnosis disease, drug screening, etc.
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                                                                                                                                                                                                 AAY51393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP. (UYSF-) UNIV SOUTH FLORIDA. (UNIW ) UNIV WASHINGTON.
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    Homo sapiens
                                                                                                                Human S182
                                                                                                                                                         04-MAY-2000
                                                                                                                                                                                                                                          AAY51393 standard; Peptide; 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                    342 SHLGPHRSTPESRAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                            protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                       (first entry)
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Pred. No. 3.6e-08;
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RESULT 17
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Best Local
Immunogenic composition comprising diagnosing Alzheimer's disease -
                                                                          WPI; 2000-146863/13
                                                                                                                       L'Hernau
                                                                                                                                                                                                                                                                                                                                                                       US|6019974-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel immunogenic composition comprising at least 1 antigenic component selected from an antigenic peptide (I) (linked to a carrier) or a multiantigenic peptide (II). The composition is useful for diagnosing or monitoring SPE-4 related protein profiles of nematodes and/or Alzheimer's disease patients, either in postmortem tissue, or from other tissue samples, where the tissue is from the brain muscle or peripheral blood cells. The immunogenic composition can be used to diagnose Alzheimer's noninvasively and has neuroprotective and nootropic activity. This sequence represents the human S182 protein which
                                                                                                                                                                                                                                                                                                                          01\FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        muscle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine
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                                                                                                                                                                           (UYEM-
                                                                                                                                                                                                                           26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY51394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY51394 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L'Hernault SW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nootropic activity. This sequence repre is used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Column 33-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344
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                                                                                                                                                                                                                                                                            (AN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHLGPHRSTPESRAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-146863/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S182 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunogen; diagnosis; nematode; Alzheimer's disease; brain; peripheral blood cell; neuroprotectant; nootropic; S182; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Similarity
15; Conser
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                         an antigenic component, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.
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RESULT 18
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Matches
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          AAW05736-W05760 represent mutated versions of the human presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a different wild type form of presenilin-1 that results from alternate splicing of the genomic DNA sequence. The presenilins are a family of highly conserved integral membrane proteins with a common structural
                                                                                                                                                                                                                                                      31-JUL-1995;
28-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel immunogenic composition comprising at least I antigenic component selected from an antigenic peptide (I) (linked to a carrier) or a multiantigenic peptide (II). The composition is useful for diagnosing or monitoring SPE-4 related protein profiles of nematodes and/or Alzheimer's disease patients, either in postmortem tissue, or from other tissue samples, where the tissue is from the brair muscle or peripheral blood cells. The immunogenic composition can be used to diagnose Alzheimer's noninvasively and has neuroprotective and nootropic activity. This sequence represents the murine S182 protein which is used in the method of the invention.
                                                                                                               New presenilin genes - useful for screening of familial Alzheimer's
                                                                                                                                                     WPI; 1996-497631/49.
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                                                                                                                                                                                                                                             28-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Presenilin-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Presenilin-1-1 C263R mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW05750 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Column 35-40;
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                                                                                       Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465
                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody;
                                                                                                                                                                              Rommens
                                                                                                                                                                                                                    RES & DEV LP
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                                                                                                                                                                                                        TORONTO GOVERNING COUNCIL.
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95US-0431048.
95US-0496841.
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                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 263
                                                                                    178pp;
                                                                                                                                                                                                                                                                                                                                                                        /label= C263R
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MC
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splicing
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                                                                                                                                                                             George-Hyslop
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patterns,
                                                                                                               diagnosis, therapy and drug disease, cerebral disorders,
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hes 0;
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and common mutational
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                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy; mutein
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RESULT 19
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28-APR-1995;
28-JUN-1995;
                        AAW05736-W05760 represent mutated versions of the human presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a different wild type form of presenilin-1 that results from alternate splicing of the genomic DNA sequence. The presenilins are a family of highly conserved integral membrane proteins with a common structural motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral
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AAW05736-W05760 represent mutated versions of the human presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a different wild type form of presenilin-1 that results from alternate splicing of the genomic DNA sequence. The presentlins are a family of highly conserved integral membrane proteins with a common structural motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding the wild type sequences can be used for disgnosis of these diseases. The wild type proteins, or vectors that express them or containing antisense sequences, antibodies selective for these mutant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,MC
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RESULT 21
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Best Local S
Matches 15
           highly conserved integral membrane proteins with a common structural motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding the wild type sequences can be used for diagnosis of these diseases. The wild type proteins, or vectors that express them or containing antisense sequences, antibodies selective for these mutant forms of the proteins and modulators of PS gene expression are
                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1995;
28-APR-1995;
28-JUN-1995;
                                                                                                                                    AAW05736-W05760 represent mutated versions of the human presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a different wild type form of presenilin-1 that results from alternate splicing of the genomic DNA sequence. The presenilins are a family of
                                                                                                                                                                                                                                         New presentiin genes - useful for screening of familial Alzheimer's
                                                                                                                                                                                                                  Claim 3;
                                                                                                                                                                                                                                                                                     WPI; 1996-497631/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Presenilin-1-1 E280A/G mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 SHLGPHRSTPESRAA 360
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15; Conserv
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95US-0496841.
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/note= "X = Ala, Gly"
  for treatment of
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  AD etc.
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RESULT 22
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                             nighly conserved integral membrane proteins with a common structural motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations the DNA encoding the wild type sequences can be used for diagnosis of these diseases. The wild type proteins, or vectors that express them or containing antisense sequences, antibodies selective for these mutant forms of the proteins and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are
                                                                                                                                                                                                                                                                                                                                                                              31-JUL-1995;
28-APN-1995;
28-JUN-1995;
                                                                                                                                                         AAW05736-W05760 represent mutated versions of the human presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a different wild type form of presenilin-1 that results from alternate splicing of the genomic DNA sequence. The presenilins are a family of
                                                                                                                                                                                                                                                   New presentilin genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders,
                                                                                                                                                                                                                             Claim
          for affinity purification
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                      seful as models for drug screening. The antibodies can also
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RESULT 23
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                                          AAW05736-W05760 represent mutated versions of the human presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a clifferent wild type form of presenilin-1 that results from alternate splicing of the genomic DNA sequence. The presentlins are a family of highly conserved integral membrane proteins with a common structural compactific common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial common factor as cerebral containing antisense sequences, antibodies selective for these mutant common for the proteins and modulators of PS gene expression are cuseful as models for drug screening. The antibodies can also be used e.g. common factor affinity purification and in immunoassays.
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Sequence
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28-APR-1995
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                                                                                                                                       Local Similarity
                                                  SHLGPHRSTPESRAA 15
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SHLGPHRSTPESRAA 360
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Alzheimer's disease; cerebral haemorrhage; schizophrenia;
                                                                                                                                                                                                                     467
                                                                                                          Conservative
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/ TORONTO GOVERNING
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95US-0431048.
95US-0496841.
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                                                                                                                                    100.0%;
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                                                                                                                                    Score 15;
Pred. No.
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                                                                                                          Mismatches
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RESULT 26
AAW05759
ID AAW05759
XX AAW057XX
AX AAW05
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KW Prese
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28-APR-1995;
28-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                              splicing of the genomic DNA sequence. The presentiins are a family of highly conserved integral membrane proteins with a common structural motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding the wild type sequences can be used for diagnosis of these diseases. The wild type proteins, or vectors that express them or containing anticons company.
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                      containing antisense sequences, antibodies selective for these mutant forms of the proteins and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for drug screening. The antibodies can also be used e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW05736-W05760 represent mutated versions of the human presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a different wild type form of presenilin-1 that results from alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New presentiin genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                           for affinity purification
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SHLGPHRSTPESRAA
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                                                                                                              15;
                                                                                                                                        Similarity
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                                                                                                              Conservative
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95US-0496841
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                                                                                                           Score 15; DE Pred. No. 3.6
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3.6e-08;
hes 0;
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RESULT 27

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AAW05733
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RESULT 28
AAW05735
ID AAW05
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AC AAW05
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AC AAW05
XX
DT 23-JU
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                                                                                                                                                                                                                                                                                                                                                                            AAW05733 and AAW05734 represent the two different forms of wild type CC human presentilin-1 (PS-1). The form represented by AAW05734 results from CC alternate splicing of the genomic DNA sequence. AAW05762 represents the CC coding sequence for wild type human PS-2. The presentilins are a family of highly conserved integral membrane proteins with a common structural CC motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial CC Alzheimer's disease (AD) and possibly other diseases such as cerebral CC haemorrhage, schizophrenia, depression etc., so detection of mutations in CC the DNA encoding these sequences can be used for diagnosis of these CC diseases. These proteins, or vectors that express them or containing CC antisense sequences, antibodies selective for mutant forms of these CC potentially useful for treatment of AD etc. Transgenic animals are useful CC as models for drug screening. The antibodies can also be used e.g. for CC affinity purification and in immunoassays.
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Best Local Similarity
Matches 15; Conserv
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                                           AAW05735;
                                                                           AAW05735 standard; Protein; 467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 128-130; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New presenilin genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders, etc.
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    23-JUL-1997
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28-APR-1995)
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V TORONTO GOVERNING COUNCIL.
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                                                                                                                                                                                                                                                                  Conservative
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  (first entry)
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95US-0431048.
95US-0496841.
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                                                                                                                                                                                                                                                                                   100.0%;
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Pred. No. 3.6e-08;
                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                     Length 467;
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Matches 15
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Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
                                                                                                 23-JUL-1997
                                                                                                                                         AAW05736;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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28-APR-1995
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                                                                                                                                                                                                                                                                              346 SHLGPHRSTPESRAA
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 15; Conserv
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This sequence represents the wild type murine presentlin-1.

CC AAW05733 and AAW05734 represent the two different forms of wild type
CC human presentlin-1 (PS-1). The form represented by AAW05734 results from
CC alternate splicing of the genomic DNA sequence. AAW05762 represents the
CC coding sequence for wild type human PS-2. The presentlins are a family
CC of highly conserved integral membrane proteins with a common structural
CC spot regions. Mutations in PS genes are implicated in familial
CC Alzheimer's disease (AD) and possibly other diseases such as cerebral
CC the DNA encoding these sequences can be used for diagnosis of these
CC diseases. These proteins, or vectors that express them or containing
CC antisense sequences, antibodies selective for mutant forms of these
CC potentially useful for treatment of AD etc. Transgenic animals are useful
CC as models for drug screening. The antibodies can also be used e.g. for
CC affinity purification and in immunoassays.
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Presenilin-1-1 A79X mutation.
                                                                                                                                                                                      AAW05736 standard; Protein; 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New presenilin genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser PE, Rommens JM,
                                                                                                                                                                                                                                                                                                                                                                                              1 SHLGPHRSTPESRAA 15
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UNIV TORONTO GOVERNING COUNCIL.
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                                                           (first entry)
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95US-0496841.
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Pred. No.
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3.6e-08;
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Best Local
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                                                                                                                                                                                                                                                                                           highly conserved integral membrane proteins with a common structural motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations ithe DNA encoding the wild type sequences can be used for diagnosis of these diseases. The wild type proteins, or vectors that express them or containing antisense sequences, antibodies selective for these mutant forms of the proteins and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for drug screening. The antibodies can also be used e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-1995;
28-APR-1995;
28-JUN-1995;
                     Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
                                                                             23-JUL-1997
                                                                                                   AAW05737
          depression;
                                                      Presenilin-1-1 V82L mutation
                                                                                                                           AAW05737
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW05736-W05760 represent mutated versions of the human presenilin-1-protein (see AAW05734 for wild type sequence). AAW05734 represents a different wild type form of presenilin-1 that results from alternate splicing of the genomic DNA sequence. The presenilins are a family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3;
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Modified-site
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                                                                                                                                                                                                      1 SHLGPHRSTPESRAA 15
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15; Conserv
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                                                                                                                          standard; Protein; 467
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V TORONTO GOVERNING COUNCIL.
         antibody; gene expression modulator; therapy; mutein
                                                                                                                                                                                                                             Conservative
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                                                                             (first entry)
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95US-0431048.
95US-0496841.
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                                                                                                                                                                                                                                       100.0%;
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3.6e-08;
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                                                                                                                                                                   RESULT 31
AAW05738
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                                                    Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
                    Homo sapiens
                                         depression; antibody; gene expression modulator; therapy; mutein.
                                                                                       Presenilin-1-1 V96F mutation.
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AAW05736-W05760 represent mutated versions of the human presenilin-1-1 CC protein (see AAW05733 for wild type sequence). AAW05734 represents a CC different wild type form of presenilin-1 that results from alternate splicing of the genomic DNA sequence. The presenilins are a family of highly conserved integral membrane proteins with a common structural cc motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial CC Alzheimer's disease (AD) and possibly other diseases such as cerebral chaemorrhage, schizophrenia, depression etc., so detection of mutations in CC the DNA encoding the wild type sequences can be used for diagnosis of the pank encoding the wild type spences can be used for diagnosis of containing antisense sequences, antibodies selective for these mutant CC containing antisense sequences, antibodies selective for these mutant corrections of the proteins and modulators of PS gene expression are useful as models for drug screening. The antibodies can also be used e.g. for earlier and in immonsease.
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28-APR-1995;
28-JUN-1995;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page -; 178pp; English.
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                                                           for affinity purification
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UNIV TORONTO GOVERNING
467
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Matches
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Best Local
23-JUL-1997
                                 AAW05738 standard; Protein;
                AAW05738;
                                                                           346 SHLGPHRSTPESRAA
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                                                                                                            l Similarity
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3.6e-08;
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Location/Qualifiers

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AC AAW0
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DT 23-J
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Best Local S
Matches 15
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28-APR-1995;
28-JUN-1995;
                                                                                                                                                                            Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; mutein.
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                                                                                                                                                                                                                                                                                           Presenilin-1-1 Y115H mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rommens JM,
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95US-0431048.
95US-0496841.
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/label= V96F
                                                                           Location/Qualifiers
                           /label= Y115H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15; DB 17;
Pred. No. 3.6e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNCIL
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Best Local S
Matches 15
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28-APR-1995;
28-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New presenilin genes - useful for screening of familial Alzheimer's
                                                                                                                                      Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; mutein.
                                                                                                                                                                                                 Presenilin-1-1 M139T/V mutation.
                                                                                                                                                                                                                            23-JUL-1997
                                                                                                                                                                                                                                                         AAW05740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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(UTOR ) UNIV TORONTO GOVERNING
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                                                                                                              Homo
                                                                     odified-site
                                                                                                                                                                                                                                                                                                                                                           346 SHLGPHRSTPESRAA 360
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15; Conserv
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95US-0431048.
95US-0496841.
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                                                                     Location/Qualifiers
                                          /note- "X - Thr, Val'
                                                      /label- M139X
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Pred. No. 3.6e-08;
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W09634899-A2

AD;

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RESULT 34
AAW05741
ID AAW057
XX AAW05
XX AAW05
XX AAW05
XX AAW05
XX AAW05
XX Prese
XW Prese
XW Prese
XW Famil
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XX W096:
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28-APR-1995;
28-JUN-1995;
                                                                                                                                                                                                                                                                                                                               Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; mutein.
  29-APR-1996;
                                                          31-OCT-1996.
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                                                                                                                                                                                                                                                                                 Homo sapiens
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V TORONTO GOVERNING COUNCIL.
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95US-0431048.
95US-0496841.
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                                                                                                                                                                                               Location/Qualifiers 143
                                                                                                                                                                     /label= I143T
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Pred. No.
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RESULT 35
AAW05742
ID AAW05742
AC AAW05
AC AAW05
XX DT 23-JU
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KW Prese
KW Famill
KW depre
OS Homo
XX Key.
FT Modif
FT W0463
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31-JUL-1995;
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28-APR-1995;
28-JUN-1995;
                               29-APR\1996;
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                                                                                                                                                                                                                                                                                                       Presenilin-1-1 M146L/V mutation.
                                                                                                                                                                                                                                                                                                                                      23-JUL-1997
                                                                                                                                                            Modified-site
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15; Conserv
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UNIV TORONTO GOVERNING COUNCIL.
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95US-0431048.
95US-0496841.
                               96WO-CA00263
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                                                                                                                                             /label= M146X
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Pred. No.
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RESULT 36
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Best Local
 31-JUL-1995;
28-APR-1995;
28-JUN-1995;
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                                                            29-APR-1096;
                                                                                        31-oct
                                                                                                                      W09684099-A2
                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                        depression;
                                                                                                                                                                                                                                                                                    Presenilin-1; human;
                                                                                                                                                                                                                                                                                                                Presenilin-1-1 H163R/Y mutation.
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28-JUN-1995;
                                                                                                                                                                                                                                                                   Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 SHLGPHRSTPESRAA 360
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UNIV TORONTO GOVERNING COUNCIL.
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 95US-0509359.
95US-0431048.
95US-0496841.
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95US-0496841.
                                                            96WO-CA00263
                                                                                                                                                                               Location/Qualifiers 163
                                                                                                                                                /label= H163X
/note= "X = Arg, Tyr"
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                                                                                                                                                                                                                                                       gene
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                                                                                                                                                                                                                                                       expression modulator;
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Pred. No.
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3.6e-08;
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RESULT 37
AAW05744
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                                        31-JUL-1995;
28-APR-1995;
28-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page -; 178pp; English.
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                                                                                                                                                                                                                                                                            Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                 23-JUL-1997
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(HSCR-) HSC RES & DEV LP.
                                                                                             29-apr-1996;
                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                               depression;
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                                                                                                                                                                                                                                                               antibody; gene expression modulator; therapy; mutein
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95US-0431048
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                                                                                                                                                                              /label= L171P
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Pred. No. 3.6e-08;
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RESULT 38
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28-APR-1995;
28-JUN-1995;
                            Fraser PE,
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                                                                                                                                                                                                                                                                                  29-APR-1/996;
                                                                                                                                                                                                                                                                                                                                      31-OCT\1996
                                                                                                                                                                                                                                                                                                                                                                                             W09634099-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                (HSCR-) HSC RES & DEV LP.
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                            Rommens JM,
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                       St George-Hyslop PH;
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Pred. No.
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Best Local
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28-APR-1995;
28-JUN-1995;
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                                                             WPI; 1996-497631/49
                                                                                                                       Fraser PE,
                                                                                                                                                                           (HSCR-) HSC RES & DEV LP.
(UTOR ) UNIV TORONTO GOVERNING
                                                                                                                                                                                                                                                                                                                                                                                            29-APR 1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Presenilin-1-1 I211T mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New presenilin genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-497631/49.
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                                                                                                                    Rommens JM,
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95US-0431048.
95US-0496841.
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New presentlin genes -

useful for diagnosis, therapy and drug

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RESULT 40
AAW05747
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28-APR-1995;
28-JUN-1995;
Claim 3; Page -; 178pp; English
                                                     New presentlin genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders,
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                                                                                                                                                                                                                                                 RES & DEV LP.
V TORONTO GOVERNING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody;
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                                                                                                                                                                                              George-Hyslop
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                                                                                                                                                                                                                                                    COUNCIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy;
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                                                        etc.
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RESULT 41
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                                                                                                                                                                                                       31-JUL-1995;
28-APR-1995;
28-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzhelmer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding the wild type sequences can be used for diagnosis of these diseases. The wild type proteins, or vectors that express them or containing antisense sequences, antibodies selective for these mutant forms of the proteins and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for drug screening. The antibodies can also be used e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW05736-W05760 represent mutated versions of the human presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a different wild type form of presenilin-1 that results from alternate splicing of the genomic DNA sequence. The presenilins are a family of highly conserved integral membrane proteins with a common structural
                                                                                                                                                               (HSCR-)
                                     Claim 3; Page -; 178pp; English.
                                                                 screening
                                                                                                                                        Fraser PE,
                                                                                                                                                                                                                                                                29-APR-1996
                                                                                                                                                                                                                                                                                          31-OCT-1996
                                                                                                                                                                                                                                                                                                                    W09634099-A2
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                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                 depression; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Presenilin-1-1 A246E mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW05748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW05748 standard; Protein; 467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 SHLGPHRSTPESRAA
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                                                                                                                                                                                                                                                                                                                                                              ified-site
                                                                  presenilin genes - useful for
eening of familial Alzheimer's
                                                                                                            1996-497631/49.
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15; Conserv
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UNIV TORONTO GOVERNING COUNCIL.
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                                                                                                                                     Rommens JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression modulator;
                                                                                                                                     St George-Hyslop
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Pred. No. 3.6e-08;
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                                                                  diagnosis, therapy and drug disease, cerebral disorders,
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AAW05736-W05760 represent mutated versions of the human presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a

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AAW05749
ID AAW05749
XX AAW05749
AC AAW05
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28-APR-1995;
28-JUN-1995;
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AAW05736-W05760 represent mutated versions of the human presenilin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 represents a different wild type form of presenilin-1 that results from alternate splicing of the genomic DNA sequence. The presenilins are a family of highly conserved integral membrane proteins with a common structural
                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-QCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Presenilin-1-1 A260V mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 SHLGPHRSTPESRAA
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                                                                                                                                                                                                               presenilin genes - useful for diagnosis, therapy and drug sening of familial Alzheimer's disease, cerebral disorders
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                                                                                                                                                                                                                                                                                                 1996-497631/49
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15; Conserv
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nilarity 100.
Conservative
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V TORONTO GOVERNING
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                                                                                                                                                                                                                                                                                                                                                      JM,
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                                                                                                                                                             English
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                                                                                                                                                                                                                                                                                                                                                   St George-Hyslop PH
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                                                                                                                                                                                                                 cerebral disorders,
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RESULT 43
AAW27177
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Best Local S
Matches 15
           The present sequence represents the human mutant S182 gene, PS1, product. Mutant PS1 produces a gene product that increases the probability of Alzheimer's disease. A nucleic acid sequence able to hybridise to sequences coding for a mutant PS1 polypeptide can be used as probes for diagnosing an increased likelihood of contracting Alzheimer's disease. Antibodies against the mutant polypeptide can also be used for this purpose. Vectors containing or expressing a nucleic acid molecule, protein or antibody specific for mutant PS1 can be administered to a patient to reduce the likelihood, or delay the onset, of Alzheimer's disease, e.g. anti-sense RNA expression can be used to decrease expression of the PS1 peptide. Transgenic animals expressing the Alzheimer's disease protein can be used to test candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      motif, common alternate splicing patterns, and common mutational hot spot regions. Mutations in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of mutations in the DNA encoding the wild type sequences can be used for diagnosis of these diseases. The wild type proteins, or vectors that express them or containing antisense sequences, antibodies selective for these mutant forms of the proteins and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for drug screening. The antibodies can also be used e.g. for affinity purification and in immunoassays.
                                                                                                                                                                                                                                                                    Chromosome 14 early-onset familial Alzheimer's disease gene PS1 mutants - useful for diagnosing likelihood of developing Alzhei disease, also anti-sense sequences, antibodies and vaccines to
                                                                                                                                                                                                                         Claim
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N-PSDB; AAT85333.
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31-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-1996;
31-AUG-1995
                                                                                                                                                                                                              Alzheimer's disease protein can be used to test candidate therapeutics and to investigate the normal role of PS1. The PS1 peptide may also be included in pharmaceutical compositions (vaccines) for Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chromosome 14 early-onset familial Alzheimer's disease gene PS1 mutants - useful for diagnosing likelihood of developing Alzheimer's disease, also anti-sense sequences, antibodies and vaccines to delay
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                                                                                                                                                                                           disease therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 72-73;
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                                                  Score 15; DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A 467-amino acid polypeptide (AAW11839) is the product of a full-length cDNA (AAT59535) of the early onset Alzhelmer's disease (EOAD) gene. A 463-amino acid polypeptide (AAW11840) is the product of another full-length cDNA (AAT59536) of an EOAD splice variant gene. The 2 polypeptides can be produced in transformed host cells and used to raise antibodies, or to identify antagonist/inhibitor cpds., useful in the treatment of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Early onset Alzheimer's disease; EOAD; neurodegenerative disease; diagnosis; therapy; inhibitor; antagonist; antibody.
                           13-OCT-1998
                                                                                AAW56770;
                                                                                                                                   AAW56770 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease, esp. EOAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Early onset Alzheimer's disease gene - useful for diagnosing a pre-disposition to Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-118980/11.
N-PSDB; AAT59535.
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13-JUL-1995;
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                                                                                                                                                                                                                                                                      346 SHLGPHRSTPESRAA
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15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 AA;
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95US-0001142
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Pred. No. 3.6e-08;
Mismatches 0;
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06-SEP-1996;
25-OCT-1996;
                                                                                                               Presenilin-1; PS1 gene; human; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; epilepsy; mental retardation; diagnosis; therapy; transgenic animal.
        Domain
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                                                                                                    Homo sapiens
                                                                                                                                                Human presenilin-1
                                                                                                                                                                20-JUL-1998
                                                                                                                                                                                AAW23964;
                                                                                                                                                                                              AAW23964 standard; Protein;
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human serum protease protein(s) - used diagnosing pre-disposition to Alzheimer's disease, etc.
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                                                                                                                                                                                                                                                                                                               sequence is that of of presenilin PS-1 the cloning and isolation of the serine
                                                                                                                                                                                                                                     SHLGPHRSTPESRAA 360
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96US-0025436.
96US-0027873.
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        /label= TM2
/note= "transmembrane
155..163
                                    /label= TM1-2
/note= "hydrophilic
                                                             /label= TM1
/note= "transmembrane
                                                                                   Location/Qualifiers
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Pred. No.
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Misc-difference 171
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177
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164..1
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                                                                                                                                                                                                                                                                                              /note= "Asp257Ala mutation site, residue 258-290 deletion
                                                                                                                                                                                                                                                                                                                                                                         /label= TM6-7
/note= "hydrophilic
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/note= "hydrophilic
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/note=_"hydrophilic
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/note= "transmembrane
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/note= "hydrophilic
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                                                                                                                                                                                                                                                                                                                                    note= "Phell7Ser mutation site
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                                                                                                                                                                                                           "Ala260Val mutation
                                                                                                                                                                                                                                          "Met146Leu mutation
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       "Val96Phe mutation site"
                      "Val82Leu mutation site"
                                                   "Cys410Tyr
                                                                   "Leu392Val mutation
                                                                                   "Leu322Val
                                                                                                 "Leu286Val
                                                                                                                 "Ala285Val
                                                                                                                                "Glu280Gly mutation
                                                                                                                                                "Glu280Ala mutation
                                                                                                                                                               "Pro267Ser
                                                                                                                                                                             "Pro264Leu mutation
                                                                                                                                                                                           "Cys263Arg mutation
                                                                                                                                                                                                                            "Leu171Pro mutation
                                                                                                                                                                                                                                                                        "residue 258-290 deletion mutant, associated with Asp257Ala mutation (Claim 1)"
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02-JAN-1997;
05-JUL-1996;
12-JUL-1996;
08-NOV-1996
                                                                                                         and epilepsy. Use of the nucleur during any particles and diagnosing derived from the presentlins is made in screening and diagnosing FAD, identifying and developing therapeutics for treatment of FAD, and in producing cell lines and transgenic animals useful as models of FAD. Methods for identifying substances that bind to, or
                                                                                                                                                                                                                                                                                                      This polypeptide comprises human presentlin-1 (hPS1). Its amino acid sequence was deduced from an isolated cDNA clone (see AAV04666). Another hPS1 sequence (see AAW23965) results from alternative splicing of the hPS1 mRNA transcript. A murine PS1 homologue (see AAW23966) and a human presentlin-2 protein (see AAW23967) are also provided. Mutations in the PS-1 and PS-2 genes are linked to the development in humans of forms of familial Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HSCR-) HSC
(UTOR ) UNIV
                                                             modulate the activity of a presenilin protein, and methods for identifying substances that affect the interaction of a presenilin interacting protein with a presenilin protein are a
                                                                                                                                                                                                                (FAD) and may be causative of other disorders, e.g. cognitive, intellectual, neurological or physiological disorders such as cerebral haemorrhage, schizophrenia, depression, mental retardation and epilepsy. Use of the nucleic acids and proteins comprising or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 180-182; 238pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated mutant presenilin-1 genes - useful for developing products for use in detection, diagnosis and therapy of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W00801549-A2
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  467 AA
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V TORONTO GOVERNING COUNCIL.
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96US-0021700.
96US-0029895.
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146
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163
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231
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211
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139
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246
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209
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26..29
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384
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291..319
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RESULT 48
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                        Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                             Presenilin-1; PS1 gene; mouse; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; epilepsy; mental retardation; diagnosis; therapy; transgenic animal.
       WO9801549-A2
                              Misc-difference
                                             Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 82..100
                      /note-
                                                                         /label= TM6-7
/note= "hydrophilic loop"
                                                                                                                                                                                                                                                                                                                 /label= TM1-2
/note= "hydrophilic loop"
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                                                                                                                                                                     note- "hydrophilic loop'
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                                                                                                                                                                                                                                                                   /label= TM2-3
/note= "hydrophilic loop"
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                                     'note- "Phe177Ser mutation site
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'note= "transmembrane domain
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note= "hydrophilic loop"
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                      "Ile439Val mutation
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Pred. No. 3.6e-08;
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                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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05-JUL-1996;
12-JUL-1996;
08-NOV-1996;
                                                                                                                               Presenilin peptide; PS1/429; immunogen; immune response; PS1 gen Alzheimer's disease; mitochondrial pathology; neurodegeneration; apoptosis; PS1/467.
                             03-JUN-1997;
    18-JUL-1996;
                                                      11-DEC-1997
                                                                                W09746678-A1
                                                                                                        Homo sapiens
                                                                                                                                                                                  PS1/467 protein.
                                                                                                                                                                                                           04-JUN-1998
                                                                                                                                                                                                                                      AAW41430
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated mutant presenilin-1 genes - products for use in detection, diagnosis
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V TORONTO GOVERNING
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96US-0021673.
96US-0021700.
96US-0029895.
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                             97WO-US09272.
    96US-0683315
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Pred. No.
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3.6e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for developing and therapy of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                    Length 467;
                                                                                                                                                      PS1 gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crisis sequence is the PS1/467 presentlin peptide. This sequence is CC specifically stated as not being in the nucleic acid of the invention, CC which encodes the PS1/429 presentlin peptide PS1/429 (II). Cells CC transformed with the DNA are used to produce recombinant (II) and CC analogues, useful e.g. as immunogens for generating an immune response against PS1/429. (II) is a new product of the PS1 gene, mutations in CC which cause Alzheimer's disease (AD). The nucleic acids are generally CC useful as probes for detection and quantification of PS1/429, and CC particularly for diagnosis of AD, especially the target sequences that CC particularly for diagnosis of AD, especially the target sequences that CC particularly for diagnosis are isolated for sequencing. Antibodies (Ab) can also be used to identify epitopes and for affinity purification of CC also be diagnosed at the protein level using Ab as immunoassay reagents. CC Ab can also be used to identify epitopes and for affinity purification of CC of the PS1/429 gene, and both nucleic acids and peptides are useful as size markers in electrophoresis, chromatography etc. The transgenic computation are used as models for AD, e.g. for testing drugs. Regulators of the PS1/429 gene or polypeptide can be used to treat e.g. Ab or diseases involving mitochondrial pathology, apoptosis and neurodegeneration. CC Typical regulators are antisense sequences, ribozymes, aptamers, CC synthetic or natural compounds. (II) may also be used to target other coding sequences to particular cellular locations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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(FARB ) BAYER CORP.
                                                                                 18-JUL-1996;
06-JUN-1996;
                                                                                                                                                                             03-JUN\1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis; PS1/467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Presenilin peptide; PS1/429; immunogen; Alzheimer's disease; mitochondrial path
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DB; AAV17358.
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15; DB Pred. No. 3.6); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.6e-08;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune response; PS1 gene;
plogy; neurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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0;

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RESULT 51
AAY24419
ID AAY24
XX
AC AAY24
XX
DT 23-SE
XX
DT 23-SE
XX
Press
OS Homo
XX
Phomo
XX
PD 15-J1
XX
PR 07-J1
XX
PR 08-J
XX
PR 08-J
XX
PR WPI;
DR N-PS
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Muta
PT Muta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC specifically stated as not being in the nucleic acid of the invention, cwhich encodes the PS1/429 presentlin peptide PS1/429 (II). Cells children encodes the PS1/429 presentlin peptide PS1/429 (II) cells contained with the DNA are used to produce recombinant (II) and canalogues, useful e.g. as immunogens for generating an immune response against PS1/429. (II) is a new product of the PS1 gene, mutations in CC which cause Alzheimer's disease (AD). The nucleic acids are generally cuseful as probes for detection and quantification of PS1/429. (CO particularly for diagnosis of AD, especially the target sequences that CC hybridise with probes are isolated for sequencing. Antibodies (AD) can calso be diagnosed at the protein level using Ab as immunoassay reagents. Ab can also be used to identify epitopes and for affinity purification of peptides. Antisense nucleic acid may also be used to regulate expression compounds are used as models for AD, e.g. for testing drugs. Regulators of the PS1/429 gene, and both nucleic acids and peptides are useful as compounds are used as models for AD, e.g. for testing drugs. Regulators of the PS1/429 gene or polypeptide can be used to treat e.g. AD or diseases involving mitochondrial pathology, apoptosis and neurodegeneration. CC synthetic or natural compounds. (II) may also be used to target other coding sequences to particular cellular locations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                              WPI; 1999-430307/36.
N-PSDB; AAX90184.
                                                                                                                                                                      07-JAN-1999;
                                                                                                                                                                                                                                                                                                  Presenilin-1;
                                                                                                                                                                                                                                                                                                                                 Human presenilin-1.
                                                                                                                                                                                                                                                                                                                                                                23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                               AAY24419;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY24419 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
 Mutant presenilin-1 gene-introduced animals, useful as model animals
                                                                              Takeda J,
                                                                                                           (DAUC ) DAIICHI PHARM CO LTD
                                                                                                                                        08-JAN-1998;
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                                                                                                                                                                                                                                     WOQ934670-A1
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 SHLGPHRSTPESRAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding presentlin peptide PS1/429 and its analogues - useful diagnosis and treatment of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHLGPHRSTPESRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Fig 3; 77pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                              Takeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                   mutation;
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                                                                                                                                        98JP-0002191
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                                                                                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                                                                                  gene mutant
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Pred. No.
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                                                                                                                                                                                                                                                                                                   animal;
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1.6e-08;
                                                                                                                                                                                                                                                                                                  Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 467;
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RESULT 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant presentilin gene. The mutant presentlin gene causes amino acid substitutions at 1 or more positions of 79, 82, 96, 115, 120, 135, 139, 143, 146, 163, 209, 213, 231, 235, 246, 250, 263, 264, 267, 269, 280, 285, 286, 290, 318, 384, 392, 410, 426 and 436, with corresponding N-terminals being e.g. A79V, V82L, A426 and P436S, particularly by replacing isoleucine of position 213 by another amino-acid especially threonine. The gene mutant animals e.g. mice can be used as model animals for the study of human Alzheimer's diseases and to screen and evaluate substances as candidates for prevention and/or therapy of Alzheimer's diseases in patients. They can over-produce amyloid beta protein by the presention-1 gene to cause nerve cell death or pathologically close to human patients with Alzheimer's diseases. The pathologically close to human patients with Alzheimer's diseases. The
                                                                                                                                                                                                                    Mutant presenilin-1 gene-introduced animals, useful as model animals for study of Alzheimer's diseases in human and screening substances for prevention and/or treatment of the diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JAN 1999;
                                                                                                                                                                                                                                                                                                                                  WPI; 1999-430307/36.
N-PSDB; AAX90185.
                                                                                                                                                                                                                                                                                                                                                                                                                     Takeda J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Presenilin-1; mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DAUC ) DAIISHI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY24420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY24420 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse presenilin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 SHLGPHRSTPESRAA
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15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                     Takeda M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 51-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98JP-0002191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-JP00015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.08;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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The present invention describes a gene mutant animal having a non-human mutant presentilin gene. The mutant presentilin gene causes amino acid substitutions at 1 or more positions of 79, 82, 96, 115, 120, 135, 139, 143, 146, 163, 209, 213, 231, 235, 246, 250, 260, 263, 264, 267, 269, 280, 285, 286, 290, 318, 384, 392, 410, 426 and 436, with corresponding

Disclosure;

Page 54-56; 64pp; Japanese

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RESULT 53
AAY23897
ID AAY23
AC AAY23
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                                                                                          The present sequence represents wild type human presenilin 1 (PS1) protein. The specification describes a method for identifying substances that alter the interaction of a presenilin with a presentlin-binding protein. The method comprises contacting the interacting domain of a presenilin protein to a presenilin-binding protein in the presence of a test substance, and measuring the interaction of the presenilin and the presenilin-binding protein. The method can be used to screen individuals for presentlin alleles associated with Alzheimer's disease and related disorders, such as senile dementia's, psychiatric diseases such as schizophrenia and depression, and neurological disease, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-terminals being e.g. A79V, V82L, A426 and P436S, particularly by replacing isoleucine of position 213 by another amino-acid especially threonine. The gene mutant animals e.g. mice can be used as model animals for the study of human Alzheimer's diseases and to screen and evaluate substances as candidates for prevention and/or therapy of Alzheimer's diseases in patients. They can over-produce amyloid beta protein by the presentiin-1 gene to cause nerve cell death or peeling off in the hippocampus earlier. Such animals are being pathologically close to human patients with Alzheimer's diseases. The present sequence represents mouse presentlin-1, as given in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; presenilin 1; PS1; presenilin-binding protein; presenilin allele; Alzheimer's disease; senile dement: psychiatric disease; schizophrenia; depression; neuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying substances that alter presenilin interactions, useful for screening individuals for presenilin alleles associated with Alzheimer's disease - useful for diagnosis of Alzheimer's diseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser PE)
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dementia;
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                                                                                  The present sequence represents a human presentlin I (PSI) polypeptide. Human Neural Plakophilin Related Armidillo Protein (hNPRAP) polypeptide is known to interact with PSI and PS2. The specification describes a method for stimulating the growth of nerve cells, comprising contacting them with hNPRAP. The hNPRAP polypeptide and polynucleotide are useful for treating nerve damage caused by a variety of diseases or physical traumas, including Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS), multiple sclerosis, stroke, ischemia associated with stroke, neural paropathy, motor neuron diseases, sciatic crush, peripheral neuropathy, neuropathy associated with diabetes, spinal cord injuries and facial nerve crush.
                                                                                                                                                                                                                                                                                             Stimulation of nerve cell growth using human Neural Plakophilin Related Armidillo Protein (hNPRAP) polypeptide, useful for the treatment of diseases such as Alzheimer's, Parkinson's, and stroke -
                                                          Sequence
                                                                                                                                                                                                                                                                  Disclosure; Page 19-20; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; presenilin; PS1; PS2; nerve cell growth; nerve damage; hNPRAP; neural plakophilin related armidillo protein; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; ALS; stroke; multiple sclerosis; ischemia; stroke; neural paropathy; sciatic crush;
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                                                           467 AA;
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nerve crush.
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               Score 15; DB 21;
Pred. No. 3.6e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying presentilin or catenin p120 activity modulator useful modulating presentilin-catenin p120 interaction and thus for treat cognitive disorder e.g., Alzheimer's disease comprises enhancing cognitive function -
                                                                                                                                                                                                                               AAG63936 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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KIAA0253; presenilin; Alzheimer's disease
                                                        Amino acid sequence of human presenilin 1.
                                                                                                                    29-OCT-2001
                                                                                                                                                                         AAG63936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 41-42; 48pp;
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DB; AAD18120.
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Pred. No. 3.6e-08;
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Best Local S
Matches 15
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            10-JAN-2000;
                                                                  08-JAN-2001;
                                                                                                                           19-JUL-
                                                                                                                                                                                    WO200151671-A2
                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                    nerve
                                                                                                                                                                                                                                                                                                                            NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralysis; peripheral neuropathy; motorneuron disorder; neurodegenerative disorder; parkinson's disease; Mentere's disease; multiple sclerosis; Bell's paley; Huntington's chorea; Down's syndrome; amyotrophic lateral sclerosis; ALS;
                                                                                                                                                                                                                                                                                                                                                                                                                Human; Par-4; presenilin; PS1; neuroprotective; nuclear factor kappa I NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human presenilin (PS1) protein.
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2000US-0175200
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                                                                                                                                                                                                                                                                                                Alzheimer's disease; epilepsy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human Par-4 protein, presenilin protein (PS1 and PS2) and their corresponding DNA molecules. The invention also relates to a method for identifying inhibitors of neuronal degeneration, comprising cotransfecting eukaryotic host cells expressing presentlin (PS), with a Par-4 DNA, and an NF-kappa B dependent reporter construct, exposing the cotransfected cells to a candidate molecule and monitoring the ability of the candidate molecule to induce NF-kappa B activation. Presentlin proteins participates in nuclear factor kappa B (NF-kappa B) signalling and activation. The inhibitors of neuronal degeneration are useful for treating neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and also for treating neurodegeneration and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the proteins and the prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating peripheral neuropathies, motorneuron disorders such as amyotrophic lateral sclerosis (ALS), Bell's palsy and various conditions involving spinal muscular atrophy and paralysis. The present sequence
     08-JAN-2001; 2001WO-US00526
                                                           19-JUL-2001
                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human presentlin PS1-FAD mutant M146V.
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                                                                                                                 WO200151671-A2
                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is human presenilin (PS1) protein.
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15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ā,
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                  /note= "Wild type Met substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
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thes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 467;
                                                                                                                                                                    Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huntington's and also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cc relates to a method for identifying inhibitors of neuronal degeneration, cc comprising cotransfecting enkaryotic host cells expressing presentlin cc (PS), with a Par-4 DNA, and an NF-kappa B dependent reporter construct, cc exposing the cotransfected cells to a candidate molecule and monitoring ct the ability of the candidate molecule to induce NF-kappa B activation. Cc Presentlin proteins participates in nuclear factor kappa B (NF-kappa B) cc signalling and activation. The inhibitors of neuronal degeneration care useful for treating neurodegenerative disorders such as Alzhelmer's cdisease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, Meniere's disease and also for treating peripheral neuropathies, motorneuron disorders such as cc amyotrophic lateral sclerosis (ALS), Bell's palsy and various conditions in human presentlin psl-FAD (familial Alzheimer's disease) mutant. Cc Note: This sequence is not shown in the specification but is derived from chuman presentlin (PSI) protein [SEQ ID NO: 4] shown in page 60-61 of the specification (AAE05466).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                           huntington's ch
nerve deafness;
                                                                                                                                                                                           Human; Par-4; presentiti; rat, neuronal muscular atrophy; paralysis; NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralysis; peripheral neuropathy; motorneuron disorder; neurodegenerative disorder; peripheral neuropathy; motorneuron disorder; neuropathy; motorneuron disorder; neuropathy; palsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying inhibitors of neuronal degeneration useful for treating e.g. Alzheimer's disease, by determining the ability of a compound induce nuclear factor kappa B activation, with the involvement of presentlin or Par-4
                                                                                                        Synthetic
                                                                                                                                                                                                                               Human; Par-4; presenilin; PS1; neuroprotective; nuclear factor kappa NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralysis
                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                             AAE05564 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-451872/48
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04-JAN-2001;
                                                       Misc-difference
                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                       24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mccarthy J, Cordell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SCIO-) SCIOS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 SHLGPHRSTPESRAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS2) and their corresponding
                                                                                                                                                                                                                                                                                    presenilin PS1-FAD mutant E280G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
15; Conserv
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                                                                                                                                                                              chorea;
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2001US-0754949.
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates to human Par-4 protein, presenilin protein their corresponding DNA molecules. The invention als
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                   Location/Qualifiers 280
                                                                                                                                                           orea; Down's
Alzheimer's
                                  /note= "Wild type Glu substituted with Gly"
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                                                                                                                                                          syndrome; amyotrophic lateral sclerosis;
disease; epilepsy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                               467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              derived from 50-61 of the
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WO200151671-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human Par-4 protein, presentlin protein (PS1 CC and PS2) and their corresponding DNA molecules. The invention also CC relates to a method for identifying inhibitors of neuronal degeneration, CC comprising cotransfecting eukaryotic host cells expressing presentlin (CC exposing the cotransfected cells to a candidate molecule and monitoring CC exposing the cotransfected cells to a candidate molecule and monitoring CC the ability of the candidate molecule to induce NF-kappa B activation. CC Presentlin proteins participates in nuclear factor kappa B (NF-kappa B) signalling and activation. The inhibitors of neuronal degeneration CC are useful for treating neurodegenerative disorders such as Alzheimer's CC disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's CC treating peripheral neuropathies, motorneuron disorders such as CC treating peripheral neuropathies, motorneuron disorders such as CC amyotrophic lateral sclerosis (ALS), Bell's palsy and various conditions in human presentlin PSI-FAD (familial Alzheimer's disease) mutant. CC Note: This sequence is not shown in the specification but is derived from chaman presentlin (PSI) protein (SEQ ID NO: 4) shown in page 60-61 of the CC specification (AAE05466).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                       Sel-12;
amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying inhibitors of neuronal degeneration useful for treating e.g. Alzheimer's disease, by determining the ability of a compound induce nuclear factor kappa B activation, with the involvement of presentlin or Par-4
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04-JAN-2001; 2001US-0754949.
                   04-APR-1997
                                                                             US6376239-B1
                                                                                                         Unidentified.
                                                                                                                                                                                    Presenilin protein
                                                                                                                                                                                                                   02-SEP-2002
                                                                                                                                                                                                                                                                               AAO18049 standard; Protein; 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-451872/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccarthy J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCIO-) SCIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JAN-2001; 2001WO-US00526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-Jub-2001.
                                              23-APR-2002
                                                                                                                                                                                                                                                                                                                                                            346 SHLGPHRSTPESRAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
hes 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                        SHLGPHRSTPESRAA 15
                                                                                                                                       presenilin; neuronal
precursor protein; AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page -; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                   (first entry)
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                 97US-0832867.
                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                      disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15; DB 22; Pred. No. 3.6e-08;
                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                      familial Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the sel-12 gene from Caenorhabditis elegans operably linked to a heterologous DNA sequence encoding a protein of interest. The sequence has be used to develop drugs for the treatment, prevention or delay of a neuronal disorder. In particular, the neuronal disorder may be familial Alzheimer's disease. The present sequence is a presentlin protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated DNA molecule comprising promoter of the sel-12 gene from Caenorhabditis elegans operably linked to heterologous gene, direct expression in neural cells and is useful to develop drugs to treat
                                                                                                                                                                                                                                                                                                                   Human; integrin-linked kinase; ILK; presenilin-1;
gamma secretase; apoptosis; Alzheimer's disease; F
neuroprotective; cytostatic; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 4; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression in neural cells and is useful to develop drugs neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-478281/51.
N-PSDB; AAL47323.
                       Disclosure; Page 43-45; 53pp; English.
                                                      Identifying agent that modulates interaction between integrin-linked kinase and presenilin-1, useful for treating Alzheimer's disease, and identifying agent that modulates protein kinase B or gamma secretase activity -
                                                                                                               WPI; 2002-351896/38
                                                                                                                                          Hiles ID,
                                                                                                                                                                  (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                             12-SEP-2000;
                                                                                                                                                                                                                  12-SEP\2001; 2001WO-GB04094
                                                                                                                                                                                                                                              21-MAR-2002
                                                                                                                                                                                                                                                                     WO200222862-A2
                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                          Human presenilin-1, PS-1.
                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             AAU79416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU79416 standard; protein; 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to DNA molecules comprising the promoter of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baumeister
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELEG-) ELEGENE GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SHLGPHRSTPESRAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHLGPHRSTPESRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
15; Conserv
                                                                                                                                         Ellis C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                             2000GB-0022333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0832867.
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Pred. No.
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. 3.6e-08;
ches 0;
                                                                                                                                                                                                                                                                                                                                     protein kinase B;
PS-1; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 467;
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                                                               disease, and
na secretase
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                                                                                                                                                                                                                                                                                                                                                  PKB;
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The invention relates to identifying an agent modulating interaction

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RESULT 62
AAE17045
ID AAE17
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                            WPI; 2002-140082/18.
N-PSDB; AAD27443.
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                                                                                                             Carter DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                    (РНАА ) РНАКМАСТА
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                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutant presentlin-processing protesse in vivo, and for screening anti-
Alzheimer's disease drugs in vivo. A transgenic non-human
enimal is useful for analysing the interaction between APP and mutant
presentlin-processing protesse in vivo, and for screening anti-
Alzheimer's disease drugs in vivo. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated mutant presentlin 1 and presentlin 2 polypeptides, useful for screening of drugs for treating pathologies associated with aberrant amyloid precursor protein processing, such as Alzhelmer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to mutant presentlin 1 (PS1) and presentlin 2 (PS2) polypeptides. Presentlin are involved in the processing of amyloid precursor protein (APP) from which major amylodogenic peptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 68-70;
                                                                                                                                                                                  Human; presenilin 1; PS1; amyloid precursor protein; APP; drug screening; Alzhelmer's disease; Parkinson's disease; multiple sclerosis; stroke; Huntington's disease; amylotrophic lateral sclerosis; Picks disease; head injury disease; frontal lobe dementia; cerebellar degeneration; ischaemic injury; schizophrenia; mutant; mutein.
                                                                                                                                                                                                                                                                                      Human mutant presenilin 1 (PS1) protein
                                                                                                                                                                                                                                                                                                                       18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                       AAE17047 standard; Protein; 467
                                                     Misc-difference
                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA & UPJOHN CO
                                                                                    Misc-difference
                                                                                                                                                        OMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SHLGPHRSTPESRAA 15
                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHLGPHRSTPESRAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-140082/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                       (first entry)
/label- Unknown
/note- "Wild typo
by NNN"
                                                   /note-
258
                                                                                   Location/Qualifiers 207..210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80pp; English.
                                                                 "Encoded by GTGGTGTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                   type Leu substituted with Xaa; Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            presenilin 1 (PS1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23,
3.6e-08;
0;
                                                                                                                                                                                                                                                                                      #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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RESULT 6
AAE17051
ID AAE
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                                                                                                                                                                                                                                                                           CC (PS2) polypeptides. Presentlin are involved in the processing of amyloid CC precursor protein (APP) from which major amylodogenic peptides are cleaved. Mutant presentlins are useful for identifying agents that CC modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant presentlin is also useful as a target for screening drugs useful in the treatment of pathologies associated with aberrant amyloid precursor protein processing, such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, Huntington's disease, amylotrophic lateral sclerosis, head injury disease, Picks disease, frontal lobe dementia, cerebellar C degeneration, stroke, ischaemic injury and schizophrenia. A transgenic non-human animal is useful for analysing the interaction between APP and mutant presenilin processing protease in vivo, and for screening anti-C Alzheimer's disease drugs in vivo. The present sequence is human animal suseful for analysing the interaction between APP and mutant presenilin-processing protease in vivo, and for screening anti-C Alzheimer's disease drugs in vivo. The present sequence is human
                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 67; Page 74-75; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated mutant presenilin 1 and presenilin 2 polypeptides, useful for screening of drugs for treating pathologies associated with aberrant amyloid precursor protein processing, such as Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carter DB,
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                                     AAE17051;
                                                               AAE17051 standard; Protein;
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                    mutant PS1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to mutant presentlin 1 (PS1) and presentlin
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                                                                                                                                                                                                 Local
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                                                                                                                                                                                      l Similarity
15; Conser
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/note= "Wild type
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Pred. No.
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                                                                                                                                                                                   DB 23;
. 3.6e-08;
ches 0;
                                                                                                                                                                                                              Length 467;
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18-APR-2002

(first entry)

Human

mutant presenilin 1 (PS1) wild type protein

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RESULT 66
AAW05785
ID AAW0
XX
AC AAW0
XZ
DT 28-:
XX
DE Pres
XX
KW Pres
KW Fam.
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                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                       modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant presentilin is also useful as a target for screening drugs useful in the treatment of pathologies associated with aberrant amyloid precursor protein processing, such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, Huntington's disease, amylotrophic lateral sclerosis, head injury disease, picks disease, frontal lobe dementia, cerebellar degeneration, stroke, ischaemic injury and schizophrenia. A transgenic non-human animal is useful for analysing the interaction between APP and mutant presentiln-processing protease in vivo, and for screening anti-Alzheimer's disease drugs in vivo. A transgenic non-human animal is useful for analysing the interaction between APP and mutant presentilin-processing protease in vivo, and for screening anti-Alzheimer's disease drugs in vivo. The present sequence is human per strong protease in vivo, and for screening anti-
                                                      Presenilin-1-1 residues 346-359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to mutant presentlin 1 (PS1) and presentlin 2 (PS2) polypeptides. Presentlin are involved in the processing of amyloid precursor protein (APP) from which major amylodogenic peptides are cleaved. Mutant presentlins are useful for identifying agents that
                                                                                         28-JUL-1997
                                                                                                                           AAW05785;
                                                                                                                                                          AAW05785 standard;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for screening of drugs for taberrant amyloid precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carter DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-2001; 2001WO-US16508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W0200202601-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; presentlin 1; PS1; amyloid precursor protein; APP; drug screening; Alzheimer's disease; parkinson's disease; multiple sclerosis; stroke; Huntington's disease; amylotrophic lateral sclerosis; Picks disease; head injury disease; frontal lobe dementia; cerebellar degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                          PS1 wild type protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ischaemic injury; schizophrenia.
                                                                                                                                                                                                                                                    346
                                                                                                                                                                                               66
                                                                                                                                                                                                                                                                                   1 SHLGPHRSTPESRAA 15
                                                                                                                                                                                                                                                  SHLGPHRSTPESRAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated mutant presenilin 1 and presenilin 2 polypeptides, 1 for screening of drugs for treating pathologies associated with ant amyloid precursor protein processing, such as Alzheimer's
                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                           467
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                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                       (first
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                                                                                                                                                          peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80pp;
                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                      Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                     .6e-08;
                                                                                                                                                                                                                                                                                                                                                    Length 467;
                                                                                                                                                                                                                                                                                                                     Indels
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RESULT 67
AAW34093
ID AAW34
XX AAW34
AC AAW34
XX O5-MA
XX Pepti
XX Pepti
XX Prese
KW Prese
KW Prese
KW Prese
XX Syntl
OS Homo
XX W0974
XX W0974
XX W0974
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAW05768-W05788 represent antigenic fragments of the human common presentin-1-1 protein (see AAW05733 for wild type sequence). AAW05734 crepresents addifferent wild type form of presentin-1 that results from calternate splicing of the genomic DNA sequence. The presentins are a family of highly conserved integral membrane proteins with a common constructural motif, common alternate splicing patterns, and common constructural motif, common attended in PS genes are implicated in familial Alzheimer's disease (AD) and possibly other diseases such as cerebral haemorrhage, schizophrenia, depression etc., so detection of cutations in the DNA encoding the wild type sequences can be used for diagnosis of these diseases. The wild type proteins, or vectors that express them or containing antisease sequences, antibodies selective for these mutant forms of the proteins and modulators of PS gene expression are potentially useful for treatment of AD etc. Transgenic animals are useful as models for day screening. The antibodies can also be used e.g.
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                  Matches
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28-APR-1905;
28-JUN-1995;
                                                         Synthetic.
Homo sapiens
                                                                                                    prevention;
                                                                                                                   Presenilin-1;
                                                                                                                                             Peptide derived from the C-terminal of the Presenilin-1 protein.
                                                                                                                                                                           05-MAY-1998
                                                                                                                                                                                                       AAW34093;
                                                                                                                                                                                                                                  AAW34093 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New presenilin genes - useful for diagnosis, therapy and drug screening of familial Alzheimer's disease, cerebral disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-0¢T-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                depression; antibody; gene expression modulator; therapy; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  for affinity purification and in immunoassays.
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                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           14
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                                                                                                    l; antibody;
Alzheimer's
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95US-0431048.
95US-0496841.
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                                                                                                                                                                                                                                 peptide;
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                                                                                                   cleavage;
disease; c
                                                                                                                                                                                                                                                                                                                                                                                 .08;
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Pred. No.
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                                                                                                   cleavage
                                                                                                                  cleavage inhibition; treatment;
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2e-08;
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                                                                                                    assay;
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                                                                                                    prognosis
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WO9741443-A2

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RESULT 68
ARE12898
ID ARE1
XX ARE1
AC ARE1
XX ARE1
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Novel gamma secretase protein, useful in the production of amyloids, capable of cleaving beta-amyloid precursor protein to produce beta
                                                                                                                                                                                                                                                                                                                                                                      WO2001 75435-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g compounds that inhibit cleavage of presenilin-l prevention and prognosis of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide,
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d precursor protein; betaAPP; presenilin; PS1.
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                                                                                                                         Hendrick JP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma-secretase activity. Gamma-secretase activity is necessary for amyloid production. The present invention also relates to methods for isolating integral membrane proteins and protein complexes, including the gamma-secretase protein of the invention. The method is useful monitoring the cleavage of beta-amyloid precursor protein (betaAPP) by gamma-secretase. The present sequence is a synthetic peptide antigen of presenilin peptide, PS1. This sequence is used in the
The invention relates to the field of plaque amyloid deposits that the hallmarks of Alzheimer's disease. In particular, the invention relates to an isolated, functionally-active protein that has
                                                                        Novel gamma secretase protein, useful in the production capable of cleaving beta-amyloid precursor protein to pramyloid peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's disease; gamma-secretase; integral-membrane protein; beta-amyloid precursor protein; betaAPP; presenilin; PS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to the field of plaque amyloid deposits that the hallmarks of Alzheimer's disease. In particular, the invention relates to an isolated, functionally-active protein that has
                                                                                                                           WPI; 2001-648575/74.
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                                                Example 8;
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                                                                                                                                                                                                                                                                                                                Modified-site
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                  p. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma-secretase activity. Gamma-secretase activity is necessary for amyloid production. The present invention also relates to methods for isolating integral-membrane proteins and protein complexes, including the gamma-secretase protein of the invention. The method is useful for monitoring the cleavage of beta-amyloid precursor protein (betaAPP) by gamma-secretase. The present sequence is a synthetic peptide antigen of presenlin peptide, PS1. This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
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                                                                                                                                                                                                                                 polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by
                                                                                                                                                                                                                                                                                            Sequences
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Note: The sequence data for this patent did not form part of t specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
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presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELTSA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                              polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
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28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
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02-JUN-2000: 2000US-208841P.
07-JUL-2000: 2000US-216747P.
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N-PSDB; AAS59515.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID No 2853; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2001.
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25 TPESRAA 31
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99US-0161993.
99US-0162142.
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100.0%;
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, Jen S, Carter
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Pred. No.
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RESULT 73
AAU04044
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                                 The sequence represents the MmyT protein encoded by the mmyT gene carried con the expression cassette present on plasmid SCP1. The expression cassette is the regulatory region of the methylenomycin cluster (mmc) from Streptomyces coelicolor A3(2), which encodes the MmyR, MmfP, MmfH, MmfL, MmfR, MmyO, MmyO, MmyO apartial Mmr polypeptides. The expression cassette is useful for expressing a nucleic acid of interest, substantially only when the host cell culture reaches high cell density at or close to the stationary phase of host cell culture. In particular the system is useful in regulating methylenomycin production. Reduced or no expression of the nucleic acid of interest is observed earlier in growth, avoiding toxic effects of some gene products on growth and the system does not require addition of exogenous inducer. The methylenomycin cluster naturally present on a highly transmissible plasmid permits properly regulated expression in diverse Streptomyces host and the expression is driven by a strong promoter, leading to high yield of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                           Novel expression cassette for expressing a nucleic acid of interest, derived from the regulatory region of methylenomycin gene cluster of SCP1 plasmid of Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-425675/45
N-PSDB; AAS07627.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus coelicolor
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                                                                                                                                                                                                                                                                 25; Fig 8f; 142pp; English.
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mmfR; MmyT; MmyO; MmyG;
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7; Conserv
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                          product.
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Mmr;
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heterologous gene expression..
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                                                                                                                                                                             Query Match
                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cyrochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthirties and treatment of diseases (e.g. rheumatoid arthirties).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antiinflamilating; cene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interfeukin; G-protein coupled receptor; thioesterase; inflammation;
                                                                                                                                                                                                                                                                                                                              arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic nucleic acids encoding e.g. amylases, oncogenes and histones, useful for diagnosing and cancer, autoimmune diseases and infections -
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27-DEC-2000; 2000US-0173419.
                                                                                                                                                                                                                                            Sequence
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206 TPESRAA 212
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nes 6; Conserv
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                                                                                                                       Conservative
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                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic nucleic acids encoding e.g. amylases, oncogenes and histones, useful for diagnosing and cancer, autoimmune diseases and infections -
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27-DEC-2000;
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                                                                                                                                 Sequence
                                                                                                                                                                                              system and an infection of
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                       congenital heart disease
                                            Human; gene expression;
cardiovascular disease;
                                                                                                                 Protein #5478
                                                                                                                                                           23-JAN-2002
                                                                                                                                                                                                        ABB23479;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
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27-SEP-2000;
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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                                                                                                          encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoded by human foetal liver single exon probe.
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                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                             40.0%; Dr
100.0%; Pr
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                                          hypertension;
                                                               heart; microarray;
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                                                                                                          for measuring heart cell gene
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Mismatches
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                                          rray; vascular system;
cardiac arrhythmia;
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                                                                                                            expression
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09-AUG-2001. WO200157275-A2 Homo sapiens.

30-JAN-2001; 2001WO-US00667

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RESULT 78
AAM58920
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                 Human; brain expressed exon; gene expression analysis;
microarray; Alzheimer's disease; multiple sclerosis; so
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epilepsy;
                                                                  Human brain expressed single
                                                                                                      05-NOV-2001
                                                                                                                                                                      AAM58920 standard;
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                                                                                                                                        AAM58920;
                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
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26-MAY-2000;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                    (first entry)
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                                                                  probe encoded protein
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D. 22;
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0532366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024283.
                                                                 04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0632366.

21-SEP-2000; 2000US-0233687.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-02346359.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                          microarray;
                                                                                                                                                                                                                                                                          06-NOV-2001
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           WPI; 2001-488900/53
                                                                                                                                              30-JAN-2001; 2001WO-US00668
                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                    WO200157276-A2
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                    Human;
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                                                DYNAMICS
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; leukaemia; lymphoma; myeloma.
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100.0%;
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RESULT 80
AAM19095
ID AAM19
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KW Probe
KW Probe
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Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                  The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present
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                                                cervical cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DK,
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Note: The sequence data for this patent did not form specification, but was obtained in electronic format

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RESULT 81

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Best Local
                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI37546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
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27-SEP-2000;
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                                                                                                                                                                                   Local
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100.0%; Pr
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CC nucleic acid probes for measuring gene expression in a sample derived CC from human lung comprising single exon nucleic acid probes having one of CC 12614 nucleic acid sequences mentioned in the specification, or their CC complements or the 12387 open reading frames derived from the 12614 (CC probes; the novel set of probes which hybridise at high stringency to a CC nucleic acid expressed in the human lung; measuring gene expression in a CC sample derived from human lung; measuring gene expression in a CC sample derived from human lung; measuring gene expression in a CC sample derived from human lung; comprising the array with CC mRNA, and (b) measuring the label detectably bound to each probe of CC the array; identifying exons in a eukaryotic genome, comprising CC of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included CC in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several CC tissues and/or cell types using hybridisation to a single exon cc microarrays having a probe with the exon, where a common pattern of CC expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one compression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one compression on from expression of the exons in a gene, particularly using human lung derived mRNA and for identifying exons in a gene, particularly can be a single exons one coded by the expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for heat of the compression of these compression of the exons in a gene, particularly can be a single exons to
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26-MAY-2000;
30-JUN-2000;
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spatially-addressable set of single exon nucleic acid probes, used measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chronic obstructive pulmonary disease; interstitial lung disfamilial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID
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2000US-207456P.
2000US-0608408.
2000US-0632366.
2000US-234687P.
2000US-236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30913; 634pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; COPD; ILD interstitial lung
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Best Local :
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
food su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pulmonary alveolar proteinosis, Kāragener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous scierosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary hastlocytosis, lymphangioleiomyomtosis,
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23-AUG-2000;
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                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                   biodiversity
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DB; AAS70390.
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upplement; medical imaging; diagnostic; genetic disorder.
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6; Conser
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2000US-0649167
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RESULT 84
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Best Local :
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        polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG000110-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                  Claim
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                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                               biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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DB; AAS70614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          supplement;
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medical imaging; diagnostic; genetic disorder.
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100.0%; Pr
polynucleotide
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29;
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RESULT 85
AAU42555
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Best Local
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         pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The
                                                                                                    polypeptides. The proteins and their associated DNA sequences are us the treatment, prevention and diagnosis of medical conditions caused P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                    Propionibacterium acnes vaccinating against and
                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                            Example 1; SEQ ID No 3750; 1069pp;
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                                                                                                                                                                                                        treating acne vulgaris
                                                                                                                                                                                                                                                                                                                  Skeiky YAW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dermatological; osteopathic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory lesion; acne vulgaris; enzyme linked
                                                                                                                                                                                                                                                                                                   ceiky YAW, Persing maisonneuve J, Zha
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DB; AAS59518.
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used
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100.0%;
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as
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                    polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, formerics are usefuls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (BLISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
              diagnostics,
                                                                                                                                                                                                                                                                              diagnostics, forensics, responsible for genetic biodiversity
 responsible for
                                                                                                                                                                                                             The invention relates to isolated polynucleotide (1)
                                                                                                                                                                                                                                               Claim 20; SEQ
                                                                                                                                                                                                                                                                           biodiversity
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                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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supplement; medical imaging; diagnostic; genetic disorder
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Consider involving abstrant protein expression or biological activity.

Considers involving abstrant protein expression or biological activity.

Considers involving abstrant protein expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polynucleotic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and calming acid sequences. ABG00010-ABG30377 represent novel human
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Note: The sequence data for this patent did not appear in the pri specification, but was obtained in electronic format directly fro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of muta responsible for genetic disorders or other traits and to assure the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the 
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food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to isolated polynucleotide (I) and probes
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        diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human dispussitic amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 36572; 103pp; English.
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Note: The sequence data for this patent did not appear in the printed model of the content of the printed and the printed are the printed and the printed and the printed and the printed and the printed are the printed and the printed and the printed and the printed and the printed are the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the printed and the prin
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                                         specification,
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at ftp.wipo.int/pub/published_pct_sequences
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23-AUG-2000; 2000US-0649167
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ftp.wipo.int/pub/published_pct_sequences
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                                                          for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
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                      Note: The sequence data for this patent did not specification, but was obtained in electronic for
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                                                                                   diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
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CC Note: The sequence data for this patent did not appear in the printed content types of the invention.

CC at fire wiso introductions of the invention.
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                                                                       AAY40001-92 are derived from human secreted proteins. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the polynucleotide. Specific uses include developing products for the diagnosis or treatment of cancer, tumors, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, sepsis, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, obesity, osteoporosis, arthritis, infections, AIDS, connective tissue disorders, transplant rejection, and reproductive disorders. The polypeptides or polynucleotides can also be used as food additives or preservatives, such as to increase carbohydrate, vitamins, minerals, cofactors or other nutritional
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26-FEB-1998;
26-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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26-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        additive; food preservative; storage capability.
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                        Sequences ABP31028-ABP35561 represent 4534 novel human proteins classing attack of the compasses and proteins of designated ORF (open reading frame) 1-4534, and sequences ABN75054-BN75054 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides and polypeptides, methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, tissue growth, angiogenesis, activin or inhibin activity, chemotactic/ chemokinetic activity, haemostatic activity, thrombolytic activity,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 2444; 2508pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABN79455
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                                                                                                                                                                             Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
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02-JUN-2000; 2000US-208841P.
07-JUL-2000\ 2000US-216747P.
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N-PSDB; AAS59506.
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes polypeptides. The proteins and their associated DNA sequences

immunogenic are used in

Example 1; SEQ ID No 468; 1069pp; English.

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Constitution of the inventor of the printed constitution of the printed constitution, but was obtained in electronic format directly from WIPO
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polypeptide (II) sequences: (I) is useful as hybridisation probes, polymerase chain reaction (PCN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                          31-MAR-2000;
23-AUG-2000;
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                                                                                                  Claim 20;
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food supplement; medical imaging; diagnostic; genetic disorder.
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                                                               The invention relates to isolated polynucleotide (I) and
                                                                                                                                biodiversity
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, Oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
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                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                            biodiversity
                                                                                                                                                                                                                                                                                                     diagnostics, forensics,
responsible for genetic
biodiversity -
                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene-therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
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quantitating a polypeptide
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)B; AAS70395.
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supplement; medical im
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maging; diagnostic; genetic disorder.
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RESULT 99
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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23-AUG-2000; 2000US-0649167.
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food supplement; medical imaging; diagnostic; genetic disorder.
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    is useful as hybridisation probes,

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Note: The sequence data for this patent did not appear in the prispecification, but was obtained in electronic format directly from the prispecification.
diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                        Claim
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Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
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CC and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

CC and to general sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed septention, but was obtained in electronic format directly from WIPO
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23-AUG-2000;
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medical imaging; diagnostic; genetic disorder.
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40.0%; Score 6; DB 22; Length 125; 100.0%; Pred. No. 45; 0; Indels	Cy 3 LGPHRS 8	simi 6;	ь
	rotein; 126 AA. entry) r antigen, Seq ID No 276. r antigen; cytostatic; uropathic; diagorhromosomal marker; forensic; urinary lood-related disorder; thrombosis. US01328. U	40.0%; Score 6; DB 22; Length 125; ty 100.0%; Pred. No. 45; ervative 0; Mismatches 0; Indels 0;	
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RESERVE SERVE                                                                                                                                            RESULT 106
                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel isolated human prostate cancer antigen complying proventing. (I) and polypeptides (II). (I) and (II) are useful for preventing, treating or ameliorating a medical condition when candinistered. (I), (II) and the antibody to (II) are useful for treating, complying and condition when prospective complying prostate cancers; urinary disorders e.g. chronic complying and detection e.g. as a chromosomal marker and in forensics. (II) can be used complying and detection e.g. as a chromosomal marker and in forensics. (I) and the anti-(II) antibody can be used in testing and detection in communoassays. AAU22702-AAU22913 represent the human prostate cancer complying amino acid sequences, and related amino acid sequences of the complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete comp
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Human reproductive system related antigen SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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||||||
61 SHLGPH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11;
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N-PSDB; AAL00703.
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05-JAN-2001; 2001US-0259678.
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce

ID NO 15003; 1399pp + Sequence Listing; English.

Isolated nucleic acids and polypeptides, diagnosing and treating e.g. leukaemia, i disorders -

, useful for preventing inflammation and immune

WPI; 2001-514838/56. N-PSDB; AAI81042.

(HYSE-) HYSEQ INC.

YT,

Liu C, Drmanac

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28-FEB-2000; 2000US-0515126 18-MAY-2000; 2000US-0577409 26-FEB-2001; 2001WO-US04927

P-2001.

Claim 20;

SEQ